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Review Article
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CONSERVATION AGRICULTURE PRACTICES IN PERENNIAL HORTICULTURAL CROPPING SYSTEMS TO IMPROVE SOIL HEALTH

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ABSTRACT

Conservation agriculture practices in perennial horticulture cropping systems aims to provide and maintain optimal conditions in the root-zone, ensure that water enters the soil, increase beneficial biological activity in the soil and avoid physical or chemical damage to roots and soil organisms that would disrupt their effective functioning.It is based on three principles *viz.,* minimal mechanical soil disturbance; permanent soil cover through the preservation of crop residues and cover crops; and crop rotation. Conservation principles minimise soil disturbance and makes use of soil biological activity, practising crop rotations; using fertilizers as appropriate and relying on integrated pest and weed management in order to minimize damage to the environment and provide organic matter and nutrients.Conservation practices minimises nutrient losses through the appropriate use of deep-rooting cover crops that recycle nutrients leached from the topsoil, conserves soil moisture by minimising evaporation losses, enhancing infiltration and minimising surface runoff. Cover crops of variable rooting depths and root spread on the orchard floor offers little scope for the plant nutrients to be lost through leaching. Long-term soil conservation management in perennial horticultural crops improved the quality of soils through soil aggregates and water stability, enhancing soil microbial diversity, the organic carbon fraction, especially near the surface, lowered the soil bulk density and enhanced the infiltration rate, thereby contributed in increasing orchard crop productivity. Through conservation agriculture practices old and senile orchards can be revived. Conservation agriculture is now receiving global attention for its carbon sequestration potential.

Keywords: Conservation, agriculture, perennial, orchard crops, soil health

The productivity of tropical orchards is declining due to deterioration in soil health. To enhance factor productivity and increase fruit yields, improvement of orchards soil health is a requisite. Continuous soil disturbance through cultivation and particularly through soil inversion has led to the degradation of soil structure, soil compaction, and decreased levels of organic matter in soil. This, consecutively, has caused a wide range of environmental impacts, including soil degradation, water and wind erosion, eutrophication, increased carbon emissions released from the soil due to exposure of soil predisposing soil organic carbon for oxidation through use of high energy-consuming machinery, and an overall reduction in beneficial soil organisms. The foremost reasons which degrade soil quality could be listed as: i) loss of fertile topsoil and organic matter associated with clay size fractions due to water erosion, ii) intensive tillage resulting in a fast decomposition of remnants of crop residues and breaking of stable soil aggregates hastening the process of oxidation of entrapped organic carbon, iii) loss in microbial diversity, iv) mono-cropping, v) imbalanced fertilizer application, vi) low nutrient use efficiency ascribed nutrient losses due to leaching, volatilization and denitrification, vii) indiscriminate use of herbicides, pesticides, fungicides, etc., resulting in poor soil and water quality, and viii) water logging, salinity, alkalinity and acid soils.

A way of minimizing these negative impacts on the agricultural environment is offered by the conservation agriculture approach. Conservation agriculture attaches great significance to improving soil health through improving soil structure and biodiversity. Soil carbon lost during tillage can be accrued through conservation practices *viz.,* zero tillage, inter and cover crops, moisture conservation etc. (Conant *et al.,* 2007). Enhanced biological activity as a consequence of enhanced soil organic matter is directly responsible for improvement of soil structure, nutrient storage and reduced pests and diseases. Conservation agriculture maintains a permanent or semi-permanent organic soil cover. This can be a growing crop or dead mulch. Its function is to protect the soil physically from sun, rain and wind and to feed soil biota. The soil micro-organisms and soil fauna take over the tillage function and soil nutrient balancing. Mechanical tillage disturbs this process. Therefore, zero or minimum tillage and direct seeding are important elements of conservation agriculture. A varied crop rotation is also important to avoid disease and pest problems (FAO, 2009).

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The principles of conservation agriculture linked to specific purposes in perennial horticulture cropping systems. The two principles, permanent soil cover and minimal soil disturbance ensure soil and water conservation, generate *in-situ* organic matter, enhance soil biological activity and prevent soil erosion. The principle of minimum soil disturbance enhances soil aggregation. Crop rotation is associated with the promotion of healthy and lively soils, thereby reducing pesticide and herbicide requirements, environmental pollution as well as enhancing natural biodiversity. To gain the full benefit of conservation agriculture all the three principles have to be applied at the same time. Practising conservation agriculture can be a challenge in India, though it is a common practice in many western countries. It means a different way of farming and requires change of mind-set of the farmers. Conservation agriculture practices may have an additive or synergistic effect on soil health in terms of reduced soil bulk density, increased soil porosity, increased soil water holding capacity, increased soil aggregate stability, increased soil carbon and nitrogen reservoirs, increased microbial indices, and reduced weed pressure. Conservation agriculture also enhances biological N_2 fixation, enhances availability of many of the insoluble sources of soil nutrients, enhances soil enzymatic activities and improves soil aggregate stability.

In perennial horticulture systems while assessing the management system for sustainability we need to address such management systems that will not exhaust the resource base, imparts resilience to vulnerability and enhance or maintain productivity. In soil quality evaluations, we basically measure changes in physical, chemical and biological characteristics of the soil. Rapport (1995) defined a healthy soil as a stable system with high levels of biological diversity and activity, internal nutrient cycling, and resilience to disturbance. Changes in soil quality are not only associated with management, but also with the environmental context, such as temperature and precipitation (Andrews *et al.,* 2004). The key characteristics of soil health management in conservation agriculture is protecting the long term fertility of soils by maintaining organic matter levels, encouraging soil biological activity. Soil building practices such as crop rotations, intercropping, cover crops and minimum tillage are central to conservation practices. Those practices encourage soil formation and structure and creating more stable systems.

Perennial based horticulture cropping systems offers a perennial-annual integrated conservation agriculture system that provides many of the same ecosystem services that "natural" forests do. In addition to the water, soil, and climate benefits they serve as critical habitat for many kinds of life as their diversity is much higher than monoculture conventional orchards and annual agriculture. Through conservation agriculture practices old and senile orchards can be revived, heal degraded land and bring them back to biological productivity and health. Perhaps the most beneficial aspect of conservation agriculture is that it not only fights climate change, but is also resilient in the face of increased intensity and frequency of droughts, floods, and other extreme weather events. Trees and perennials typically have stronger and deeper root systems than annuals and can survive and continue to yield in conditions that would ruin many annual crops.

I. Conservation agricultural practices in perennial horticulture crops addresses:

Horticultural production: Conservation agriculture has tremendous potential for achieving sustainable yield increases by improving the growth conditions for crops and the efficiency of input. Trees can be an important component in many agro-ecosystems. With their deep and extensive root systems, they can capture nutrients not accessible by crops and make them available to crop production again through litter fall. From a conservation agriculture point of view, not only do the trees store carbon in their above ground biomass, they also contribute to below ground biomass through their root systems and their input of litter to the soil (branches and leaves). Trees may also play a role in reducing nutrient losses from wind erosion. Litter produced by woody perennials like mango is beneficial because of its higher content of polyphenols (lignin and tannins), which slows the decomposition rate (Abril and Bucher, 2001), when compared with grasses and annual herbs.

Natural resource base: Perennial crops generally improve soil structure while annual vegetable crops grown either in rows or on beds and furrows often result in structural degradation mainly as a result of loss of soil organic matter and ground cover due to soil disturbance. Soil structure and aggregates are strongly influenced by processes such as tillage, cropping systems and climate. Conservation agriculture reverses soil degradation processes and builds up soil

organic matter. Organic matter affects both the chemical and physical properties of the soil and its overall health. Properties influenced by organic matter include: soil structure; moisture holding capacity; better infiltration of rainwater and enabling the recharge of groundwater which reduces erosion and leaching and, in turn, water pollution, diversity and activity of soil organisms, both those that are beneficial and harmful to crop production; and nutrient availability. It also influences the effects of chemical amendments, fertilizers, pesticides and herbicides.

Biodiversity: Conservation agriculture conserves and enhances biodiversity in the field. Conservation practices enhance natural biological processes above and below the ground by reducing interventions such as mechanical soil tillage to an absolute minimum. Soils under conservation tillage have been shown to have higher soil microbial biomass and enzymatic activity than those under conventional tillage systems (Madejón *et al.,* 2007; Melero *et al.,* 2008), indicating an activation of microorganisms through carbon source inputs from organic residues.

Labour shortage: Conservation agriculture eliminates power-intensive soil tillage and intercultural operations thus reducing the drudgery and labour required for crop production by more than 50 per cent for small scale farmers. For mechanized farms, it reduces fuel requirements by 70 per cent and the need for machinery by 50 per cent. Conservation practices prevents hardpans from being formed, protects the soil, increases soil moisture, and restores soil fertility, so stabilizing yields and improving production over the long term.

Climate change: Conservation agriculture reduces crop vulnerability to extreme climatic events. In drought conditions, it reduces crop water requirements by 30 per cent, makes better use of soil water and facilitates deeper rooting of crops. In extremely wet conditions, conservation agriculture facilitates rain water infiltration, reducing the danger of soil erosion and downstream flooding.

Livelihoods: Due to the reduction in runoff and soil loss and better conservation of moisture, soil health is maintained. Under such conditions higher crop yield can be comprehended with subsequent increase in the income of farmers who opt conservation agriculture practices in perennial horticulture cropping systems. Also, conservation agriculture gives farm families opportunities to improve their livelihoods through intercrops, mixed crops and cover crops.

II. Conservation agriculture practices in perennial horticulture cropping systems aims:

- To provide and maintain optimal conditions in the root-zone (maximum possible depth for crop roots) in order to enable them to grow and function effectively and without hindrance in capturing plant nutrients and water.
- To ensure that water enters the soil so that (i) plants have sufficient water to express their potential growth; and (ii) excess water passes through soil to groundwater and streamflow, not over the surface as runoff where it can cause erosion. There is greater potential for increased cropping efficiency as more water is held in the soil profile than under conventional systems.
- To increase beneficial biological activity in the soil in order to: (i) maintain and rebuild soil architecture for enhanced water entry and distribution within the soil profile; (ii) compete with potential soil pathogens; (iii) contribute to decomposition of organic materials to soil organic matter and various grades of humus; and (iv) contribute to the capture, retention and gradual release of plant nutrients.
- To avoid physical or chemical damage to roots and soil organisms that would disrupt their effective functioning.

III. Impact of conservation agriculture practices on soil health in perennial horticulture cropping systems

Soil health, also referred to as soil quality, is defined as “the capacity of soil to function within ecosystem boundaries to sustain biological activity, maintain environmental quality, and promote plant and animal health” (Doran and Zeiss, 2000). A healthy soil should possess the characteristics like high organic matter content, good soil tilth and structure, high water infiltration and retention, resistance to compaction, high soil biological activity, plant nutrient recycling and availability, resistance to erosion, devoid of toxic chemicals, low in weed and disease pressures etc. Soil health management implies executing practices that either maintain or augment the soil’s physical, chemical, and biological attributes to improve soil functions. These attributes function synergistically and

interact in a complex way to deliver specific soil services and to enhance ecosystem functions, such as nutrient availability, ero-sion control, and water infiltration. Building and improving the soil health through conservation practices will ensure continued productivity, enhanced farmers' income, and promote food and nutritional security.

The effects of conservation agriculture practices in dryland mango orchards on Alfisols under four distinct management situations *viz.,* mango orchards under clean cultivation and intensive management; mango orchards under weed cover and intensive management; mango orchards under weed cover and intensive management brought under conservation horticultural practices since 10 years and clean cultivation vegetable field was assessed by quantifying the soil physical, chemical, biological and biochemical properties by Ganeshamurthy *et al.* (2019). It has been shown that conservation agriculture practices improved the quality of soil, especially near the surface, by lowering the bulk density and enhancing infiltration rate. Clean cultivation in mango orchards had resulted in higher bulk density (1.34 Mg/m^{-3}) than weed infested plots and this in turn recorded higher bulk density than conservation agriculture plots (1.01 Mg/m^{-3}). Plots under conservation agriculture with cover crop had higher steady state flow (388 mm/h) as compared to mango orchards under clean cultivation (173 mm/h). The soil aggregate formation and water stability have enhanced in plots with conservation practices because of higher production of glomalin compared with vegetable and orchard plots where conventional practices were followed.

The increasing carbon emission is of major concerns for entire world as well addressed in Kyoto protocol. Sequestering carbon in tree-based systems, thus, has the potential to offset a substantial portion of the future atmospheric increase in CO_2 concentration. Conservation practices in perennial horticulture cropping systems enhance soil biodiversity, which is known to increase carbon sequestration. Any action taken to sequester carbon in biomass and soils will generally increase the organic matter content of soils, which in turn will have a positive impact on environmental, agricultural and biodiversity aspects of ecosystems. In studies on carbon sequestration potential of 35-year-old mango orchards under different management practices, it has been documented that mango orchards under conservation horticulture practices and mango orchards under weed cover with intensive management expressively enhanced the soil carbon stock in the top 1 m of orchard soils. Comparative to clean cultivation vegetable field, mango orchards under conservation horticulture practices and mango orchards under weed cover with intensive management increased soil carbon sequestration by 15.2 t ha^{-1} and 12.9 t ha^{-1}, respectively. Soil carbon is the largest pool of carbon followed by above-ground biomass, below-ground biomass and litter [3] weed. Soil carbon was higher by 2.54, 2.75 and 2.37-fold in intensively managed mango orchards, mango orchards under weed cover with intensive management and mango orchards under conservation horticulture practices, respectively than tree carbon. The highest total carbon content (107.63 t ha^{-1}) was found under mango orchards under conservation horticulture practices, followed by mango orchards under weed cover with intensive management (100.05 t ha^{-1}) and the least was under intensively managed mango orchards (97.31 t ha^{-1}), suggesting that mango orchards under conservation horticulture practices offers promising potential for total carbon sequestration. Averaged across the three different management systems, highest potential for carbon storage was observed to be 101.7 t ha^{-1} for mango orchard, 1.68 fold higher than in vegetable system (Rupa *et al.,* 2022).

a. Minimum soil disturbance (Zero tillage / minimum tillage)

Tillage is one of the major practices that reduce the organic matter level in the soil. Each time the soil is tilled, it is aerated. As the decomposition of organic matter and the liberation of carbon are aerobic processes, the oxygen stimulates or speeds up the action of soil microbes, which feed on organic matter. Repetitive tillage degrades the soil structure and its potential to hold moisture, reduces the amount of organic matter in the soil, breaks up aggregates, and reduces the population of soil fauna such as earthworms that contribute to nutrient cycling and soil structure. Organic matter production and conservation is affected dramatically by conventional tillage, which not only decreases soil organic matter but also increases the potential for erosion by wind and water. The impact occurs in many ways. There is improvement in soil physico-chemical and biological properties due to little soil disturbance.

Activities that promote the accumulation and supply of organic matter, such as the use of cover crops and refraining from burning, and those that reduce decomposition rates, such as reduced and zero tillage, lead to an increase in the organic matter content in the soil (Sampson and Scholes, 2000). Earthworms, micro arthropods and centipedes are basically primary shredders of most dry organic materials; hence their population tend to increase with increasing amounts of organic material applied as soil cover. Ploughing reduces the quantity of food sources for primary shredders and disturbs their burrows and living space, hence populations of certain species decrease drastically. Moreover, reduction of earthworm numbers reduces their impact, through burrowing, in increasing porosity and aeration (particularly continuous macropores) and lowers their ability to bury. There may also be less use of irrigation water as the deep percolation losses of water are checked.

Conservation principles minimise soil disturbance and protect and nourish the soil life through reducing or eliminating tillage operations; practising crop rotations; using fertilizers as appropriate and relying on integrated pest and weed management. These practices minimises nutrient losses through the appropriate use of deep-rooting cover crops that recycle nutrients leached from the topsoil, conserves soil moisture by minimising evaporation losses, enhancing infiltration and minimising surface runoff and improved collection, storage and application of wastes from orchards. In reduced or zero-tillage systems, soil fauna resume their bio-turbating activities gradually loosening and mixing the soil components (also known as bio-tillage). In zero tillage systems, the action of soil macro-fauna gradually incorporates cover crop and weed residues from the soil surface down into the soil. The activity of microorganisms is also regulated by the activity of the macro-fauna, which provide them with food and air through their burrows. In this way, nutrients are released slowly and can provide the following crop with nutrients.

Under conservation tillage systems with inter crops and cover crops in mango orchards, the absence/ reduction of soil disturbance produced a modification of surface soil conditions, which improved soil physical properties and reduced soil organic matter decomposition. Franzluebbers et al. (1995) reported that active fractions of soil organic matter increased in superficial soil layers in no tillage compared to traditional tillage. It has been shown by several workers that aggregate stability is strongly related with soil organic carbon (Shepherd et al. 2001). Simmons and Coleman (2008) attributed the difference in fungal population between zero and conventional tillage systems to the ability of an ecosystem to withstand & disturbance, whereas bacterial-dominated systems are more resilient than fungal dominated systems due to the different energy pathway (Bardgetta and Cook, 1998). Moore *et al.* (2003) postulated that recovery times from disturbance of each energy channel may be different, and results in an alteration of the food web. Soils in zero tillage systems would evolve fungal dominated, 'slow' energy channels, while soils in conventional tillage would break down substrate via a bacterial dominated, or 'fast' energy channel (De Ruiter *et al.,* 1998; Hendrix *et al.,* 1986). The practice of zero tillage/minimum tillage is eco-friendly, results in less emission of GHGs and thus helps in mitigating adverse effects of climate change.

b. Crop residues

In conservation agriculture, incorporation of crop residues in soil or retention on surface reduces wind and water erosion, increases water infiltration and moisture retention, and reduces surface sediment and water runoff. With improved soil characteristics, higher level of soil moisture can contribute to higher productivity and sustainability. Leaving substantial amounts of crop residues evenly distributed over the soil surface also promotes stable soil aggregation by enhancing soil biological activity and the production of various binding agents (such as fungal hyphae, polysaccharides, mucilage, and lipids) and by protecting the aggregates from direct physical impacts of raindrops and wind.

Surface residues also reduce evaporative loss of soil water and increase plant available water by shielding soil from solar radiation and reducing air movement just above the soil surface (Donk and Klocke, 2012). It increases hydraulic conductivity and reduce bulk density of soil by modifying soil structure and aggregate stability. Mulching with plant residues raises the minimum soil temperature in winter due to reduction in skyward heat flux from soil and decreases soil temperature during summer due to shading effect. Soil cover in the form of crop residues increased biological activity (Woltering, 2005; Mutema *et al.*, 2013) which

is indicative of the fact that early stages and the primary shredders of organic matter continue to be a more active group as fresh addition of organic residues is a continuous process in conservation agriculture practices plots.

Crop residues in turn adds soil organic matter and facilitates availability of nutrients, prevent leaching of nutrients, increase cation exchange capacity, provide congenial environment for biological N fixation, increase microbial biomass and enhance activities of enzymes such as dehydrogenase and alkaline phosphatase. Increased microbial biomass can enhance nutrients availability in soil as well as act as sink and source of plant nutrients. In mango based cropping system, a legume cover crop like M*ucuna* added more organic residues to the system followed by intercrop with cowpea. But in sweet potato plot a non-legume crop, available organic residue (above ground plant biomass) was small as huge biomass was removed off site through tubers (Ganeshamurthy *et al.,* 2019). Tillage practices and low organic inputs cause rapid loss of organic carbon and stable aggregation and also affect the distribution and stability of soil aggregates (Six *et al.*, 2000).

It has been reported that long-term soil conservation management in perennial fruit crop orchards improved the quality of soils through enhancing the organic carbon fraction and biological status, especially near the surface. Addition of litter and other crop residues lowered the soil bulk density and enhanced the infiltration rate. Soil aggregates and water stability improved under conservation practices. Soil microbial diversity and extra cellular enzymes level improved over conventional management. Absence of earthworms and centipedes in vegetable plot and conventional mango orchards showed deterioration in soil properties under conventional intensive systems (Ganeshamurthy *et al.,* 2016) as compared to mango plot under conservation agriculture practices. In general dehydrogenase, urease, phosphomonoestrase and aryl sulphatase activities were higher under plots following conservation practices than under plots with conventional practices in mango or vegetable field. The rhizosphere of leguminous crops may secrete higher amounts of exudates more actively than in vegetable crops, and may therefore supply more carbon and nitrogen to the soil for enhanced microbial activity leading to enhanced levels of enzymes (Hazarika *et al.,* 2013., Nuruzzaman *et al.,* 2005).

Crop residue burning in the field is a common practice. Residues are usually burnt to help control insects or diseases or to make fieldwork easier in the following season. Burning destroys the litter layer and so diminishes the amount of organic matter returned to the soil. Many farmers remove residues from the field for use as animal feed and bedding or to make compost. Later, these residues return to contribute to soil fertility as manures or composts. However, residues are sometimes removed from the field and not returned. This removal of plant material impoverishes the soil as it is no longer possible to recycle the plant nutrients present in the residues.

c. Crop rotation

The key functions of orchard ecosystems are governed by the diversity of the flora and fauna in the ecosystem. Monoculture with conventional practices evade many of the congenial environments needed for survival of many of the flora and fauna. This is aggravated further by use of herbicides and pesticides. Continuously growing same species year after year results in declined levels of soil organic matter, decreased aggregate stability, increased soil bulk density, increased soil erosion, increased disease prevalence, reduced crop yields, etc. Subsequently, crop rotations have consistently been recommended as a best management practice to improve production and help conserve soil health.

For maintaining / enhancing soil fertility and control of insects, weed and diseases in perennial horticulture cropping systems, there should be rotation of annual crops on the same orchard land over a period of two years or more. Grow-ing the same crop in the interspaces of the orchard crops continuously in the same soil habitually leads to the buildup of disease causing organisms called pathogens. This can be avoided by growing a plant belonging to another family, the pathogen cycle becomes disrupted because the new crop belonging to a different family can-not serve as a host for the pathogen. Use of legumes in rotation improves soil fertility. Crop rotation is associated with the promotion of healthy and lively soils, thereby reducing pesticide and herbicide requirements, environmental pollution as well as enhancing natural biodiversity.

Crop rotations and cover crops involving legumes in perennial horticulture cropping systems

encourage N_2 fixation. Enhanced population of beneficial organisms like nutrient mobilizers and PGPRs will enable the soil system in holding nutrients in most appropriate forms that are readily absorbed by the plant roots. Conservation agriculture provides more habitats for birds, small mammals, reptiles, earthworms, microorganisms and spiders, amongst others, and more food for eco-function players, including organics, insects and seeds, which in turn lead to an increase in species and population. Having crops cover of variable rooting depths and root spread on the orchard floor offers little scope for the plant nutrients to be lost through leaching into the aquifer hence conservation agriculture practices in orchards create conditions that are similar to natural forest ecosystem.

d. Mulch / Permanent soil cover / Cover cropping

The mulches are materials placed on the soil surface to protect it against raindrop impact, erosion, and helps promote more stable soil aggregates as a result of increased microbial activity and to improve its fertility. One way to improve the condition of the soil is to mulch the area requiring amelioration. Crop residue mulching is a system of maintaining a protective cover of vegetative residues such as straw, maize stalks, palm fronds, *mucuna* and stubble on the soil surface. Mulching add organic matter to the soil, reduces weed growth, and virtually eliminates erosion during the period when the ground is covered with mulch. Mulching systems can be either '*in situ* mulching systems' (plant residues remain where they fall on the ground) or 'cut-and-carry mulching systems' (plant residues are brought from elsewhere and used as mulch.

Cover crops are plants that are grown between the rows of perennial horticultural crops (when the soil would otherwise be left bare) for improving soil physical, chemical and biological properties, to minimize erosion, or to improve soil fertility. Growing a cover crop is one way to in-crease the soil organic matter through the addition of biomass to the soil. A cover crop may be any crop grown within the system to provide soil cover, irrespective of whether it is later incorporated into the soil. These cover crops may be an annual or a biennial or even some perennial herbaceous plants grown in a pure or mixed stand mainly during monsoon period or may be throughout the year. Legume crops, *Mucuna,* sweet potato, green manure crops etc. are excellent cover crops for perennial horticulture cropping systems because they are dense and produce huge biomass. Good amount of biomass is helpful for improvement of physico-chemical properties of the orchard soil if incorporate them.

Growing of crops in the interspaces of the orchard not only generates extra income but the practice also helps to check the soil erosion through ground coverage and improves the soil physico-chemical properties. Selection of suitable intercrops in perennial horticultural crops for optimum returns as well as to improve the soil fertility primarily depends on agro-climatic condition of the area. Orchard soil improvement is accelerated when ground cover is enhanced, organic matter addition is enhanced and soil is least disturbed. An inter-crop or cover crops in an orchard of fruit crops acts in multiple ways. It does not allow rain drops to hit the ground directly. The roots of the crops on the floor of the orchard hold soil tightly so that the top soil is not carried away by the water. Thus conservation agriculture practices in perennial fruit orchards lead to a significant reduction in erosion, and thus to a reduction in water pollution.

Cover crop biomass must be returned to the soil after the desired growing period for the soil health benefit to be fully realized. However growing legume cover crops is still the best practice for improving organic matter levels hence, soil quality. Cover crops improve soil tilth and drainage. Deep-rooted cover crops penetrate subsurface hardpan and thereby, improve soil aeration. Some cover crops deliver other benefits to the soil. For example, legumes have the capacity to fix nitrogen. Cover crops grown in orchards will flourish only when sufficient soil moisture and plant nutrients are available, and they compete for these with the orchard crop. Nutrient management skill is prerequisite to regulate the growth of the cover crop so as to maximize benefits to the orchard.

Benefits of cover crops

- Protect the soil, when it is not cultivated
- Provide an additional source of organic matter to improve soil structure and create an improved top soil
- Recycle nutrients and mobilizing them in the soil profile in order to eliminate layers with slow moving nutrients like phosphorus and potassium

- Encourage “biological ploughing” of the soil; the roots of some crops are pivotal and able to penetrate compacted or very dense layers, increasing water percolation capacity of the soil
- Utilize easily leached nutrients
- Permit a rotation in a monoculture
- Help control weeds, pests or break soil compaction

In summary, conservation agriculture practices in perennial horticulture crops makes use of soil biological activity and cropping systems to reduce the excessive disturbance of the soil and to maintain crop residues on the soil surface in order to minimize damage to the environment and provide organic matter and nutrients. Conservation practices in perennial horticulture cropping systems are designed to reduce soil erosion and land degradation through mulch cover; reduce soil temperature and conserve moisture; increase organic matter and improve soil structure and fertility; enhance soil health through increased soil biodiversity; reduce CO_2 emissions and build carbon levels; reduce reliance on cultivation and fossil fuel use; reduce fuel and labour inputs; achieve viable and sustainable productivity; improve yields over the long term; and reduce vulnerability to climate change.

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Research Article
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IN SILICO ANALYSIS TO CHARACTERISE THE RICE CHITINASE 1 (*Oschib1*) GENE INDUCED DURING SHEATH BLIGHT INFECTION

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ABSTRACT

Chitinase enzyme catalyzes the hydrolysis of chitin a-1,4 linkages. Plant chitinases are pathogenesis-related proteins induced in response to pathogen attack and play a critical role in defense against pathogens. Transcriptomic analysis was done to identify the host pathogen interaction in rice to identify many candidate genes inaddition to class III chitinase 1. Class III chitinase 1 (*Oschbi1*) was identified through transcriptomic data and real time PCR. In this *in silico* characterization study, we investigated the class III chitinaseI- *Oschib1* (Os10g0416500) gene in rice. The databases like RAP-DB, NCBI, RGAP were used for the retrieval of locus information, the nucleotide and amino acid sequences of gene. Using the Pfam database, the chitinase 1 (*Oschib1*) motifs were identified as glycoside hydrolase-GHL18 and GHL10 family members. Based on the expression and co-expression analysis of rice chitinase gene, plants cannot produce chitin, suggesting that plant chitinases are induced only under biotic or abiotic stress which was not produced under normal condition. Some disease resistance proteins CRKs, AdZADH2 and PBZ1 are co-expressed with chitinase (*Oschib1*) indicating that the disease resistance genes may have connectivity and are co-inducible. NCBI-Blast and NCBI- multiple sequence alignment viewer provided the distance tree results and homology of nucleotides in different cultivars of rice. Interestingly, two more genes belonging to class III chitinase of GHL18 family (Os10g0416100, Os10g0416800) showed high amino acid similarity. Furthermore, major analysis will be done through transgenic approach to characterize the *Oschib1* by overexpression of the gene.

Keywords: Chitinase, Glycoside hydrolase, *In silico*, NCBI Blast, RAP-DB

Chitinases are a group of pathogenesis related (PR) proteins that catalyze the hydrolysis of *N*-acetyl-â-D-glucosaminide 1, 4-linkages in chitin and chitodextrins (Jitonnom *et al*., 2011). Plant cell wall is devoid of chitin. The chitinous components present in the fungal cell wall are the targets of chitinases thereby inhibiting the fungal pathogens (Rawat *et al*., 2017). The expression of chitinase encoding genes is induced during fungal infection leading to systemic acquired resistance (SAR) (Návarová *et al*., 2012). Overexpression of the chitinase and the glucanase genes enhanced the protection against fungal attack in transgenic tobacco (Zhu *et al*., 1994). Chitinase activities were detected 24h after inoculation of moderately resistant cultivars.

Betichikon, Dudruchi, Khatochalani, Padi Pulut Malat, Kakua, IR72, Khakibinni rice varieties for sheath blight resistance. But in the susceptible cv. IR58, chitinase activity was detected only 36h after inoculation (Shresta *et al*., 2008). The co-expression of tobacco osmotin (ap24) and rice chitinase (chi11) genes resulted in enhanced resistance in rice plants against the sheath blight disease caused by *Rhizoctonia solani* (Sripriya *et al*., 2017). Karmakar *et al*. (2016) showed improved resistance of rice plants against sheath blight disease by the co-expression of chitinase and oxalate oxidase 4 genes. Similarly, the chitinase gene LOC_Os11g47510 overexpression in rice plants also showed improvement in the resistance against sheath blight disease. (Richa *et al*., 2017). Moreover, chitinases are also involved in the growth and development of plants. Mutation of the Arabidopsis Class II chitinase (*AtCTL1)* causes abnormalities in cell morphology and changes internode and root length (Zhong *et al*., 2002). Similarly mutation of OsCLP gene in rice affects the calcium signaling in root and causes the retardation of root length (Wu *et al*., 2017). Mutation of chitinase *BC15*/*OsCTL1* gene causes reduced cellulose content and mechanical strength leads to the culm and leaves brittle without alterations in plant

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growth- suggesting a possible mechanism for chitinase regulated cellulose biosynthesis and cell wall remodeling (Wu *et al*., 2012). Other biological processes, such as cell separation or loosening, embryonal development, and programmed cell death are associated with plant chitinase activity (Agusti *et al*., 2008). In addition, some plant hormones- auxin and cytokinin accumulation reduces the chitinases activity in tobacco (Shinshi *et al*., 1987) and abiotic stress resistance for salinity was appeared in tobacco lines due to over expression of chitinases (Dana *et al*., 2006; Grover, 2012). Many reports indicate that plant chitinases are induced not only during the pathogen attack but also on various abiotic stresses, such as osmotic pressure, drought, salinity, wounding, and frost (Pinheiro *et al*., 2001; Tateishi *et al*., 2001).

According to Neuhaus and others (1996), plant chitinases are divided into six classes (I, II, III, IV, V, and VI) based on their amino acid sequence similarity. The classes I, II, and IV correspond to family glycoside hydolases 19 (GH-19), whereas classes III and V to family GH-18 according to the CAZy (Carbohydrate active enzyme) database (Henrissat, 1991; http://afmb.cnrs-mrs.fr/CAZY/). Until now, 25 and 49 chitinase family genes have been identified in Arabidopsis and rice, respectively based on TAIR and TIGR databases (Grover, 2012). A study was conducted and identified 43 tomato chitinases via database analysis to identify their phylogeny, structure, chromosomal location and duplication, and synteny were then investigated (Cao *et al*., 2019).

In this study, we analysed the Class III chitinase 1 (*Oschib1*) gene identified through transcriptomic analysis (data not given) of rice during *R. solani* infection by retrieving the details from databases and analyzing the possible relationship, diversity and homology of the chitinase 1 (*Oschib1*) with other chtinase genes in rice. *In silico* tools were used to characterize the *Oschib1* for its homology with other cultivars, motif families, for its expression and co-expression analysis with other genes responsible for disease resistance.

MATERIAL AND METHODS

Identification of pathogen induced candidate gene

The whole-genome transcriptomic analysis was conducted at ICAR-Indian Institute of Rice Research (ICAR-IIRR) to identify the key genes involved in rice-*R. solani* interaction. A few genes were shortlisted based on their functional annotation for quantitative expression analysis using quantitative Real Time PCR (qRT-PCR). Based on the relative expression analysis, *Oschib1* (Os10g0416500) was selected for the functional characterization. This *Oschib1* gene expression was highly upregulated after inoculation of rice plants with *R. solani,* in comparision with some other genes whose relative expression was not higher than *Oschib1.*

Sequence retrieval and analysis of chitinase 1 (*Oschib1*) gene

The *Oschib1* details were retrieved from the RAP-DB (https://rapdb.dna.affrc.go.jp/), NCBI (https://www.ncbi.nlm.nih.gov/) and RGAP (http://rice.uga.edu/) databases. The nucleotide and amino acid sequences were retrieved from the RAP-DB and RGAP databases whereas the blast analysis was done using NCBI. In RAP-DB the database, the *Oschib1* was designated as Os10g0416500 whereas in RGAP it is designated as LOC_Os10g28080.1. From these databases entire details of the *Oschib1* gene were retrieved which include nucleotide sequence, amino acid sequence, location of the gene on chromosome, gene size and structure, transcript size, and untranslated region (UTR) length. In addition, the expression data and coexpression network of this gene were also retrieved. The protein motifs details were analysed and extracted from motif search database for Pfam motifs (https://www.genome.jp/tools/motif/).

Phylogenetic relationship and sequence similarity analysis

From RAP-DB 35 chitinases were retrieved and tabulated. The details of the chitinases and their transcripts length were collected (Table 1). The amino acid sequence similarity was done using Clustal W; the two chitinases were showing similarity with the chitinase 1 of our study (Figure 1, Table 2). Later, the *Oschbi1* sequence homology was studied in different cultivars of rice using BLAST software. The distance tree results of cultivars and homology analysis was also done using BLAST. The multiple sequence alignment was performed with clustalW (https://www.genome.jp/tools-bin/clustalw) and the insertions and deletions (InDels) were observed in Multiple Sequence Alignment Viewer (https://www.ncbi.nlm.nih.gov /projects/ msaviewer/)

Table 1. Details of the chitinases present in rice according to RAP-DB database

S.No.	Accession ID	Description	Transcript length	Functionally characterized chitinases	References
1	OS01G0287600	SIMILAR TO CHITINASE 10.	1055 BP		
2	OS01G0303100	SIMILAR TO CHITINASE PRECURSOR (EC 3.2.1.17)	1239 BP		
3	OS01G0660200	ACIDIC CLASS III CHITINASE OSCHIB3A (EC 3.2.1.14)	1236 BP		
4	OS01G0687400	SIMILAR TO CHITINASE (EC 3.2.1.14).	1186 BP		
5	OS01G0860500	SIMILAR TO HEVAMINE A PRECURSOR [INCLUDES: CHITINASE (EC 3.2.1.14); LYSOZYME (EC 3.2.1.17)]	1193 BP		
6	OS01G0937050	HOMOLOG OF XYLANASE INHIBITOR, CHITINASE-LIKE PROTEIN, DEFENSE RESPONSE AGAINST PATHOGENS, GROWTH REGULATION THROUGH CALCIUM SIGNALING	1275 BP		
7	OS02G0605900	SIMILAR TO CHITINASE (EC 3.2.1.14) A.	976 BP		
8	OS03G0132900	SIMILAR TO CHITINASE 11.	1086 BP		
9	OS03G0418000	SIMILAR TO BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14). (OS03T0418000-00)	1043 BP	CLASS II, CHITINASE 10,11,12; RCH10	KIM ET AL., 2003, MAO ET AL., 2014
10	OS04G0493400	SIMILAR TO CHITINASE	1078 BP		
11	OS04G0494100	SIMILAR TO CHITINASE	1022 BP		
12	OS05G0138200	SIMILAR TO CHITINASE (CLASS II) (EC 3.2.1.14)	1025 BP		
13	OS05G0247100	SIMILAR TO GLYCOSYL HYDROLASES FAMILY 18; CHITINASE III PROTEIN, XYLANASE INHIBITOR, REGULATION OF ABIOTIC STRESS RESPONSE, RESISTANCE TO HERBIVORES	1199 BP		
14	OS05G0399300	CLASS I CHITINASE, DEFENSE AGAINST FUNGAL PATHOGENS (OS05T0399300-01)	1314 BP	CLASS I, CHITINASE II , PR-3, RC7	DATTA ET AL., 2000; NANDA KUMAR ET AL., 2007;
15	OS05G0399400	CHITINASE 9	1005 BP		
16	OS05G0399700	CHITINASE (EC 3.2.1.14)	1303 BP		
17	OS06G0149400	SIMILAR TO CHITINASE A.	1562 BP		

S.No.	Accession ID	Description	Transcript length	Functionally characterized chitinases	References
18	OS06G0726100	PATHOGENESIS RELATED (PR)-3 CHITINASE 3, RESISTANCE AGAINST SHEATH BLIGHT PATHO	1169 bp	Class I, PR-3, Oschi11,	Lin et al., 1995; Baisakh *et al.,* 2001; Kumar *et al.,* 2003; Sridevi *et al.,* 2003; Rao *et al*., 2011; Karmakar *et al.,2017*
19	Os06g0726200	Similar to Chitinase 1	1217 bp		
20	Os08g0518800	Similar to Class III chitinase homologue (OsChib3H-h)	660 bp		
21	Os08g0518900	Chitinase (EC 3.2.1.14)	1367 bp		
22	Os09g0494200	Membrane-associated chitinase-like protein, Cellulose biosynthesis (Os09t0494200-01);Similar to Chitinase-like protein (EC 3.2.1.14). (Os09t0494200-02)	1648 bp, 1453 bp		
23	Os10g0416100	Class III chitinase RCB4 (EC 3.2.1.14)- (Os10t0416100-01); Similar to Chitinase (Fragment)- (Os10t0416100-02)	1210 bp, 1096 bp		
24	Os10g0416500	Similar to Chitinase 1 precursor (EC 3.2.1.14) (Tulip bulb chitinase-1) (TBC-1)	1069 bp	Class III, Oschib1	
25	Os10g0416800	Similar to Chitinase 2 (EC 3.2.1.14) (Tulip bulb chitinase-2) (TBC-2)	1134 bp		
26	Os10g0542900	Similar to chitinase	1072 bp		
27	Os10g0543400	Chitinase 8	528 bp		
28	Os11g0700900	Class III chitinase homologue (OsChib3H-b)	1280 bp		
29	Os11g0701000	Class III chitinase homologue (OsChib3H-c)	1314 bp	Class III, Oschib3H	Richa et al., 2017
30	Os11g0701100	Similar to Class III chitinase homologue (OsChib3H-h) (Fragment); Similar to Xylanase inhibitor protein 2.	1150 bp		
31	Os11g0701400	Chitinase (EC 3.2.1.14) III C10150-rice (EC 3.2.1.14).	1076 bp		
32	Os11g0701500	Similar to Class III chitinase homologue (OsChib3H-g)	1019 bp		
33	Os11g0701800	Chitinase (EC 3.2.1.14) III C10701-rice (EC 3.2.1.14) (Class III chitinase homologue (OsChib3H-a)H-). (Os11t0701800-01)	1175 bp		
34	Os11g0702100	Similar to Class III chitinase homologue (OsChib3H-h)	1167 bp		
35	Os12g0238550	Similar to Chitinase 6	446 bp		

Table 2. Genes coexpression with Os10g0416500 (*Oschib1*) in rice

Hierarchy	LocusID	Description
1	Os04g0121800	Non-protein coding transcript, putative npRNA
1	Os10g0535800	Protein of unknown function Cys-rich family protein
2	Os09g0502500	Alcohol dehydrogenase superfamily, zinc-containing protein.
2	Os12g0555000	Similar to Probenazole-inducible protein PBZ1

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NP_001064605.1   1   MGSAKLIAVVLLPALLAFQAPMATAVNSNLFRDYIGAIFNGVKFTDVPIN   50
NP_001064608.1   1   ----------MTNGYLFREYIGAQFTGVRFSDVPIN                26
NP_001064607.1   1   ----------MVNGYLFREYIGAQFTGVRFSDVPVN                26

NP_001064605.1   51  PKVRFDFILAFIIDYT--TETNPPTPTNGKFNIFWQNTVLTPSAVASIKQ   98
NP_001064608.1   27  PNLSFNFILSFAIDYTSPAGGATPAPTNGVFSPYWDTANLSPADVAAVKA   76
NP_001064607.1   27  PGLSFHFILAFAIDYFMATQSSKPAPANGVFAPYWDTANLSPAAVAAAKA   76

NP_001064605.1   99  SNPNVRVAVSMGGATVNDRP--VFFNIT-SVDSWVNNAVESLTGIIQDNN  145
NP_001064608.1   77  AHPNVSVMVGLGGDSVQDTA-KVFFSPT-SVDSWVANAVASVSGIIDAYG  124
NP_001064607.1   77  AHPNLSVILALGGDTVQNTGVNATFAPTSSVDAWVRNAADSVSGLIDAYG  126

NP_001064605.1   146 LDGIDIDYEQF----QVDPDTFTECVGRLITVLKAKGVIKFASIAPFGNA  191
NP_001064608.1   125 LDGVDVDYEHFNDDGGAGVDTFVECIGRLLTELKARHPNITTSIAPFEDA  174
NP_001064607.1   127  LDGVDVDYEHF----AAGVDTFVECIGRLLTELKARHPNIATSIAPFEHP  172

NP_001064605.1   192 EVQRHYMALWAKYGAVIDYINFQFYAYGASTTEAQYVDFFNQQIVNYPGG  241
NP_001064608.1   175 VVQRYYQPLWRRYAGVIDLVNFQFYGYGDNTDVPTYVMFYDEQAANYPGG  224
NP_001064607.1   173 VVQRYYQPLWRRYAGVIDYVNFQFYGYGANTDVATYVMFYDEQAANYPGS  222

NP_001064605.1   242 NILASFTTAATTTSVPVETALSACRTLQKEGKLYGIFIWAADHSR--SQG  289
NP_001064608.1   225 KVLASFKTGDVAGLLWPEQGIAGAKELQRQGKLPGLFIWSADSSKVSSYG  274
NP_001064607.1   223 KLLASFKTGNVTGLLSPEQGIAGAKELQRQGKLPGLFIWSADSSMVSSYK  272

NP_001064605.1   290 FKYETESQALLANATISY                                307
NP_001064608.1   275 FEYEIKAQEIIANH----                              288
NP_001064607.1   273 FEYETKAQEIVANH----                              286
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PROTEIN ACC.	*GENE*	*ORGANISM*
NP_001064605.1	*OS10G0416100*	*O.SATIVA*
NP_001064608.1	*OS10G0416800*	*O.SATIVA*
NP_001064607.1	*OS10G0416500*	*O.SATIVA*

Figure 1. Amino acid sequence analysis of other chitinase genes with Oschib1 and their protein accessions

RESULTS AND DISCUSSION

Most of the chitinases transformed until now are more often from the chromosomes 3, 5, 6, 11 and members of class I, II, III (Molla *et al*., 2020; Li *et al*., 2021). None of these chitinases have shown complete resistance to sheath blight (Molla *et al*., 2020; Li *et al*., 2021). Until now four chitinases- Os03g0418000 (RCH10), Os05g0399300 (RC7), Os06g0726100 (Oschi11), Os11g0701000 (Oschib3H) were transformed into rice cultivars (Table. 1). Especially, *Oschi11* gene transformation was done many times into many different cultivars (Table 1). Earlier reports mentioned that class I chitinases are involved in antifungal activity (Sasaki *et al*., 2006), recently a study was reported regarding the antifungal activity of class III chitinase (Richa *et al*., 2017). This is the first attempt we transformed class III chitinase 1 (*Oschib1*) from chromosome 10. It is a class III chitinase 1 gene belongs to PR8 protein and it is a member of GHL18 family. Under controlled growth condition the *Oschib1* expression levels are very low but when rice plants were infected with *R.solani*, the gene up regulation

was very high. In this context, we have chosen the *Oschib1* gene for functional validation.

Many differentially expressed genes (DEGs) were identified through transcriptomic analysis of rice-*R. solani* interaction studies. The DEGs were validated using relative expression studies that indicated very high up-regulation of *Oschib1* gene during host-pathogen interaction (data not provided).

Details of chitinase1 gene (Os10g0416500)

Os10g0416500 is a PR-8 protein, a member of Glycohydrolase18 (GHL18) class. It is denoted with *Oschib1*, PR-8, PR8, OsPR8. The gene is located at chr10:14590045..14591113 (+strand) in the rice genome on chromosome10. The transcript size (cDNA) of the gene is 1069bp (Figure 2), coding sequence CDS size is 861 bp, and the amino acid or protein sequence is of 287aa (Figure 3). The molecular weight of the chitinase 1 protein is 31.09 kDa. The total transcript size along with its UTR and CDS size is given in (Table 3). The expression of O*schib1* under controlled growth condition was observed. The *Oschib1* expression levels are very low under normal condition except in root parts at specific stages (Figure 4). Mutation of Class II chitinase (*AtCTL1)* in Arabidopsis causes abnormalities in cell morphology and changed internode and root length (Zhong *et al*., 2002). Same mutation in rice *OsCLP* gene affects the calcium signaling in root and causes the retardation of root length (Wu *et al*., 2017). These earlier reports supports that chitinases are induced in roots under normal conditions and the expression levels increase during fungal pathogen attacks or under abiotic stress in plants (Hamel and Bellemare, 1995; Tateishi *et al*., 2001; Sasaki *et al*., 2006). Some other genes like Os04g0121800- non protein coding transcript, putative npRNA, Os10g0535800- protein of unknown function Cys-rich family protein, Os09g0502500- alcohol dehydrogenase super family, zinc-containing protein and Os12g0555000- similar to probenazole-inducible protein PBZ1 showed co-expression with the Os10g0416500-chitinase 1 (Figure 5). The genes coding the plant-specific Cys-rich motif (domain of unknown function 26 [DUF26]) make up a large gene family, and the motif was initially found in the extracellular region of cysteine-rich receptor-like kinases (CRKs) and Cys-rich secretory proteins from Arabidopsis (*Arabidopsis thaliana*; Chen, 2001). Several CRKs are involved in resistance to bacterial and fungal pathogens, hypersensitive response-related cell death, oxidative stress responses, and salicylic acid-dependent defense pathways (Du and Chen, 2000; Wrzaczek *et al*., 2010; Rayapuram *et al*., 2012). Zinc binding alcohol dehydrogenases 2 (AdZADH2) are NAD(P) dependent oxidoreductases involved in hydride ion transfer from alcohols to NAD^+ catalyzing reversible oxidation of alcohols to aldehydes or ketones. They are found in all plants, playing important roles in plant growth, pollen, and seedling development and fruit ripening (Thompson *et al.,* 2010). However, a study reported AdZADH2 was significantly upregulated in a wild peanut, *Arachis diogoi* treated with conidia of late leaf spot (LLS) pathogen, *Phaeoisariopsis personata*. This up-regulation was not observed in a comparative analysis of cultivated peanut, which is highly susceptible to LLS (Kumar *et al.,* 2016). Probenazole (PBZ) induces a non-race specific resistance in rice plants against rice blast fungus and PBZ1 (PR protein)

Table 3. Details of the chitinase 1 transcript in rice

Region	Length on chromosome	Size
5' UTR	*CHR10:14590045..14590100 (+ STRAND)*	*56 BP*
CDS	*CHR10:14590101..14590961 (+ STRAND)*	*861BP*
3' UTR	*CHR10:14590962..14591113 (+ STRAND)*	*152 BP*

ATGCGCCGCGTCCACAGCTCGATCGCTAGCCCTACTCGCTAGCTAGATCGGCGGCATGGTGAACGGCTACTTGTTC
CGGGAGTACATCGGCGCGCAGTTCACCGGCGTGCGCTTCTCCGACGTGCCCGTCAACCCGGGCCTCAGCTTCCACTTCAT
CCTCGCCTTCGCCATCGACTACTTCATGGCGACGCAGTCCTCCAAGCCGGCGCCAGCCAACGGCGTGTTCGCCCCGTACTGG
GACACGGCCAACCTGTCCCCGGCCGCCGTCGCCGCGGCCAAGGCGGCGCACCCCAACCTCAGCGTCATCCTCG
CCCTCGGCGGCGACACCGTCCAGAACACCGGCGTCAACGCCACGTTCGCGCCGACGTCGTCCGTCGACGCGTG
GGTGCGCAACGCCGCCGACTCCGTCTCCGGCCTCATCGACGCCTACGGCCTCGACGGCGTCGACGTCGACTACGAGCACTTCGCCGC
CGGCGTGGACACGTTCGTGGAGTGCATCGGTCGCCTCCTCACCGAGCTCAAGGCGCGGCACCCGAACATCGCCA
CCTCCATCGCGCCGTTCGAGCACCCCGTGGTGCAGCGCTACTACCAGCCGCTGTGGCGGCGCTACGCCGGCGTGATCGACTACGTCAA
CTTCCAGTTCTACGGCTACGGCGCCAACACCGACGTGGCGACGTACGTGATGTTCTACGACGAGCAGGCGGCGAACTACCCCGGCAGCAAGC
TGCTCGCCAGCTTCAAGACCGGGAACGTCACCGGGCTGCTCTCGCCGGAGCAGGGGATCGCCGGCGCGAAGGAGTTGCAGCGGCAGGGGAA
GCTGCCGGGGTTGTTCATCTGGTCAGCGGATAGCTCCATGGTCAGCAGCTACAAGTTTGAGTACGAGACCAAGGCTCA
GGAGATCGTCGCCAACCACTGATCGTCCATCGAACGGTCGTGATAATACTTATGAAATAAGAGCAAATAAATTGCGAAATAATGGTCGTATTA
TATATCGAGCGTCATTATGCACGACTTACGTGCTAAATAAGAAATGGACTTATGTGCCGATTGGTAATCGGCGATATATGG

Figure 2. Nucleotide sequence details of the *Oschib1* gene

was identified as a PBZ-inducible gene from rice (Nakashita *et al*., 2001). It is a PR protein which indicates that the expression of chitinase 1 might induce the PBZ gene expression or vice versa. Two motifs identified within the chitinase 1 are Glycosyl hydrolases family 18 and Glycosyl hydrolase-like 10 (Table 4). GH18s are proteins that consist of discrete domains, which can be arranged in different orders in different proteins (Henrissat and Davies, 2000). Besides the catalytic domain, there is very often a substrate-binding domain present. These substrate- binding domains are not necessary for chitinolytic activity, although they seem to enhance the efficiency of the enzymes (Limon *et al*., 2001).

MVNGYLFREYIGAQFTGVRFSDVPVNPGLSFHFILAFAIDYFMATQSSKPAPANGVFAPYWDTANLSPAAVAAAKAAHPNLSVILALGGDTVQ
NTGVNATFAPTSSVDAWVRNAADSVSGLIDAYGLDGVDVDYEHFAAGVD TFVECIGRLLTELKARHPNIATSIAPFEHPVVQRYY
QPLWRRYAGVIDYVNFQFYGYGANTDVATYVMFYDEQAANYPGSKLLASFKTGNVTGLLSPEQGIAGAKELQRQGKLPGLFIWSA
DSSMVSSYKFEYETKAQEIVANH*

Figure 3. Sequence details of the Oschib1 protein or amino acid (287 aa)

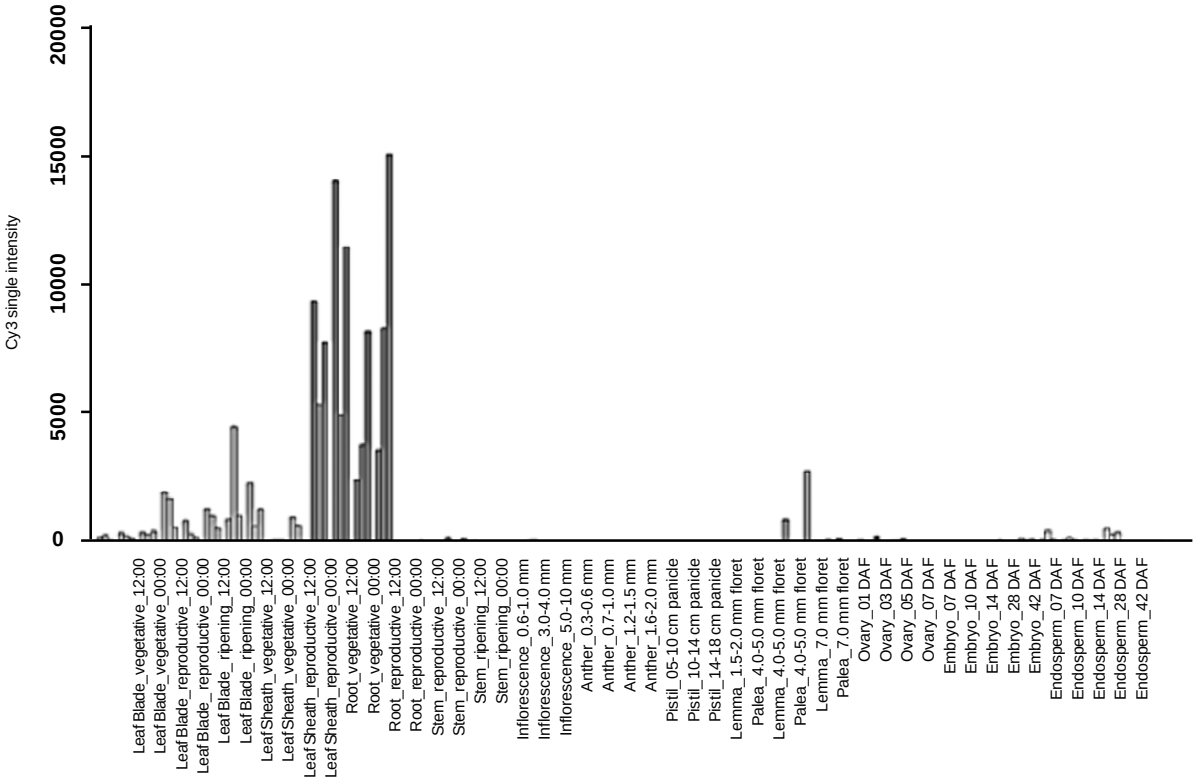

Figure 4. Graph indicating the expression of *Oschib1* in different developmental stages of rice under normal growth conditions

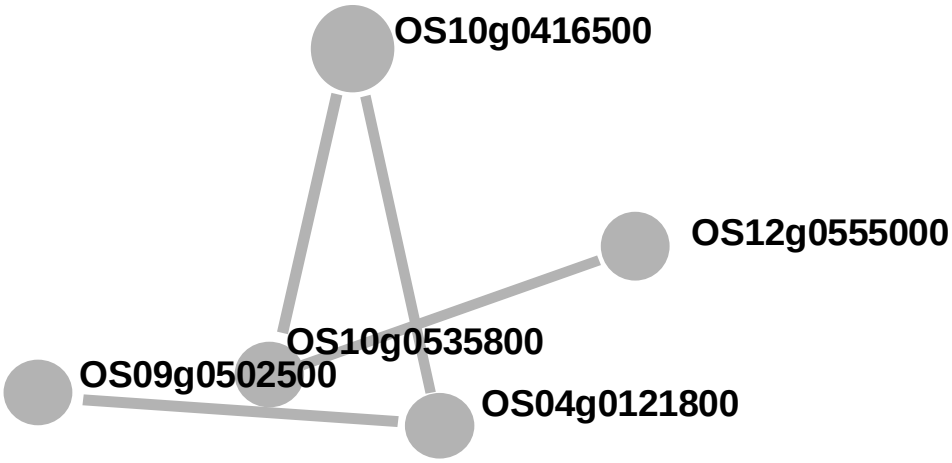

Figure 5. Coexpression network of Os10g0416500 with other disease resistance genes

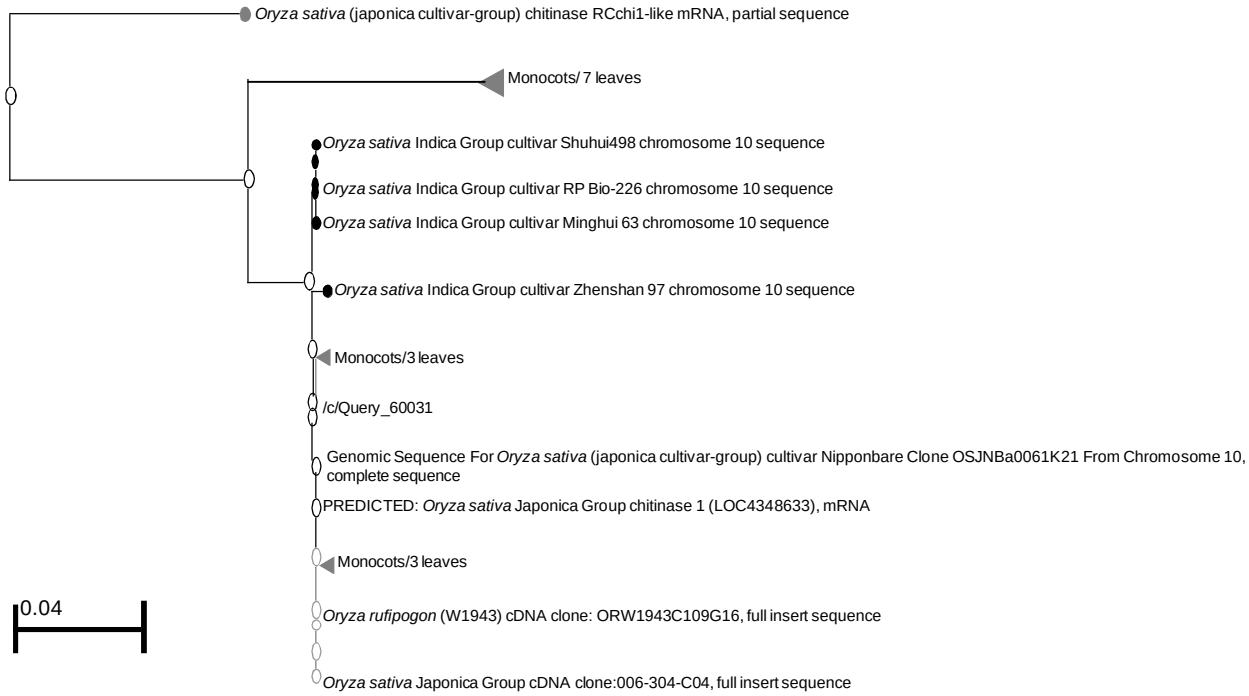

Figure 6. Distance tree results of *Oschib1* with other cultivars in rice

Phylogenetic relationship and sequence similarity of chitinase 1 with other chitinase genes of rice

According to RAP-DB database, there are 35 chitinase genes in rice. The MSU ID for the Os10g0416500 is LOC_Os10g28080. Only two chitinases out of 35 chitinase genes synthesize two variants of transcripts. The chitinase Os09g0494200 produce membrane-associated chitinase-like protein, cellulose biosynthesis (Os09t0494200-01) and similar to chitinase-like protein (Os09t0494200-02); chitinase gene Os10g0416100 produces two variants of transcripts Class III chitinase RCB4 (Os10t0416100-01) and similar to Chitinase Fragment (Os10t0416100-02) (Table 4). Chitinase 1 (Os10g0416500) comes under Glycohydrolase family 18. Based on the amino acid sequence analysis the chitinases Os10g0416100-Class III chitinase RCB4 (Os10t0416100-01), Os10g0416800- similar to Chitinase 2 were showing highest similarity with Os10g0416500 (*Oschib1*) sequence and their protein accession ID was given (Figure 5). Several chitinases from rice were produced using the *Pichia pastoris* expression system, and the enzymatic properties were characterized (Park *et al*., 2002; Truong *et al*., 2003). Among the class III enzymes from rice, the chitinase activity of OsChib1b was found to be lower than that of OsChib1a. According to a study, the class I enzyme gene was found to be constitutively expressed in the entire developmental stages, whereas the class III gene was not expressed at any developmental stages and in any plant organs (Sasaki *et al*., 2006). On the contrary, the class III enzyme gene was found to be expressed when the *Arabidopsis* plants were exposed to various environmental stresses, such as cold, drought, high light, salt, and chemical treatment with paraquat and ethephon (Sasaki *et al*., 2006). Obviously, the class III enzyme has a different physiological function from that of the class I enzyme and is likely responsible for the transduction of environmental stress signals. Our study suggests that these three chitinases Os10g0416500, Os10g0416100 and Os10g0416800 (chitinase 1, chitinase 2 RCB4, chtinase 2) belongs to the class III chitinase and showing aminoacid sequence similarity.

Based on the nucleotide sequence retrieved from the RAP-DB database the predicted chitinase 1 (OS10g0416500) was showing sequence identity of 99.53 % with many other rice cultivars like Shuhui-498,

Table 4. Pfam motifs of Oschib1 protein using motif search

Pfam	Description
Glyco_hydro_18	PF00704, Glycosyl hydrolases family 18
GHL10	PF02638, Glycosyl hydrolase-like 10

Table 5. Details of *Oschib1* sequence identity with different cultivars of rice

Description	Per. ident	Accession
PREDICTED: Oryza sativa Japonica Group chitinase 1 (LOC4348633), mRNA	100	XM_015757491.1
Oryza sativa Japonica Group DNA, chromosome 10, cultivar: Nipponbare, complete sequence	100	AP014966.1
Genomic Sequence For Oryza sativa (japonica cultivar-group) cultivar Nipponbare Clone OSJNBa0061K21 From Chromosome 10, complete sequence	100	AC016780.6
Oryza sativa subsp. japonica BAC clone nbxb0032I20, complete sequence	100	AF229187.1
Oryza sativa Japonica Group cDNA clone:006-203-G07, full insert sequence	99.91	AK059767.1
Oryza rufipogon (W1943) cDNA clone: ORW1943C109G16, full insert sequence	100	CU405868.1
Oryza sativa Indica Group cultivar Shuhui498 chromosome 10 sequence	99.53	CP018166.1
Oryza sativa Indica Group cultivar RP Bio-226 chromosome 10 sequence	99.53	CP012618.1
Oryza sativa Indica Group cultivar Zhenshan 97 chromosome 10	99.53	CP056061.1
Oryza sativa Indica Group cultivar Minghui 63 chromosome 10	99.53	CP054685.1
Oryza sativa Japonica Group cDNA clone:006-304-C04, full insert sequence	100	AK104202.1
Oryza sativa Japonica Group cDNA clone:006-201-G07, full insert sequence	100	AK104100.1
Oryza sativa subsp. japonica class III chitinase (chib1) gene, complete cds	99.9	AF296279.1
Oryza sativa Japonica Group cDNA clone:006-202-C10, full insert sequence	100	AK104397.1
PREDICTED: Oryza sativa Japonica Group chitinase 2 (LOC4348634), mRNA	88.47	XM_015759537.2
Oryza sativa Japonica Group cDNA clone:006-303-H08, full insert sequence	88.47	AK060033.1
Oryza sativa Japonica Group cDNA clone:001-007-F06, full insert sequence	88.47	AK104292.1
Oryza sativa Japonica Group cDNA clone:006-306-E05, full insert sequence	88.47	AK104222.1
Oryza sativa Japonica Group cDNA clone:J023025I19, full insert sequence	88.47	AK099101.1
Oryza sativa (indica cultivar-group) cDNA clone:OSIGCSN066K01, full insert sequence	88.36	CT830371.1
Oryza sativa Japonica Group cDNA clone:001-208-E12, full insert sequence	88.36	AK119555.1
PREDICTED: Oryza brachyantha chitinase 2-like (LOC102718393), mRNA	85.71	XM_015841621.2
Oryza sativa (japonica cultivar-group) chitinase RCchi1-like mRNA, partial sequence	82.04	EF472966.1

RP Bio-226, Minghui 63, Zhenshan 97 (Table 5). The distance tree relationship of the many cultivars showing highest identity was also observed in these cultivars (Figure 6). The multiple sequence alignment of *Oschib1* from japonica with other cultivars of rice was analyzed by using NCBI multiple sequence analysers to know the InDels and SNPs (Figure 7). Phylogenetic analysis of chitinases in *Brassica juncea* and *Camelina sativa* revealed four distinct sub-groups, representing different classes of chitinases (I-V) (Mir *et al*., 2020). GH19 family chitinases adopt the single displacement catalytic mechanism due to high percentage of alpha-helices, whereas all the GH18 family chitinases have

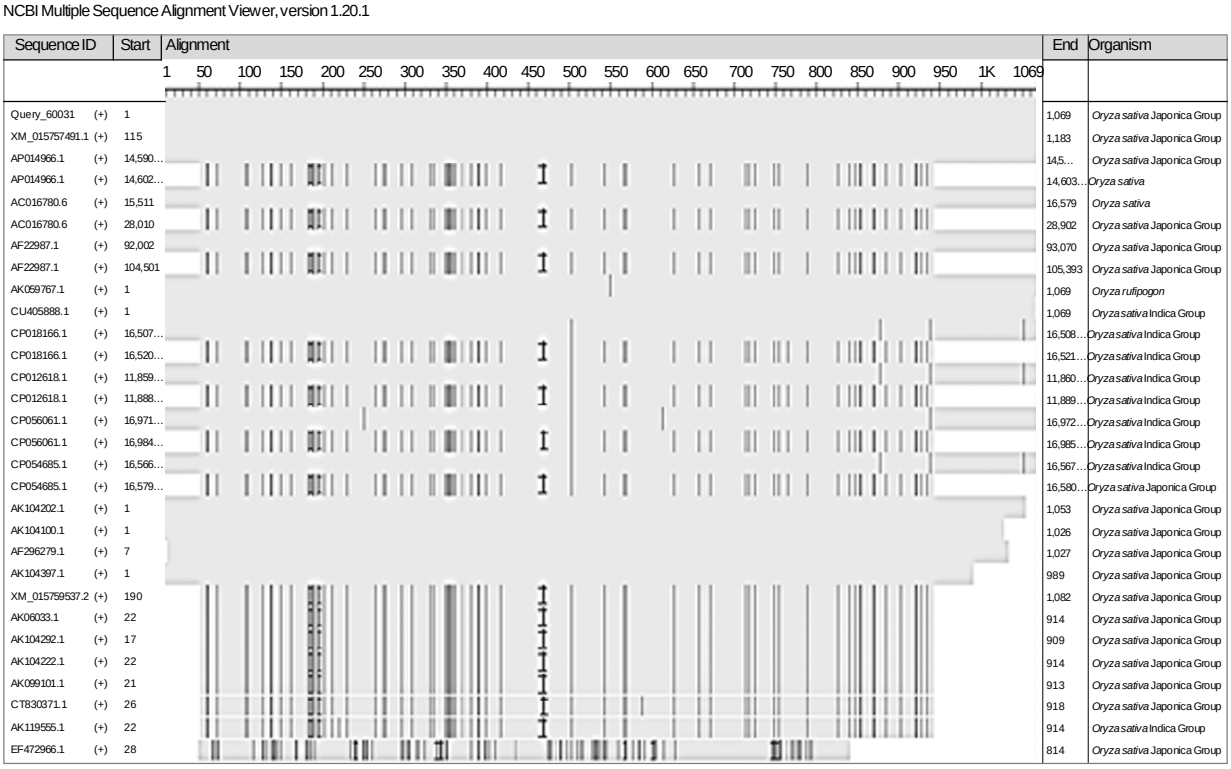

Figure 7. Multiple Sequence Alignment of *Oschib1* in other cultivars of rice

triosephosphateisomerise (TIM barrel) as catalytic domains fold with a conserved DxDxE motif, and through substrate-assisted mechanism they catalyze the hydrolytic reaction (Vaaje-Kolstad *et al*., 2004; van Alten *et al*., 2001; Hoell *et al*., 2010).

CONCLUSION

In the present study class III chitinase 1 was characterized through *in silico* tools like RAP-DB, NCBI, RGAP and NCBI-Blast etc. to identify the homology with other chitinases in rice and the distance tree relationship with the other cultivars of rice. In addition nucleotide and aminoacid sequence details of *oschib1*, the expression and coexpression analysis of rice this gene was retrieved using the RAP-DB database. In silico tools like Pfam used to identify the motifs families of chitinase 1 protein. Using NCBI-blast homology sequences in other cultivars were identified also distance tree results and multiple sequence was done. Based on these analyses we identified the class III chitinase 1-*Oschib1* (Os10g0416500) is majorly involved in the defense mechanism following the infection of fungal pathogen or expressed under many of the environmental stresses. To support its antifungal activity, a thorough functional characterization of gene is necessary by utilization of studies.

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Research Article
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AGE-SPECIFIC SURVIVORSHIP AND LIFE-FERTILITY TABLE STUDY OF INVASIVE ALIEN PEST FALL ARMYWORM ON CASTOR

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ABSTRACT

A laboratory experiment was carried out to study the demography of fall armyworm (FAW) in castor at Department of Entomology, College of Agriculture, Rajendranagar, Hyderabad, during 2020-21. Daily observations of FAW from neonates to death of adults was recorded where the age specific survivorship showed decrease in population of FAW on castor at transition of each stage representing the stair step survivorship curve. The net reproductive rate was 324.27, mean generation time (Tc) 30.07 and intrinsic rate of increase (r_m) 0.1922 indicating the susceptibility of the host plant. Finite rate of increase (or) female off-springs/female/day (ë) 1.556, doubling time (DT) 3.60 days, weekly multiplication rate (WMR) 3.83 times per week and annual rate of increase (ARI) 1.4223 x 10^{70}, indicated that castor is also a suitable host for FAW. The results on per cent contribution of larvae, pupae and adults were 97.48, 1.38 and 0.20, respectively at stable age distribution of *S. frugiperda* on castor. The life expectancy (ex) was high in early days *i.e.,* 10.32 (days) and decreased gradually with the age. The present results suggested that in the absence of maize, sorghum and other highly preferred crops, castor crop could become a potential host for FAW. Monitoring needs to be strengthened in order to determine the occurrence of FAW in castor and implement management tactics well in advance.

Keywords: Age-specific survivorship, castor, life expectancy, population parameters, *Spodoptera frugiperda*

The invasive pest fall armyworm, *Spodoptera frugiperda* (J.E. Smith, 1797) (Lepidoptera, Noctuidae) is native to two continents: South and North Americas (Casmuz *et al.*, 2010 and Murua *et al*., 2015). The pest is highly polyphagous causing economic damage in various crops such as maize, sorghum, beans and cotton (Abrahams *et al.,* 2017; Day *et al.,* 2017). It made its first transcontinental migration to Africa in early 2016 (Georgen *et al*., 2016), and to India and Yemen in 2018. The pest came to Asia either through natural migration with the monsoon winds or through imported plant material. As in January 2019, it has been reported in Bangladesh, Myanmar, Sri Lanka, Thailand and China (FAO, 2019). In 2020, Australia, South Korea, Cambodia, Papua New Guinea, Timor Leste, New Caledonia, Jordan, Syria, and United Arab Emirates officially stated the occurrence of the pest (Prasanna *et al*., 2021).

Due to its perennial pest status, strategies for management of FAW are imperative. For an ecologically sound integrated pest management program, it is crucial to understand thoroughly ecology of the pest. The life table generates an integrated and comprehensive description of development, survival, fecundity and life expectancy of a population, and is often used to project the growth and populations (Chi, 1990). The background information provided by life and fertility table studies can be used for developing sustainable management strategies for FAW.

MATERIAL AND METHODS

Rearing of FAW in laboratory

S. frugiperda was reared in the laboratory of Department of Entomology, College of Agriculture, Rajendranagar after collecting the larvae from maize fields, during 2020-21, the larvae which were in various stages of development were put into multiwell trays containing artificial diet. After becoming pre-pupae, they were placed in plastic tubs containing soil and allowed to develop into pupae. As the adults emerged, they were collected using plastic vial and released for mating into jars (10x15 cm) that contained small petriplate with sterile absorbent cotton dipped in 10 per cent honey solution. The jars were lined with yellow paper acting

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as substratum for egg laying as well as for providing darkness for moths. The top of the jars were covered with muslin cloth and secured with rubber band. After egg laying, the egg masses were collected for further experiments on life-fertility.

Age-specific survivorship experiment

Neonates that hatched from one cohort of egg mass were counted and transferred by brush on to fresh castor leaves. Primarily, the population was maintained in plastic jars (10 x15 cm) and later transferred to individual cups to prevent cannibalism. The plant parts were changed every 24 h to avoid microbial contamination. The larvae were maintained till adult emergence. Mortality data was recorded daily till all the adults died. Age-specific survivorship was used for constructing the life tables as suggested by Morris and Miller (1954). The survivorship curves were drawn by plotting the number living at a given age (lx) against the age (x). The shape of curve describes the distribution of mortality with age (Slobodkin, 1962).

Life- fertility experiment

The pupae that were developed from a cohort were segregated into males and females after examining the seventh, eighth and ninth sterno-abdominal segments for sex markings using a stage microscope. Sex ratio was calculated based on the emerged moths. Adult moths that emerged on a single day were collected using a plastic tube and released into a battery jar and covered with muslin cloth for ventilation. The internal wall was covered with yellow paper which acted as an oviposition substrate. A small cotton wick soaked in 10 per cent honey solution was placed in the small petriplate for adult feeding. The number of eggs laid by the female adults on each day was counted by using stage microscope till the death of the adults. The age-specific fecundity was constructed as described by Birch (1948) and Poole (1974). In the fertility tables, x represents age interval in days, lx the number of females as a fraction of initial size of cohort and mx as age-specific fecundity. Also, the population parameters were calculated as given below.

1. Potential fecundity $\sum mx$
2. Mean generation time $(T_C = \sum x.lxmx/R_0)$
3. Net reproductive rate $\left(R_0 = \sum lxmx\right)$
4. Corrected generation time $\left(T = \log_e R_0/r_m\right)$
5. Innate rate for increase in numbers (r_c) $(r_c = \log_e R_0/ Tc)$
6. Intrinsic rate of increase (r_m) $\left(\sum e^{-rm.x.mxmx} = 1\right)$
7. Finite rate of increase (λ) (antilog er_m)
8. Weekly multiplication rate (WMR) $(e/r_m)^7$
9. Doubling time (DT) (log2 e/r_m)
10. Annual rate of increase (ARI) (Antilog er_m 365)
11. Sex ratio (F:M)
12. Hypothetical female in F_2 generation $(R_0)^2$
13. Birth rate (β)
14. Instantaneous birth rate (b) $= (r_m.\beta/e^{rm} - 1)$
15. Instantaneous death rate (d)= $(b\text{-}r_m)$

Stable age distribution was worked out by observing the population schedule of birth rate and death rate when grown in limited space and life expectancy was computed by using the method suggested by Atwal and Bains (1974).

Data analysis

A computer software package MS-EXCEL was used for analysis.

RESULTS AND DISCUSSION

Age specific life-table and survivorship of FAW

The total life cycle of the FAW was 36 days (Table1). The mortality rate during the age interval 1 to 18 days was less than 10 per cent while that between 19-25 days was 0 per cent. It increased to 35.71 per cent on 30th day, thereafter decreased up till 34th day before reaching 100 per cent on 36th day. From the results, it can be inferred that during the larval instars, the mortality rate was maximum (8.65%) when 3rd instar larvae moulted to 4th instar. Mortality was also higher during pre-pupal (8.70%) and early pupal stages (8.47%) while in the adult stage mortality was highest at mid stage (35.71%).

The age specific survivorship curve (lx) and mortality (dx) of *S. frugiperda* on castor are presented in Figure 1. The survivorship curve was found to be similar to that of stair step type curves recorded for holometabolous insects and is in conformity to that reported by Odum (1971) and was intermediate to Type I and Type II survivorship curves described by Slobodkin (1962) and Deevey (1947). Choudhary and

Bhattacharya (1986) also recorded similar type of survival pattern in *Creatonotus gangis* (Linnaeus) and *Spodoptera litura* (F) on winged bean, while Chenchiah *et al*. (2007) recorded in *C. gangis* on artificial diet. Pramanik *et al.* (2012) reported stair step type of survivorship curve in *Leucinodes orbonalis* (Guenee) and Srivastava and Gupta (2015) in *Samia cynthia ricini* (Donovan) reared on castor. Also, Supriya *et al*. (2018) recorded stair step survivorship curve in *S. litura* when reared on castor for three generations.

Life-fertility of FAW in castor

The total number of surviving females that emerged were 24 out of 136 indicating lx to be 0.18 at the pivotal age of 26 days which remained so up to 30th day. Thereafter it gradually declined reaching 0.01 by 36 days, when all the adults died. The adult emergence was noticed for 9-10 days. (Table 2) (Fig 2). The potential fecundity was 2896.18 eggs with the highest egg laying being recorded on 29th day

Table 1. Age-specific survivorship of FAW on castor

Age of the insect in days(x)	Number surviving at the beginning of each age interval x out of 136(lx)	Number dying during the age interval x out of 136(dx)	Mortality rate at the ageInterval x(100qx)	Stage of the insect
1	136	2	1.47	I- INSTAR
2	134	6	4.48	
3	128	5	3.91	II-INSTAR
4	123	7	5.69	
5	116	4	3.45	III-INSTAR
6	112	8	7.14	
7	104	9	8.65	IV-INSTAR
8	95	6	6.32	
9	89	3	3.37	
10	86	5	5.81	V-INSTAR
11	81	4	4.94	
12	77	3	3.90	
13	74	5	6.76	VI-INSTAR
14	69	6	8.70	
15	63	4	6.35	
16	59	5	8.47	PRE-PUPAL
17	54	2	3.70	
18	52	1	1.92	PUPAL
19	51	0	0.00	
20	51	0	0.00	
21	51	0	0.00	
22	51	0	0.00	
23	51	0	0.00	
24	51	0	0.00	
25	51	0	0.00	
26	51	3	5.88	ADULTS
27	48	4	8.33	
28	44	4	9.09	
29	40	12	30.00	
30	28	10	35.71	
31	18	6	33.33	
32	12	2	16.67	
33	10	1	10.00	
34	9	2	22.22	
35	7	2	28.57	
36	5	5	100.00	

Table 2. Age-specific fertility of FAW on castor

Age interval in days	Number of females alive/ number of eggs at the initial stage of the cohort	Average number of eggs laid by female in each interval (x) / sex ratio			Innate rate for increase in numbers (r_c =loge R_0/ Tc) = (0.1923) r_c is 0.1923					
					Intrinsic rate of increase (r_m) by iteration When r_m value is 0.1934			Intrinsic rate of increase (r_m) " e-rm.x. lxmx=1) When r_m value is 0.1922l		
x	lx	mx	lxmx	x.lxmx	r_m.x	$e^{rm.x}$	$e^{-rmx.lxmx}$	r_m.x	e^{-rmx}	$e^{-rmx.lxmx}$
26	0.18									
27	0.18									
28	0.18									
29	0.18	880.50	158.49	4596.21	5.609	0.003666	0.5811	5.5738	0.00380	0.60163
30	0.18	227.86	41.02	1230.46	5.802	0.003022	0.1239	5.7660	0.00313	0.12847
31	0.13	641.91	83.45	2586.89	5.995	0.002490	0.2078	5.9582	0.00258	0.21568
32	0.04	694.09	27.76	888.44	6.189	0.002052	0.0570	6.1504	0.00213	0.05921
33	0.03	451.82	13.55	447.30	6.382	0.001691	0.0229	6.3426	0.00176	0.02385
34	0.02	0.00	0.00	0.0000	6.576	0.001394	0.0000	6.5348	0.00145	0.00000
35	0.02	0.00	0.00	0.0000	6.769	0.001149	0.0000	6.7270	0.00120	0.00000
36	0.01	0.00	0.00	0.0000	6.962	0.000947	0.0000	6.9192	0.00099	0.00000
		$\sum$mx = 2896.18	$\sum$lxmx = 324.47	$\sum$x.lxmx = 9749.30			$\sum e^{-rmx.lxmx}$ = 0.9927			$\sum e^{-rmx.lxmx}$ = 1.02884

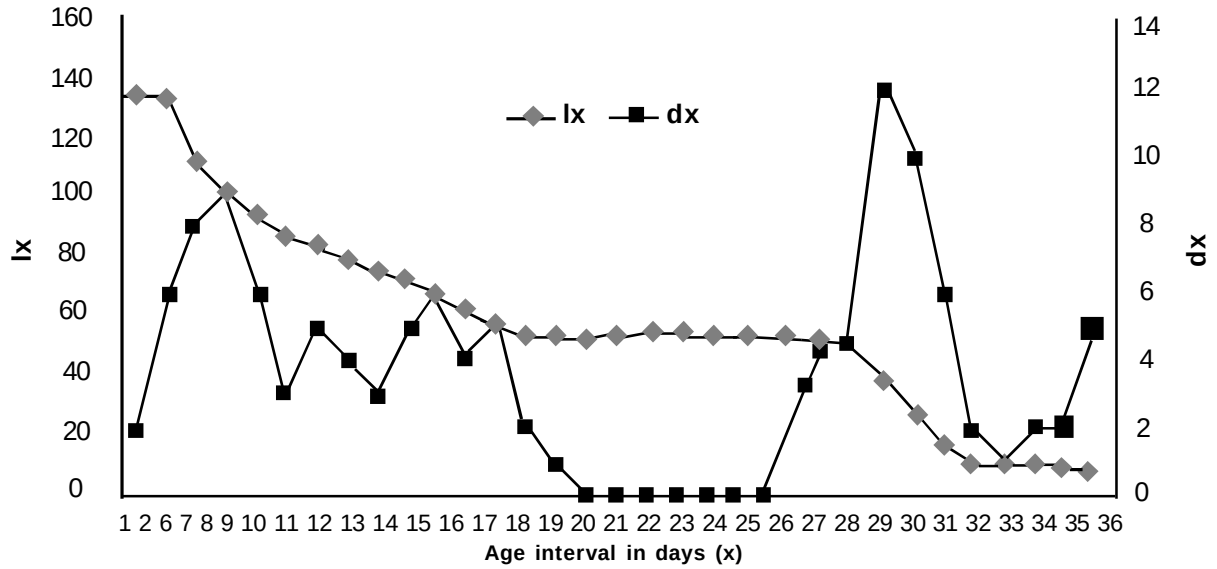

Figure 1. Age-specific survivorship (lx) and mortality (dx) of FAW on castor

(880.50 eggs). No eggs were laid from 34th day. From these observations, it can be inferred that the potential egg laying period was for 5 days. The present findings are in agreement with the results of Supriya *et al*. (2018) who reported potential fecundity of 1651.00 eggs in *S. litura* on castor during third generation. Host plant quality is a key determinant of the fecundity of herbivores insects, affecting insect reproductive strategies, egg size and quality, the allocation of resources to eggs. The choice of oviposition sites may be influenced by plant quality, as may egg or embryo resorption on poor quality host (Awmack and Leather, 2002).

The life parameters *viz*., net reproductive rate (R_0), mean generation time (Tc) and intrinsic rate of increase (r_m) were 324.27, 30.07 days and 0.1922 females/female/day, respectively (Table 2). The present findings were in agreement with the results of Sooravan *et al.* (2005) who reported that the intrinsic rate of natural increase (r_m) of *S. litura* population on the host plant ranged from 0.153 to 0.195 females / female/day. Similarly, the results of Tuan *et al.* (2013) indicated that the intrinsic rate of increase of *S. litura* reared on peanuts was 0.1828 females/female/day. The faster development of immature stages (shorter

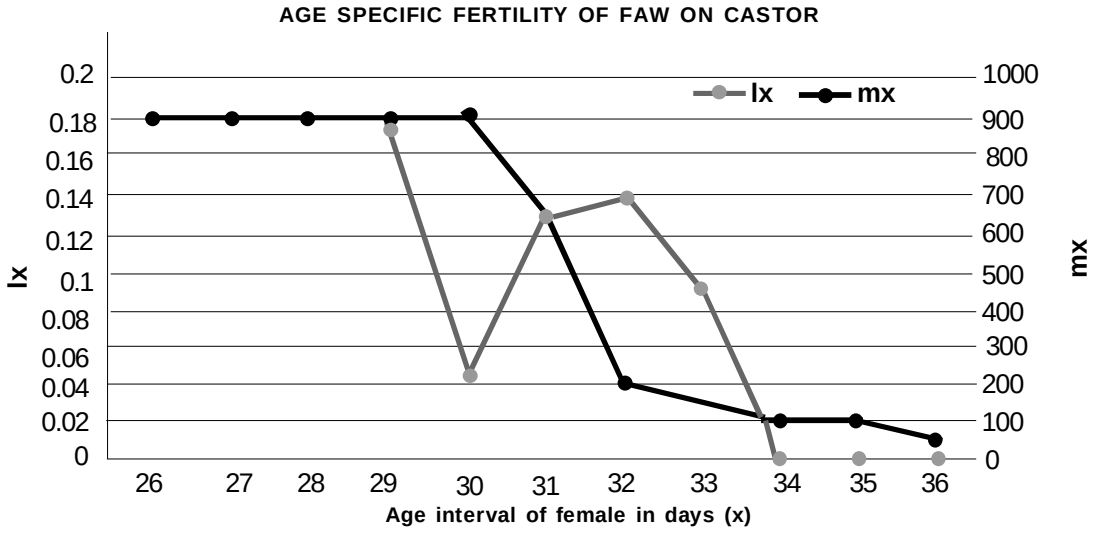

Figure 2. Age-specific survivorship (lx) and fecundity (mx) for female of FAW on castor

generation time), higher survivorship and higher fecundity rates and high value of r_m indicated the susceptibility of the host plant for insect feeding and also pointed out that increased feeding and or higher assimilation rate, both could result in an increased titre of digestive enzymes (Woods, 1999).

Life parameters of FAW on castor

Life parameters represented in (Table 3) *viz*., finite rate of increase (ë) *i.e.,* @&'s/@&/day (female off-springs/female/day) was 1.556 while other parameters like weekly multiplication rate (WMR), doubling time (DT) and annual rate of increase (ARI) were recorded as 3.83, 3.60 and 1.4223 x 10^{70}, respectively. Sunil *et al.* (2019) who reported that the *S. litura* on groundnut also recorded WMR and DT as 3.09 and 4.29 days, respectively, similar to present observations on FAW. Sex ratio (F:M) (1:1.13) indicated high male moth population compared to females.

Stable age distribution of FAW on castor

The study on the influence of each developmental stage of *S. frugiperda* on castor towards the stable age distribution was calculated by observing the age schedule of birth rate and death rate. In the present studies, the immature stages and pupae contributed to 99.74 per cent (Table 4) and indicated that immature stages contributed highest to the stable age distribution of the population. Similar pattern of distribution of stable age was observed with *S. litura* on castor (Supriya *et al*., 2018; Maghodia and Koshiya, 2008). Instantaneous birth rate and instantaneous death rate of FAW on castor were recorded as 0.501 and 0.309, respectively indicating lower death rate compared to birth rate.

Table 3. Life- parameters of FAW on castor

S.No	Life-Parameters	Formulae	Values obtained
1	Finite rate of increase @&'offsprings/@&/day	λ = antilog e^{rm}	1.556
2	Weekly multiplication rate	WMR= $(e^{rm})^7$	3.83
3	Doubling time	DT= (log2 e/r_m)	3.60
4	Annual rate of increase (ARI)	Antilog e^{rm} 365	1.4223 x 10^{70}
5	Sex ratio	F:M	1:1.13
6	Hypothetical F_2 females	$(R_0)^2$	105151.03

Table 4. Stable-age -distribution of FAW on castor

x	Lx	x+1	r_m(x+1)	e (-r_m(x+1)	e (-r_m(x+1) X Lx	Px. e(-r_m(x+1)	px.100	% Contribution
1	0.99	2	0.38440	0.68086	0.67585	0.21366	21.366	(38.46 %) I-Instar
2	0.96	3	0.57660	0.56181	0.54115	0.17108	17.108	
3	0.92	4	0.76880	0.46357	0.42778	0.13524	13.524	(24.14 %) II-Instar
4	0.88	5	0.96100	0.38251	0.33610	0.10625	10.625	
5	0.84	6	1.15320	0.31563	0.26457	0.08364	8.364	(14.90 %) III-Instar
6	0.79	7	1.34540	0.26044	0.20682	0.06538	6.538	
7	0.73	8	1.53760	0.21490	0.15722	0.04970	4.970	(11.73 %)
8	0.68	9	1.72980	0.17732	0.11995	0.03792	3.792	
9	0.64	10	1.92200	0.14631	0.09414	0.02976	2.976	IV-Instar
10	0.61	11	2.11420	0.12073	0.07412	0.02343	2.343	(5.61 %) V-Instar
11	0.58	12	2.30640	0.09962	0.05787	0.01829	1.829	

Table 4. (Contd.)

x	Lx	x+1	$r_m(x+1)$	e $(-r_m(x+1)$	e $(-r_m(x+1)$ X Lx	Px. $e(-r_m(x+1)$	px.100	% Contribution
12	0.56	13	2.49860	0.08220	0.04563	0.01443	1.443	
13	0.53	14	2.69080	0.06783	0.03566	0.01127	1.127	(2.641%) VI- Instar
14	0.49	15	2.88300	0.05597	0.02716	0.00859	0.859	
15	0.45	16	3.07520	0.04618	0.02071	0.00655	0.655	
16	0.42	17	3.26740	0.03811	0.01583	0.00500	0.500	(0.887 %) Pre-pupa
17	0.39	18	3.45960	0.03144	0.01225	0.00387	0.387	
18	0.38	19	3.65180	0.02594	0.00982	0.00311	0.311	(1.385%) Pupal
19	0.38	20	3.84400	0.02141	0.00803	0.00254	0.254	
20	0.38	21	4.03620	0.01766	0.00662	0.00209	0.209	
21	0.38	22	4.22840	0.01458	0.00547	0.00173	0.173	
22	0.38	23	4.42060	0.01203	0.00451	0.00143	0.143	
23	0.38	24	4.61280	0.00992	0.00372	0.00118	0.118	
24	0.38	25	4.80500	0.00819	0.00307	0.00097	0.097	
25	0.38	26	4.99720	0.00676	0.00253	0.00080	0.080	
26	0.36	27	5.18940	0.00558	0.00203	0.00064	0.064	(0.206 %) Adults
27	0.34	28	5.38160	0.00460	0.00156	0.00049	0.049	
28	0.31	29	5.57380	0.00380	0.00117	0.00037	0.037	
29	0.25	30	5.76600	0.00313	0.00078	0.00025	0.025	
30	0.17	31	5.95820	0.00258	0.00044	0.00014	0.014	
31	0.11	32	6.15040	0.00213	0.00024	0.00007	0.007	
32	0.08	33	6.34260	0.00176	0.00014	0.00004	0.004	
33	0.07	34	6.53480	0.00145	0.00010	0.00003	0.003	
34	0.06	35	6.72700	0.00120	0.00007	0.00002	0.002	
35	0.04	36	6.91920	0.00099	0.00004	0.00001	0.001	
36	0.02	37	7.11140	0.00082	0.00001	0.00000	0.000	
				3.16318		**100.00**		

Birth rate (β) = 3.163, px = 1/(β) = 0.316

Instantaneous birth rate (b) = (r_m. β /e^{rm}-1) = 0.501

Instantaneous death rate (d) = (b-r_m) = 0.309

Life expectancy of FAW on castor

The life expectancy (ex) of *S. frugiperda* on castor declined gradually with the advancement in development of the insect (Table 5). The life expectancy of newly hatched larvae was 10.32 days. The mortality rate (dx) increased gradually which was indicated by a decrease in the lx value, and mortality was comparatively high at 31-35 days of pivotal age. The expectation of further life was reduced to 2.00 days from 10.32 days in the beginning (Fig 3). These results are supported by Dhabi *et al.* (2009) who reported that the life expectancy of *P. xylostella* was more in early stages and declined with the advancement of age.

CONCLUSION

The present study signifies the first complete report on the life history data of *S. frugiperda* on castor. The higher survivorship of immature stages indicated the potential damage to crop by larval instars which needs to be managed by appropriate management strategies. The higher net reproductive rate, fecundity and shorter mean generation time explained the strong environmental adaptability of FAW, which is responsible for the serious damage to castor in near future. Our findings provide useful information in predicting population dynamics and understanding the potential damage that could be incurred by *S. frugiperda* infestation on castor.

Table 5. Life-expectancy of FAW on castor

Pivotal age (Days)	Number Surviving to the beginning of the age interval	Number dying during 'x'	Mortality rate per hundred alive at beginning of the age interval	Alive between age 'x' and 'x+1'	Number of the individuals life days beyond 'x'	Expectation of further life (e_x)
x	lx	dx	dx*100/lx	lx+(lx+1)/2	Tx	Tx/lx*2
1-5	136	24	17.65	192.00	701.50	10.32
6-10	112	31	27.68	152.50	509.50	9.10
11-15	81	22	27.16	110.50	357.00	8.81
16-20	59	8	13.56	84.50	246.50	8.36
21-25	51	0	0.00	76.50	162.00	6.35
26-30	51	33	64.71	60.00	85.50	3.35
31-35	18	13	72.22	20.50	25.50	2.83
36-40	5	5	100.00	5.00	5.00	2.00

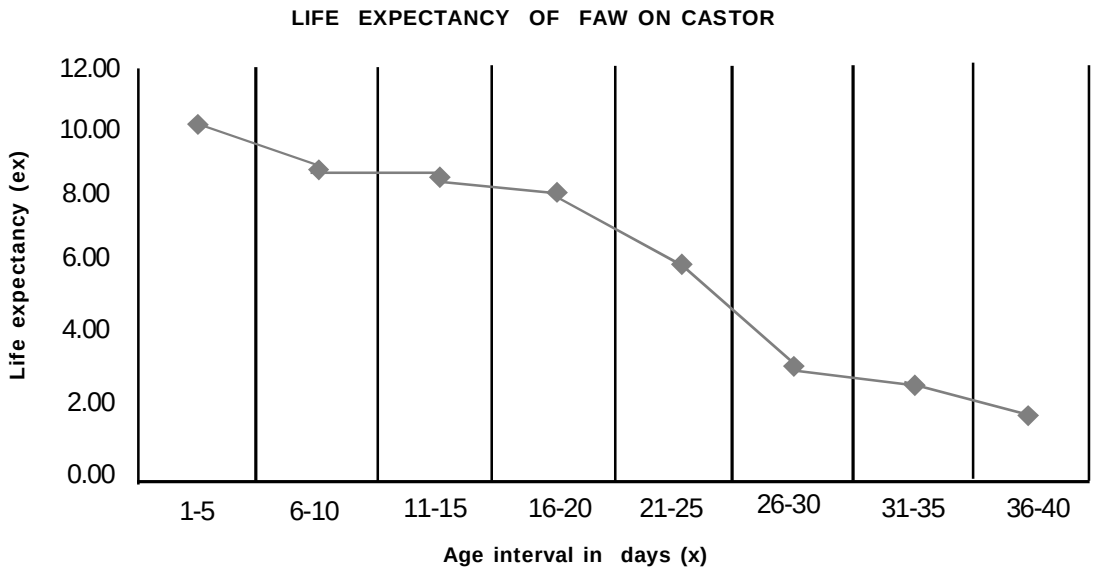

Figure 3. Life expectancy (ex) of FAW on castor

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Research Article
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GENE ACTION AND ORDER EFFECTS FOR HIGH FRUITING EFFICIENCY IN INTER AND INTRA SPECIFIC HYBRIDS OF COTTON

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ABSTRACT

Quadriallel analysis provides information on all types of gene actions *viz.,* additive, dominance and epistatic components besides giving information on order of parents in double cross combinations for obtaining superior transgressive segregants. Present study was made to obtain information on gene actions controlling the number of bolls per plant in 45 inter and intra specific cotton double cross hybrids from four *Gossypium hirsutum* L. (Adilabad kapas-1, ADB-39, ARBC-64 and CNH 115) and two *Gossypium barbadense* L. (Suvin and Phule rukhmai) genotypes. The general and specific combining ability effects were significant. Three double crosses (Adilabad kapas-1 × Phule rukhmai) (ADB-39 × Suvin), (Adilabad kapas-1 × Phule rukhmai) (ARBC-64 × CNH 115) and (ADB-39 × Suvin) (ARBC-64 × CNH 115) recorded high four line interaction effects of lines i, j, k and l due to particular arrangements. Dominance variation found to be more than additive variance while, among the epistatic interaction, additive × additive × additive was high fallowed by dominance × dominance and additive × dominance. Hence pure line development would be more successful with selection in the later generations involving parents derived from above double crosses.

Keywords: Cotton, double crosses, fruiting efficiency, inter specific crosses, quadriallel analysis

Cotton is an economically important crop globally and has high commercial value for its natural fibre. Rapid development of new technologies in the textile industry has driven the demand for higher fibre quality of cotton. Number of bolls per plant is the important yield contributing character in cotton and has been the foremost among the breeding targets for cotton breeder. Parental selection for hybridization based on *per se* performance alone may not be able to deliver superior recombinants. Therefore, the parents chosen on the basis of their genetic value and combining ability and, the breeding procedure decided on the basis of gene action involved in the expression of character is selected. In this context, quadriallel analysis is one of the proven mating schemes as this provides information on all types of gene actions *viz.,* additive, dominance and epistatic components besides giving information on order effects of parents in double cross combinations for obtaining superior transgressive segregants. A double cross hybrid is first generation progeny of a cross of two unrelated F_1 hybrids symbolized as (1 × 2) (3 × 4), where 1, 2, 3 and 4 are the four parents and (1 × 2) and (3 × 4) are the two F_1's (Rawling and Cockerham, 1962). The two cultivated tetraploid genetically diverse cotton species *Gossypium hirsutum* L. and *Gossypium barbadense* L. are included in this study for development cotton hybrids having more number of bolls coupled with good fibre properties like spun length, micronaire and bundle strength.

MATERIAL AND METHODS

The experimental material used in this study comprised of 45 double cross hybrids developed from 6 inbred lines. Four inbred lines of *G. hirsutum* L. [Adilabad kapas-1(1), ADB-39 (2), ARBC-64 (5) and CNH 115 (6)] and two inbred lines of *G. barbadense* L. [Suvin (3) and Phule rukhmai (4)] received from cotton scheme, Agricultural Research Station, Adilabad were crossed in half diallel fashion (Griffing, 1956) to obtain fifteen single crosses. Later these hybrids were again crossed in diallel fashion in such a way that only unrelated crosses were involved in obtaining 45 double crosses. These forty-five double crosses are evaluated in two replications during *kharif*, 2020 at ARS, Adilabad

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and quadriallel analysis was carried out as per Rawlings and Cokerhams (1962). Each genotype was evaluated in the 2.4 m × 6.0 m plot size with a spacing 120 cm between the rows and 60 cm between plants in a row. Ten plants from each cross were randomly chosen for recording boll number and the mean data was subjected to quadriallel analysis.

RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed significant 1-line general, 2-line specific, and 2, 3, 4-line arrangements. Since only 6 lines were used, variance due to 3 line and 4 line specific effects could not be estimated. ADB-39 had maximum 1-line general effect followed by ARBC-64 (Table 2), the cross combination ADB-39 × CNH 115 exhibited highest positive 2 line general effect (2.07) irrespective of arrangement (Table 3). The specific combination (Suvin × CNH 115) (—) had the highest two-line interaction effect (4.50) of lines i and j in a particular arrangement (ij) (—). Similarly (Suvin × -) (ARBC-64 × -) too had highest two-line interaction effect (1.15) of lines i and j in particular arrangement (i-) (j-). Whereas the above two combinations had recorded negative effects when used in opposite orders clearly indicating the significance of the parental order in crossing programme. Similar results were recorded by Sumalini (2018) in maize for days to 50 percent silking.

Table 1. Analysis of variance

Source	D. f.	Mean squares
Replications	1	113.56
Total	89	100.13
hybrids	44	171.65 **
error	44	28.30
1-line general	5	396.71 **
2-line specific	9	208.10 **
2-line arrangement	9	78.70 *
3-line arrangement	16	151.53 **
4-line arrangement	5	112.64 **

*, **Significant at p< 0.05 and p< 0.01 respectively

Table 2. One-line general (gi) effects in quadriallel analysis

Line i	gi value
Adilabad kapas-1	-0.13
ADB-39	2.17
Suvin	-1.01
Phule rukhmai	-2.39
ARBC-64	1.30
CNH 115	0.06

Table 3. Two-line interaction effect of lines i and j particular arrangement (ij) (..), i.e. t(ij)(..), (i.)(j.), i.e. t(i.)(j.) and S_{ij}, i.e. effect of i and j irrespective of arrangement

Lines	t(ij) ij	t(i.) (..)	S_{ij} (j.)	Lines	t(ij) ij	t(i.) (..)	S_{ij} (j.)
12	-1.51	0.76	-0.17	26	-0.01	0.00	2.07
13	1.42	-0.71	0.08	34	-1.75	0.88	-0.90
14	2.22	-1.11	0.43	35	-2.30	1.15	0.10
15	-1.21	0.60	0.13	36	4.50	-2.25	0.54
16	-0.92	0.46	-0.60	45	1.61	-0.81	0.00
23	-1.88	0.94	-0.83	46	-1.88	0.94	-2.08
24	-0.20	0.10	0.16	56	-1.70	0.85	0.14
25	3.59	-1.79	0.94				

1(Adilabad kapas-1), 2(ADB-39), 3(Suvin), 4(Phule rukhmai), 5(ARBC-64) and 6(CNH 115)

Three line interaction effect in particular and irrespective of arrangement

With respect to the specific order effect of three out of four parents, i.e. (ij) (k-) type, the double cross i.e. (Suvin × ARBC-64) × (Phule rukhmai × -) was found to be the best combination (Table 4). On the basis of the overall performance of any three parents in all possible combinations (Table 5), irrespective of the arrangement (S_{ijk}), the best triplet was ADB-39 × ARBC-64 × CNH-115. However, the order of these parents in a cross matters and can be seen by changing the arrangement of the parents in a particular cross. A change in the arrangement of the parents of the best combination of three parents (Suvin × ARBC-64) (Phule rukhmai × -) which had the highest desirable positive effect (6.13) had given a negative effect (-2.95) in other combination (Phule rukhmai × ARBC-64) × (Suvin × -). Similarly when the same parents are combined but in some other order (Suvin × Phule rukhmai) × (ARBC-64 × -) it had a specific combination effect in a negative direction (-3.17). The 3-line specific effect of these parents irrespective of arrangement was -0.10. This observation clearly shows the significance of the order in which the parents have to be involved in multiple crosses. Similar findings were also reported (Essam El-Hashash, 2012) in double cross hybrids of cotton for this trait.

Table 4. Three-line interaction effect of lines i, j and k due to particular arrangement (ij)(k.) i.e. tij.k

Lines (ij)(k.)	tij.k	Lines (ij)(k.)	tij.k	Lines (ij)(k.)	tij.k	Lines (k.) (ij)(k.)	tij.k
(12)(3.)	-0.92	(15)(6.)	1.98	(25)(4.)	-4.54	(36)(2.)	-4.05
(12)(4.)	4.12	(16)(2.)	2.09	(25)(6.)	0.2	(36)(4.)	-2.97
(12)(5.)	-0.95	(16)(3.)	-1.34	(26)(1.)	-1.35	(36)(5.)	2.83
(12)(6.)	-0.74	(16)(4.)	0.85	(26)(3.)	1.33	(45)(1.)	-0.23
(13)(2.)	-0.02	(16)(5.)	-0.67	(26)(4.)	1.23	(45)(2.)	-0.28
(13)(4.)	-3.12	(23)(1.)	0.93	(26)(5.)	-1.2	(45)(3.)	-2.95
(13)(5.)	0.06	(23)(4.)	-0.91	(34)(1.)	-2.81	(45)(6.)	1.85
(13)(6.)	1.66	(23)(5.)	-0.87	(34)(2.)	4.98	(46)(1.)	2.51
(14)(2.)	-5.75	(23)(6.)	2.72	(34)(5.)	-3.17	(46)(2.)	0.95
(14)(3.)	5.93	(24)(1.)	1.63	(34)(6.)	2.76	(46)(3.)	0.21
(14)(5.)	0.96	(24)(3.)	-4.07	(35)(1.)	2.91	(46)(5.)	-1.8
(14)(6.)	-3.36	(24)(5.)	4.82	(35)(2.)	-1.85	(56)(1.)	-1.31
(15)(2.)	2.92	(24)(6.)	-2.18	(35)(4.)	6.13	(56)(2.)	1.00
(15)(3.)	-2.97	(25)(1.)	-1.97	(35)(6.)	-4.88	(56)(3.)	2.05
(15)(4.)	-0.74	(25)(3.)	2.72	(36)(1.)	-0.31	(56)(4.)	-0.04

1(Adilabad kapas-1), 2(ADB-39), 3(Suvin), 4(Phule rukhmai), 5(ARBC-64) and 6(CNH 115)

Table 5. Three-line interaction effect of lines i, j and k appearing together irrespective of arrangement i.e. S_{ijk}

Line ijk	S_{ijk}	Line ijk	S_{ijk}	Line ijk	S_{ijk}	Line ijk	S_{ijk}
123	-1.26	135	0.25	234	-1.16	256	1.97
124	0.54	136	0.38	235	-0.61	345	-0.1
125	-0.22	145	0.96	236	1.37	346	-1.33
126	0.6	146	-1.43	245	0.74	356	0.66
134	0.79	156	-0.75	246	0.2	456	-1.61

1(Adilabad kapas-1), 2(ADB-39), 3(Suvin), 4(Phule rukhmai), 5(ARBC-64) and 6(CNH 115)

Four line interaction effect in particular and irrespective of arrangement

Three double cross hybrids viz. (Adilabad kapas-1 × Phule Rukhmai) × (ADB-39 × Suvin), (Adilabad kapas-1x Phule Rukhmai) × (ARBC-64 × CNH 115) and (ADB-39 × Suvin) × (ARBC-64 × CNH 115) showed maximum interaction effect of 4.73 (Table 6) with a particular arrangement of the parents. On the contrary the parents i.e. Adilabad kapas-1, Phule rukhmai, ADB-39 and Suvin in a specific order (Adilabad kapas-1 × Suvin) (ADB-39 × Phule Rukhmai) had negative interaction effect (-3.51). Soliman (2014) too had recorded similar results for seed cotton yield in 45 double cross hybrids studied. The data clearly suggest that, the order in which parents go into a double cross hybrid can be a deciding factor for its high or low performance. The double cross (Adilabad kapas-1 × Suvin × Phule Rukhmai × ARBC-64) found to have high interaction effect for lines i, j, k and l appearing together irrespective of the arrangement (Table 7) followed by ADB-39 × Suvin × ARBC-64 × CNH 115.

Table 6. Four-line interaction effect of lines i,j,k and l due to particular arrangement (ij) (kl) i.e. tij.kl.

Line (ij)(kl)	tij.kl	Line (ij)(kl)	tij.kl	Line (ij)(kl)	tij.kl
(12)(34)	-1.23	(14)(35)	-3.91	(23)(45)	-2.26
(12)(35)	2.65	(14)(36)	-0.82	(23)(46)	-2.47
(12)(36)	-1.43	(14)(56)	4.73	(23)(56)	4.73
(12)(45)	-1.43	(15)(23)	-2.47	(24)(35)	1.26
(12)(46)	2.65	(15)(24)	2.25	(24)(36)	2.25
(12)(56)	-1.23	(15)(26)	0.22	(24)(56)	-3.51
(13)(24)	-3.51	(15)(34)	0.22	(25)(34)	1.00
(13)(25)	-0.18	(15)(36)	2.25	(25)(36)	-0.82
(13)(26)	3.69	(15)(46)	-2.47	(25)(46)	-0.18
(13)(45)	3.69	(16)(23)	-2.26	(26)(34)	0.22
(13)(46)	-0.18	(16)(24)	1.26	(26)(35)	-3.91
(13)(56)	-3.51	(16)(25)	1.00	(26)(45)	3.69
(14)(23)	4.73	(16)(34)	1.00	(34)(56)	-1.23
(14)(25)	-0.82	(16)(35)	1.26	(35)(46)	2.65
(14)(26)	-3.91	(16)(45)	-2.26	(36)(45)	-1.43

1(Adilabad kapas-1), 2(ADB-39), 3(Suvin), 4(Phule rukhmai), 5(ARBC-64) and 6(CNH 115)

Table 7. Four-line interaction effect of lines i, j, k and l appearing together irrespective of arrangement i.e. S_{ijkl}.

Line ijkl	S_{ijkl}	Line ijkl	S_{ijkl}	Line ijkl	S_{ijkl}
1234	-0.95	1256	0.71	2345	-1.74
1235	-3.93	1345	3.98	2346	-0.79
1236	1.08	1346	-0.66	2356	3.82
1245	2.57	1356	0.71	2456	1.39
1246	0.01	1456	-3.66	3456	-2.55

1(Adilabad kapas-1), 2(ADB-39), 3(Suvin), 4(Phule rukhmai), 5(ARBC-64) and 6(CNH 115)

Genetic component of variance

Additive as well as non additive gene action was involved in the expression of the studied trait (Table 8). Hence, it was considered to partition the digenic component of epistatic variation and it was observed that, the dominance variation found to be more than additive variance. Among the epistatic interactions, additive × additive × additive was high followed by dominance × dominance and additive × dominance. Linghe Zeng *et al.* (2017) also reported higher magnitude of dominance component in double crosses for lint yield and fibre properties. Sumalini *et al.* (2018) also reported high additive × additive × additive type of interaction for the yield and yield contributing characters in double cross maize hybrids. Hence, predominance of dominance variation, additive × additive × additive interaction, suggests a possibility of exploitation of double cross hybrids for identification of superior lines through recurrent selection. On the contrary, Essam El-Hashash (2012), who studied 15 double crosses, reported negative genetic variance for dominance and additive × additive × additive gene interaction governing this character. Yehia (2009) reported predominance of additive × dominance, additive × additive and dominance × dominance type gene interaction in 45 double cross hybrids of Egyptian cotton which is in partially agreement with the present findings.

Table 8. Genetic components of variance

Source	Value
Additive Genetic Variance	-616.51
Variance due to Dominance Deviation	76.81
Additive × Additive Component of Variance	864.91
Additive × Dominance Component of Variance	-1567.23
Dominance × Dominance Component of Variance	2396.90
Additive × Additive × Additive Genetic Variance	3134.462

CONCLUSION

The parent ADB-39 was found to contribute high average line effect, hence can be used as best general combiner for this trait. Three double crosses viz. (Adilabad kapas-1 × Phule Rukhmai) × (ADB-39 × Suvin), (Adilabad kapas-1 × Phule rukhmai) × (ARBC-64 × CNH 115) and (ADB-39 × Suvin) × (ARBC-64 × CNH 115) exhibited similar high four line interaction effects for lines i, j, k and l due to the particular arrangement. Higher dominance variance for a trait, suggests that the hybrid development would be more rewarding than the pure lines. However double cross hybrids in cotton are not economically viable and hence pure line selections from potential double crosses can be identified through pedigree method of breeding.

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Research Article
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PATHOGENIC VARIABILITY AMONG THE ISOLATES OF *FUSARIUM OXYSPORUM* F. SP. *LYCOPERSICI (FOL)* CAUSING WILT OF TOMATO IN TELANGANA STATE

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ABSTRACT

Tomato is very often affected by several diseases incited by pathogens such as fungi, bacteria, viruses and nematodes. Among the fungal diseases, Fusarium wilt of tomato caused by *Fusarium oxysporum* f. sp. *lycopersici (Fol)*, is one of the most destructive diseases across the world causing severe economic losses, wherever tomato is grown. Roving surveys were conducted in major tomato crop growing areas of Telangana state *viz*., Adilabad, Sangareddy and Rangareddy during the year 2017- 18. Fifteen isolates of *Fusarium oxysporum* f. sp. *lycopersici* collected from different tomato growing areas of Telangana were studied for their pathogenic variability and was observed that, *Fol* isolate collected from Adilabad district was found to be more virulent in causing disease incidence and disease severity when inoculated to susceptible tomato cv. Pusa Ruby compared to the other fourteen isolates collected from different places of Telangana. All the *Fol* isolates were found to be pathogenic by causing diseased wilt symptoms on cv. Pusa Ruby. Further, all the fifteen isolates were characterized at molecular level with species specific primer ITS 1(5'TCCGTAGGTGAACCTGCGG-32) and ITS 4 (5'-TCCTCCGCTTATTGATATGC-32) and by using ISSR primers which revealed the relationship among the fifteen isolates with varied degree of coefficient.

Keywords : *F.oxysporum* f. sp. *lycopersici*, Fusarium wilt, pathogenic variability, telangana state, tomato

Tomato (*Lycopersicon esculentum* Mill.), a "fruity vegetable", native of Peru, South America, is a popular and widely grown annual vegetable crop with weak woody stem, growing to a height of 1-3 meters under family Solanaceae , also known as Nightshades throughout the world (Mirza, 2007). In India, tomato is the third important vegetable crop grown after potato and onion. The major tomato growing states in India are Odissa, Madhya Pradesh, Karnataka, Chhattisgarh, Andhra Pradesh and Telangana. In Telangana, tomato is cultivated in an area of 4,148 ha, with production 1171.50 Mt and productivity of 12 Mt ha^{-1} (Horticulture Statistics, 2018). The major tomato growing districts in Telangana are Adilabad, Rangareddy and Sangareddy. Its tangy flavour contributed to the dish, making it a favourite additive in all the regular cuisines across the world. In India, tomato is the third important vegetable crop grown after potato and onion with an area of 0.78 Mha, and production and productivity with 19,759 Mt and 25.04 Mt ha^{-1} respectively, and was grown mainly as *rabi* in plains and as a summer and rainy season crop in hills. Tomato is very often affected by several diseases incited by pathogens such as fungi (Fusarium wilt, early blight, anthracnose, Verticillium wilt *etc*) bacteria (wilt and canker), viruses (leaf curl and tomato spotted wilt) and nematodes. Among all the fungal diseases that infect tomato, Fusarium wilt of tomato caused by *Fusarium oxysporum* f. sp. *lycopersici* (Sacc.), Snyder and Hans, is one of the most serious and destructive diseases across the world (Sheu and Wang, 2006) causing severe economic losses, wherever tomato is grown (Sudhamoy *et al*., 2009). Under these circumstances, integration of cultural, chemical and biological methods have played a major role in managing the Fusarium wilt disease of tomato (Singh *et al*., 2015). Adequate information is lacking with respect to variability among the isolates and source of genetic resistance. Knowledge on pathogenic variation among the races of pathogen is very much essential for effective disease management strategy especially for breeding resistant varieties. Keeping in view the importance of tomato crop, the present investigation was carried out to find the pathogenic variability among the *Fol* isolates for effective disease management strategies.

MATERIAL AND METHODS

Wilt diseased tomato plant were identified during roving surveys from major tomato growing areas

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(Table 1) and were brought to laboratory, washed under running tap water to remove adhered soil particles, surface sterilized with 1 per cent NaOCl (Sodium hypochlorite) solution for 1 to 2 min followed by rinsing twice with sterile distilled water, then dried between sterile filter papers for 10 to 15 min. Infected and discoloured stem portions were cut into small pieces with sterilized knife and again washed with distilled water followed by disinfection for one minute with 1 per cent sodium hypo chlorite solution. They were again washed thrice with distilled water to remove residues of sodium hypo chlorite and then transferred aseptically under laminar air flow system onto sterilized Petri plates containing PDA medium. The plates were incubated at room temperature at 27 $\pm$ 2 ^{0}C for 10 days for development of typical mycelial growth of associated causal organism.

were sub cultured on Petri plates having with PDA medium and were allowed to grow at 27 $\pm$ 2^{0}C for 10 days.

To determine the *forma specials* of the collected *Fol* isolates and to prove Koch's postulates, fifteen isolates of *Fol* were tested for pathogenicity. On confirmation of pathogenicity by observing wilting diseased symptoms on tomato plants, reisolation of causal organism *i.e., Fol*, was done and the fifteen *Fol* isolates were designated serially from *Fol* 1 to *Fol* 15 and studied further for its pathogenic variability.

The wilt affected tomato plants exhibiting external symptoms *viz*., drooping of leaves, yellowing, stunted growth, initially yellowing on one side of the plant on lower leaves and branches, browning and death of entire plant at advanced stage of infection.

Table 1. List of *Fol* isolates collected from different villages of Telangana State (2017-18)

Isolate No.	Village	District	GPS Points
Fol 1	Gudihatnoor	Adilabad	19.5293° N, 78.5121° E
Fol 2	Indervelley	Adilabad	19.3014° N, 79.0826° E
Fol 3	Salewada	Adilabad	19.4281° N,78.4026° E
Fol 4	Tosham	Adilabad	19.6578° N, 78.5314° E
Fol 5	Dandumailaram	Rangareddy	17.2291° N, 78.7760° E
Fol 6	Raipole	Rangareddy	17.2038° N, 78.7150° E
Fol 7	Manchal	Rangareddy	17.1605° N, 78.2077° E
Fol 8	Yacharam	Rangareddy	17.2044° N, 78.4001° E
Fol 9	Damarigidda	Rangareddy	16.8188° N, 77.5032° E
Fol 10	Thadlapally	Rangareddy	17.6297° N, 78.0837° E
Fol 11	Gummadidala	Sangareddy	17.6847° N, 78.3686° E
Fol 12	Nallavelli	Sangareddy	**17.2751**° N**, 78.7972**° E
Fol 13	Jharasangam	Sangareddy	17.7637° N, 77.7122° E
Fol 14	Zaheerabad	Sangareddy	17.6814° N, 77.6074 ° E
Fol 15	Chinna hyderabad	Sangareddy	17.6314° N, 78.3326° E

The isolated fungus cultures associated with wilt diseased specimens were identified based on cultural and morphological characters (micro and macro conidial characters and mycelial colours) with the help of monograph, The *Fusarium* (Booth, 1971; Nelson *et al*., 1983), Illustrated Genera of Imperfect Fungi (Barnet and Hunter, 1998) and CMI descriptions.

The identified cultures were further purified by single hyphal tipping method (Rangaswami, 1958) and

On proper identification the infected plants were uprooted and checked for vascular discolouration by split opening the stem, which is chief characteristic symptom of Fusarium wilt of tomato. Pathogenic variability of *Fol* isolates were assessed by calculating Per cent disease incidence (PDI) and Disease severity separately for all the fifteen isolates.

$$\text{Per cent disease incidence (PDI)} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

Mean Per cent disease incidence was calculated as per the formula (Mandhare and Patil, 1993).

Disease severity index

Disease severity was recorded from 15th day onwards for each *Fol* isolate on 0 to 4 rating scale (Weitang *et al.,* 2004), at an interval of 10 days up to the age of 45 day old and per cent disease severity was calculated as per the given formula.

$$\text{Disease severity index} = \frac{\text{Sum of all disease ratings}}{\text{Total number of plants observed} \times \text{Maximum disease rating}} \times 100$$

Disease rating scale (Weitang *et al.,* 2004)

0 = No symptoms

1 = Slight infection (< 25 per cent showing wilted symptoms)

2 = Moderate infection (26 to 50 per cent showing wilted symptoms)

3 = Extensive infection (51 to 75 per cent showing wilted symptoms)

4 = Complete infection (> 75 per cent of the plant wilted and dead)

Fifteen *Fol* isolates were categorized based on disease severity index into five categories, as follows (Charoenporn *et al*., 2010).

Disease severity	Isolate category
0	Avirulent
< 25 per cent	Low virulent
26 to 50 per cent	Moderately virulent
51 to 75 per cent	Virulent
> 76 per cent	Highly virulent

Root dip inoculation technique

Root dip inoculation technique was employed to find pathogenic variation in fifteen isolates of *Fol* on susceptible cv. Pusa Ruby under green house conditions as per the procedure mentioned. Twenty one day old seedlings of tomato susceptible cv. Pusa Ruby were uprooted slowly from protrays, abrased gently at root portions, dipped in the spore suspension having spore load of *Fol* @ 1×10^6 /ml for 15 to 20 mins (Sheu and Wang, 2006), separately for all fifteen *Fol* isolates. After successful completion of root dip inoculation technique, seedlings were transplanted into pots having autoclaved sterilized soil of two kg each. Three replications were maintained in a completely randomized design with five seedlings per each replication. The pots were supplied with essential nutrients along with proper irrigation as per the protocol for proper establishment to express wilt symptoms similar to that of field conditions. The tomato seedlings cv. Pusa Ruby were dipped in sterile distilled water as check were transplanted into pots under similar conditions.

RESULTS AND DISCUSSION

Pathogenic variability among the fifteen *Fol* isolates were ascertained on the basis of the ability to cause disease and the temporal variation in appearance of the specific symptoms *viz*., drooping, yellowing, wilting or plant death. The results indicated that gradual increase in expression of wilt symptoms started from first fortnight to third fortnight and the appearance of characteristic wilt symptoms varied depending on the virulence level of each *Fol* isolate. Disease severity was calculated as per the appearance of the symptoms caused by each *Fol* isolate on 0-4 rating scale.

All the fifteen *Fol* isolates evaluated in the present study were found to be pathogenic in nature by causing the disease and producing characteristic symptoms *viz*., yellowing, drooping, netted appearance and wilting susceptible tomato cv. Pusa Ruby. Temporal and symptomatic wilt expression from 15th day of inoculation (DOI) to 45th DOI clearly differentiated these fifteen *Fol* isolates under five different groups *viz.,* Avirulent (denoted by DSI-0), low virulent (DSI-1), moderately virulent (DSI-2), virulent (DSI-3) and highly virulent (DSI-4).

At 15th date of inoculation (DOI)

The results (Table 2) revealed that per cent disease incidence (PDI) and disease severity index (DSI) varied significantly among fifteen *Fol* isolates which ranged from minimum PDI of 20.00 per cent (*Fol* - 1, 2, 3, 5, 6, 7, 9, 10, 11, 12, 13, 14) and grouped under DSI -1 (low virulent) to maximum PDI of 60 per cent (*Fol*- 4) which was grouped under DSI -2 *i.e.*, moderately virulent.

Among the fifteen *Fol* isolates, it was found that *Fol*-4 isolate was the only moderately virulent isolate at 15th DOI.

At 30th date of inoculation (DOI)

The results (Table 2) revealed that significant differences were observed among fifteen *Fol* isolates. *Fol* - 1, 2 and 6 recorded least per cent wilt disease incidence of 26.66 per cent with DSI 2, while maximum per cent wilt disease incidence (100.00%) was observed in *Fol* - 4 with DSI 4. The other *Fol* isolates recorded per cent incidence of 66.66 % (*Fol* - 3), 40.00 % (*Fol* - 7 and *Fol* - 9), 66.66 % (*Fol* - 3 and *Fol* - 5), 73.33 % (*Fol* - 12) and 80.00 % (*Fol* - 8 and *Fol* - 10).

At 30th DOI, *Fol* isolates - 4, 8 and 10 were found significantly different from other *Fol* isolates in causing PDI and disease severity index and were grouped under DSI 4 *i.e*., highly virulent with disease severity of > 75 per cent of the plant being affected.

At 45th date of inoculation (DOI)

The data recorded on 45th DOI revealed that pathogenic virulence varied significantly among the fifteen *Fol* isolates with minimum PDI of 66.66 per cent (*Fol* - 1, 2, 6, 9 and 13) to maximum of 100 per cent (*Fol* - 4, 8, 10 & 12) followed by per cent disease incidence of 93.33 per cent (*Fol*- 3, 14 and 15), 86.66 per cent (*Fol*- 5) and 73.33 per cent (*Fol* - 7 and 11).

Isolate *Fol* - 4 (Plate 1) was found to be highly virulent among the other *Fol* isolates, based on virulence in causing wilt disease incidence and disease severity on susceptible variety *i.e*., Pusa Ruby from 15th DOI to 45th DOI.

Table 2. Pathogenic variability of *F. oxysporum* f. sp. *lycopersici* isolates on susceptible cv. Pusa

PDI (%) and wilting severity (%) by *Fol* isolates						
Isolate	**PDI (%) (15 DAP)**	**Disease severity index (%)**	**PDI (%) 30 DAP**	**Disease severity index (%)**	**PDI (%) 45 DAP**	**Disease severity index (%)**
Fol 1	20.00(26.55)	4.00	40.00(30.77)	12.00	66.66(54.96)	33.33
Fol 2	20.00(26.55)	5.33	26.66(30.77)	11.66	66.66(54.96)	50.00
Fol 3	20.00(26.55)	4.00	66.66(54.96)	21.66	93.33(81.13)	43.33
Fol 4	60.00(50.74)	12.00	100.00(90.00)	51.66	100.00(90.00)	90.00
Fol 5	20.00(26.55)	4.00	66.66(54.96)	20.00	86.66(72.27)	51.66
Fol 6	20.00(26.55)	4.00	26.66(30.77)	16.66	66.66(54.96)	45.00
Fol 7	20.00(26.55)	6.66	40.00(39.21)	11.66	73.33(59.18)	60.00
Fol 8	33.33(34.99)	10.00	80.00(63.40)	36.66	100.00(90.00)	83.33
Fol 9	20.00(26.55)	5.00	40.00(39.21)	16.66	66.66(54.96)	53.50
Fol 10	20.00(26.55)	5.00	80.00(63.40)	23.30	100.00(90.00)	81.66
Fol 11	20.0(26.55)	5.00	33.33(34.99)	15.00	73.33(59.18)	58.30
Fol 12	20.00(26.55)	5.00	73.33(59.18)	28.33	100.00(90.00)	78.30
Fol 13	20.00(26.55)	5.00	26.60(30.77)	10.00	66.66(54.96)	40.00
Fol 14	20.00(26.55)	5.00	73.30(59.18)	31.66	93.33(81.13)	83.30
Fol 15	26.66(30.77)	6.66	73.30(59.18)	31.60	93.33(81.13)	78.30
C.D	4.645 (p=0.05)	-	10.14	-	14.8	-
S.E(m)±	1.59	-	3.48	-	5.08	-
C.V	9.52	-	12.14	-	12.35	-

Note: PDI - Percent disease index, DAP - Days after planting

Figures in parentheses are arcsine values

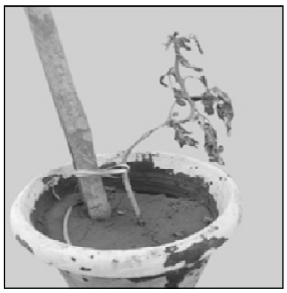

Plate 1. Wilted tomato plant by highly virulent isolate *Fol*-4

Plate 2. Control (Uninoculated)

Grouping of *Fol* isolates based on disease severity index

Based on wilt disease severity, the results revealed that (Table 3) fifteen *Fol* isolates were grouped into five groups as follows, Avirulent (DSI=0), low virulent (DSI=1), moderately virulent (DSI=2), virulent (DSI =3) and highly virulent (DSI= 4).

Similar variation in the pathogenicity of different isolates were reported by Jaruhar and Prasad (2011), Sumangala *et al*. (2013), Chopada *et al*. (2015) and Sivakumar *et al*. (2018) and based on the disease severity, isolates were grouped as most virulent and least virulent isolates. Similar results were reported by various workers, *viz.*, Abdel *et al.* (2012) and Sundaramoorthy and Balabaskar (2013) which revealed that maximum PDI of 88.80, 78.50 and from 43.40 to 46.50 was observed with virulent isolate under glass house conditions.

Nirmaladevi and Srinivas (2012) also reported that pathogenic variability among 69 *Fol* isolates when tested against five susceptible varieties of tomato by adopting root cut and dipping technique and, based on the mean disease severity (MDS), virulence of *Fol*, isolates were recorded as weak pathogenic with low (MDS: < 25%), moderate pathogenic (MDS: 25-50%) or high pathogenic (MDS: > 50%).

Reis *et al*. (2005) reported that the transmission of *F. oxysporum* f. sp. *lycopersici,* can be through by contaminated seeds of tomato which would further aggravate the establishment of different physiological variants with distinct variability from one location to other location even in same regions and districts. Mishra *et al*. (2010) reported that variation among *Fol* isolates may be due to mutation in the genome.

CONCLUSION

Pathogenic variability studies revealed that Isolate *Fol* - 4, collected from Adilabad district was found to be more virulent in causing disease incidence and disease severity when inoculated to susceptible tomato cv. Pusa Ruby. Further, all the fifteen isolates were characterized at molecular level with species specific primer ITS 1 (5'TCCGTAGGTGAACCTGC GG-32) and ITS 4 (5'-TCCTCCGCTTATTGATATGC-32) and by using ISSR primers which revealed the relationship among the fifteen isolates with varied degree of coefficient.

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Table 3. Grouping of *F. oxysporum* f. sp. *lycopersici* isolates based on disease severity

DSI	Disease Severity (%)	15th DOI	30th DOI	45th DOI
0 (Avirulent)	0	-	-	-
1 (Low virulent)	1-10	*Fol* -1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 13,14 & 15	-	-
2 (Moderately virulent)	11 - 25	*Fol*- 4	*Fol* - 3,5,6,7,9, 10, 11 & 13	-
3 (Virulent)	26 - 50	-	*Fol*-1,8,12,14 & 15	*Fol* - 1,3,6 & 13
4 (Highly virulent)	> 51	-	*Fol*- 4	*Fol* - 2, 4, 5, 7, 8, 9, 10, 11, 12, 14 & 15

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Research Article
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PROFITABILITY OF ZERO TILL MAIZE INFLUENCED BY NUTRIENT AND WEED MANAGEMENT PRACTICES

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ABSTRACT

Field experiment was carried out at College Farm, Agricultural College, Aswaraopet, Professor Jayashankar Telangana State Agricultural University, during *rabi* 2016-17 and 2017-18 with three nutrient management (M_1: 100% RDF, M_2: 75% RDF +25% N through Vermicompost and M_3: 75% RDF + 25% N through FYM) and four weed management treatments (S_1: Control; S_2: Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2,4 - D 0.5 kg ha^{-1} at 25 DAS; S_3: Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS and S_4: Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS) in both the years. Among nutrient management practices, highest total number of grains cob^{-1} (313.76, 324.38), test weight (21.97, 22.44 g), grain yield (5399, 5766 kg ha^{-1}) and straw yield (6674, 7041 kg ha^{-1}) were recorded with 75% RDF + 25% N through Vermicompost (M_2) and at par with 75% RDF + 25% N through FYM (M_3) during *rabi* 2016-17 and 2017-18 respectively. Out of weed management treatments tested, highest total number of grains cob^{-1} (365.26, 378.62), test weight (22.06, 22.54 g), grain yield (6275, 6708 kg ha^{-1}) and straw yield (7475 and 7908 kg ha^{-1}) were observed with Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS {S_4} and comparable with {S_3} Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS during *rabi* 2016-17 and 2017-18 respectively. Under various nutrient treatments, significantly 75% RDF + 25% N through Vermicompost (M_2) fetched higher net returns (47882, 53424 ₹ ha^{-1}) while B:C ratio (2.42, 2.59) was maximum with 75% RDF + 25% N through FYM (M_3) in two successive years respectively. Amongst weed management practices, significantly higher net returns (61282, 67886 ₹ ha^{-1}) were obtained with S_4 (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS) and B:C ratio (2.76, 2.95) was realized with {S_3} Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS in *rabi* 2016-17 and 2017-18 respectively.

Keywords: FYM, nutrient management, vermicompost, weed control, zero till maize

Maize, a crop of worldwide economic importance together with rice and wheat provides approximately more than 30% of the food calories to more than 4.5 billion people. In India, maize is considered as third most important crop among the cereals and used as staple food in many developing countries (Yakadri *et al*., 2015). Worldwide, maize is grown in an area of 197.20 Mha with production of 1148.49 Mt and productivity of 5824 kg ha^{-1} (FAOSTAT, 2019-20) while 9.56 M ha with 28.77 Mt production and 3006 kg ha^{-1} productivity in our country. In Telangana, maize occupies an area of 0.56 M ha with production and productivity of 2.99 Mt and 5347 kg ha^{-1} respectively (CMIE, 2019-20). Maize yields in India need to be increased significantly so as to meet food, feed and industrial needs.

In the conventional rice-maize cropping system, due to efficient land preparation after rice, the problem of rejuvenation of rice stubble is not encountered and initial weed problem is solved with pre-emergence application of atrazine. Wider spacing, erect and initially slow growth of crop encountered weed problems under zero till maize after rice harvest. However, residues retained on the soil surface, serve as physical barrier for emergence of weeds, moderate the soil temperature, conserve soil moisture, add organic matter and improve the nutrient-water interactions. Rice-maize sequence in traditional areas aids in overcoming planting difficulties in rice fallows, reduces weeds and improves fertilizers and water use efficiency with a potential benefit in saving the cost of production from ₹ 3800-5500 ha^{-1} (DMR Technical Bulletin, 2009). Due to the nutrient extraction of high-yielding crops, nutrient demand in rice-maize systems can be considerable, yet integrated nutrient management studies for maize hybrids are extremely productive, but limited in South Asia (Timsina *et al*., 2010). Hence, finding out viable nutrient and weed management strategy for the crop are still promising management recommendation in order to increase productivity of maize during both the

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seasons in any region. Therefore, the present research was carried out with an objective to study the effect of nutrient and weed management during both the seasons to maximize grain yield.

MATERIAL AND METHODS

The field experiment was conducted at College Farm, Agricultural College, Aswaraopet, Professor Jayashankar Telangana State Agricultural University situated at an altitude of 162 m above mean sea level at 17^{0}24'54" N latitude and 81^{0}10'34 E longitude which is located in the Central Telangana Agro Climatic Zone. The soil of the experimental site was sandy clay loam in texture, pH of 6.72, low in available nitrogen, medium in phosphorus and available potassium. The experiment was conducted during *rabi* 2016-17 and 2017-18 in split-plot design with three nutrient treatments (M_1: 100% RDF, M_2: 75% RDF + 25% N through Vermicompost and M_3: 75% RDF + 25% N through FYM) as main plots and four weed management practices [S_1: Control; S_2 : Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2,4 - D 0.5 kg ha^{-1} at 25 DAS; S_3 : Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS and S_4 : Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS] as sub-plots replicated thrice in *rabi* 2016-17 and 2017-18. Recommended dose of fertilizer was 180: 80: 80 kg N, P_2O_5 and K_2O ha^{-1} as urea, single super phosphate and muriate of potash was applied as per the treatments. The entire P_2O_5 and half of K_2O were applied at sowing. Nitrogen was applied in three equal splits (1/3rd each at basal, knee-high and tasseling). Similarly, the remaining potassium was applied along with urea during second top dressing at tasseling. Gross plot size and net plot size were 6.0 m x 4.8 m and 3.6 m x 3.2 m respectively during both seasons. Five cobs were randomly chosen from net plot and in each cob, the total number of grains cob^{-1} was counted and finally the mean of total number of grains cob^{-1} was determined. Weight of hundred grains was recorded from the composite sample of net plot area produce in each treatment and their weight was recorded and expressed in grams. The kernels from the air-dried cobs from each net plot were separated, cleaned and dried to obtain at least 14 per cent moisture. Weight of grains of each plot was recorded separately and expressed as grain yield in kg ha^{-1}. Stover from the net plot area was weighed after properly sun dried and indicated stover yield in kg ha^{-1}. The expenditure incurred from sowing to harvest was worked out for each treatment and expressed in ha^{-1} as cost of cultivation. Gross monetary returns (0 ha^{-1}) were calculated by multiplying the grain and stover yield with their respective prevailing market price (Perin *et al*., 1979). Net returns (0 ha^{-1}) was calculated by subtracting the cost of cultivation from gross returns for each treatment. Benefit cost ratio was calculated by dividing gross returns with cost of cultivation for each treatment. The data were analyzed statistically applying analysis of variance technique for split plot design. The significance was tested by 'F' test (Gomez and Gomez, 1984).

RESULTS AND DISCUSSION

Total number of grains cob^{-1}

Total no. of grains cob^{-1} were significantly influenced by different nutrient and weed management practices however, their interaction effect was non-significant in zero till maize and followed a similar trend during both the years of experimentation (Table 1 and figure 1).

All the nutrient treatments had recorded substantial impact on total number of grains cob^{-1}. M_2 [75% RDF + 25% N through Vermicompost] recorded significantly higher total number of grains cob^{-1} (313.76 and 324.38), which was at par with 75% RDF + 25% N through FYM {M_3} (297.68 and 309.95) during both the years. However, lowest number of grains cob^{-1} (261.20, 270.44) were realized with M_1 [100% RDF].

All the weed control treatments recorded significantly higher number of grains cob^{-1} over control. S_4 [Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS] treatment was found significantly superior with higher total number of grains cob^{-1} of 365.26 and 378.62 which was statistically at par with S_3 [Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS] (355.63, 368.54) during both years. Significantly lower number of grains cob^{-1} was observed with control (145.98, 153.49).

Constant and enhanced nutrient availability resulted in taller plants and maximum dry matter accumulation thereby increased the size of source that led to increased sink in forming the cob length and in turn resulted in more total number of grains cob^{-1} under zero till maize. Prabhat Kumar *et al*. (2018), Yadav *et al*. (2016) and De and Bandyopadhyay (2013) also reported same findings.

Table 1. Yield parameters and yield (kg ha^{-1}) of zero till maize influenced by nutrient and weed management (*Rabi*, 2016-17 and 2017-18)

Treatments	Total no. of grains cob^{-1}		Test weight (g)		Grain yield (Kg ha^{-1})		Stover yield (Kg ha^{-1})	
	2016-17	2017-18	2016-17	2017-18	2016-17	2017-18	2016-17	2017-18
Main plots: Nutrient Management								
M_1	261.20	270.44	21.29	21.86	4305	4626	5580	5901
M_2	313.76	324.38	21.97	22.44	5399	5766	6674	7041
M_3	297.68	309.95	21.78	22.28	5064	5419	6339	6694
SEm±	7.48	7.86	0.32	0.46	129	145	6198	6545
CD (*P=0.05*)	29.36	30.85	NS	NS	507	569	154	158
Sub plots: Weed Management								
S_1	145.98	153.49	21.19	21.75	2394	2603	3794	4003
S_2	296.66	305.71	21.51	22.09	4950	5277	6250	6577
S_3	355.63	368.54	21.96	22.39	6071	6494	7271	7694
S_4	365.26	378.62	22.06	22.54	6275	6708	7475	7908
SEm±	10.09	10.34	0.25	0.28	203	217	6198	6545
CD (*P=0.05*)	29.98	30.73	NS	NS	604	644	239	256
Interaction								
M × S								
SEm±	17.47	17.92	0.44	0.49	352	376	413	444
CD (*P=0.05*)	NS	NS	NS	NS	NS	NS	NS	NS
S × M								
SEm±	19.49	20.08	0.58	0.72	383	411	450	479
CD (*P=0.05*)	NS	NS	NS	NS	NS	NS	NS	NS

NS = Non Significant, *fb* = followed by, HW = hand weeding

Nutrient Management

M_1: 100% RDF

M_2: 75% RDF + 25% N through Vermicompost

M_3: 75% RDF + 25% N through FYM

Weed Management

S_1 : Control

S_2 : Atrazine 50 WP 500 g ha^{-1}+ Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2, 4-D 0.5 kg ha^{-1} at 25 DAS

S_3 : Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 gha^{-1}) at 25 DAS

S_4 : Topramezone 0.03 kg ha^{-1}+ Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS

Minimum weed growth due to tank mix application of atrazine and topramezone followed by hand weeding had curtailed the crop weed competition for growth factors and finally led to higher total number of grains cob^{-1} when compared to other treatments thus improving maize plant nutrition. Similar increase in total number of grain cob^{-1} was also noticed by Rajbir Singh *et al*. (2018), Kandasamy (2018) and Swetha (2015) due to less weed competition under farmer's practice.

Test weight (100 grain weight)

During both years, nutrient and weed management practices did not show any significant influence on the test weight of maize during both the years. However, comparatively higher test weight was recorded with *rabi* 2017-18 than *rabi* 2016-17. In both years, none of the nutrient and weed management treatments had an interaction effect on test weight, as shown in table 1 and figure 2.

The test weight was not affected by any of the nutrient treatments. Out of three nutrient management practices in *rabi* 2016-17 and 2017-18, it was portrayed that 75% RDF + 25% N through Vermicompost treatment registered highest test weight of 21.97 and 22.44 g followed by 75% RDF + 25% N through FYM (21.78 and 22.28 g). Lowest test weight of 21.29 and 21.86 g was observed with 100% RDF.

Over the course of two years, weed management practices had no discernible effect on test weight. Relatively higher test weight was obtained with S_4 [Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS] (22.06 and 22.54 g) than S_3 [Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS] (21.96 and 22.39 g), S_2 [Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2,4 - D 0.5 kg ha^{-1} at 25 DAS] (21.51 and 22.09 g) and S_1 [Control] (21.19 and 21.75 g).

Adequate nutrients promoted meristematic and physiological activities *viz.,* leaf area, root development, crop dry matter production etc., resulting in efficient absorption and translocation of nutrients. These activities promote higher photosynthetic activities leading to the production of enough assimilate for subsequent translocation to various sinks and hence the production of higher test weight of maize. The results are in conformity with Muhammad Abid *et al*. (2020) and Govardhan Rao and Ramana (2017).

Efficient translocation of photo assimilates from the source to grains due to lowest crop weed competition even during the later stages of crop growth. Similar findings were reported by Modak *et al*. (2019) and Srinivasulu *et al*. (2016).

Grain yield (Kg ha^{-1})

During two years of investigation, the effect of nutrient and weed management practices on grain yield had the pronounced effect (Table 1 and figure 3). However, statistically there was no significant interaction found between nutrient and weed treatments. In comparison to 2016-17, the yield in 2017-18 was greater. The grain yield obtained in the M_2 [75% RDF + 25% N through Vermicompost] treatment (5399 and 5766 kg ha^{-1}) was significantly higher and comparable with M_3 [75% RDF + 25% N through FYM] (5064 and 5419 kg ha^{-1}). Over two years, M_1 [100% RDF] had the lowest grain yield of 4305 and 4626 kg ha^{-1}.

S_4 *i.e.* Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS (6275 and 6708 kg ha^{-1}) engendered the highest grain yield among the weed management practices and comparable with S_3 [Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 25 DAS] (6071 and 6494 kg ha^{-1}) followed by S_2 [Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2,4 - D 0.5 kg ha^{-1} at 25 DAS] (4950 and 5277 kg ha^{-1}). Lowest grain yield was noted with S_1 [Control] (2394 and 2603 kg ha^{-1}). However, S_4 and S_3 were at par with each other.

The progressive mineralization and release of nutrients over time often results in better nutrient use efficiency with integrated nutrient management than the application of nutrients through inorganic fertilizers only. Higher growth, greater absorption and better translocation of assimilates from source to sink could have resulted in increased yield if nutrients were available at more frequent intervals. These findings are similar to those of Dibakar Ghosh *et al*. (2020) and Sigaye *et al*. (2020).

Curtailment in weed density and dry matter ensured efficient weed control by the use of topramezone and atrazine in combination which was coupled with hand weeding once. Increased exploitation of growth resources and improved reproductive potential of the crop might have contributed to the highest grain yield. The findings are consistent

with those of Mali *et al*. (2019), Modak *et al*. (2019) and Sandhya Rani *et al*. (2019).

Stover yield (Kg ha^{-1})

During *rabi* 2016-17 and 2017-18, nutrient and weed management practices had a substantial impact on the yield of zero till maize. However, their interaction was not significant, as seen in table 1. A review of data on nutrient management treatments in *rabi* 2016-17 and 2017-18 revealed that M_2 [75% RDF + 25% N through Vermicompost] (6674 and 7041 kg ha^{-1}) generated highest stover yield, followed by M_3 [75% RDF + 25% N through FYM] (6339 and 6694 kg ha^{-1}) and both were statistically identical, while M_1 *i.e.* 100% RDF registered lowest stover yield of 5580 and 5901 kg ha^{-1}.

S_4 [Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS] was produced the highest stover yield (7475 and 7908 kg ha^{-1}) and was almost analogous to S_3 [Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS] (7271 and 7694 kg ha^{-1}). However, as compared to S_1 [Control], S_2 [Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2,4- D 0.5 kg ha^{-1} at 25 DAS] (6250 and 6577 kg ha^{-1}) was superior (3794 and 4003 kg ha^{-1}).

Increased stover output might be attributed to improved nutrient availability, which led to faster cell elongation, as well as greater leaf area and photosynthesis, which resulted in increased dry matter. Subhash Babu *et al*. (2020) Radha Kumari and Sudheer (2016) reported similar findings. Better weed management may have aided crop growth, allowing for better dry matter output and enhanced stover yield. Rajbir Singh *et al*. (2018) and Mahadevaiah and Sagar (2018) found similar results.

Economics

Nutrient and weed management practices significantly influenced gross returns, net returns and B:C ratio in both the years of experimentation. Similar trend in the gross and net returns was observed as that of grain yield (Table 2).

Cost of cultivation (₹ ha^{-1})

Cost of cultivation was invariably altered by various nutrient and weed management practices imposed in zero till maize. During both the years of study, same costs were incurred in the production of maize and no change was observed in the trend. Regarding nutrient treatments of zero till maize, cost of cultivation was higher with M_2 [75% RDF + 25% N through vermicompost] (35780 ₹ ha^{-1}) followed by M_3 [75% RDF + 25% N through FYM] (31746 ₹ ha^{-1}) and lowest with M_1 [100% RDF] (29157 ₹ ha^{-1}).

Among four weed management practices imposed, higher costs were incurred to S_4[Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* intercultivation/HW at 35 DAS] (35618 ₹ ha^{-1}) which was closely followed by S_3 [Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS] (33986 ₹ ha^{-1}) and S_2 [Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2,4 - D 0.5 kg ha^{-1} at 25 DAS] (31021 ₹ ha^{-1}). The cost of cultivation was lowest with control (28285 ₹ ha^{-1}).

Gross returns (₹ ha^{-1})

Among three nutrient management practices, gross returns were highest with M_2 [75% RDF + 25% N through vermicompost] (83602, 89204 ₹ ha^{-1}) which was in parity with M_3 [75% RDF + 25% N through FYM] (78507, 83992 ₹ ha^{-1}). However, the lowest gross returns were noticed with M_1 [100% RDF] (66929, 71823 ₹ ha^{-1}) in two years. With respect to weed management practices across two years, S_4 [Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS] realized maximum gross returns of 96900, 103504 ¹ ha^{-1} which was at par with S_3 [Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS] (93783, 100229 ₹ ha^{-1}) when compared to S_2 [Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2, 4 - D 0.5 kg ha^{-1} at 25 DAS] (76795, 81777 ₹ ha^{-1}) and least with control (37906, 41091 ₹ ha^{-1}).

Highest gross returns might be due to higher grain and stover output attributed to integrated use of fertilizers and organic manures. The results were in accordance with Subhash babu *et al*. (2020) and Maruthupandi and Jayanthi (2018). Higher grain yield might be due to better uptake of growth resources by the crop than weeds throughout the crop growth period resulting in taller plants stature, increased leaf area index, dry matter production and ultimately final yield (Dibakar Ghosh, 2020, Sandya Rani, 2020 and Patil, 2020).

Table 2. Economics of zero till maize influenced by nutrient and weed management (*Rabi*, 2016-17 and 2017-18)

Treatments	Cost of cultivation (Rs. ha^{-1})		Gross returns (Rs. ha^{-1})		Net returns (Rs. ha^{-1})		B:C Ratio	
	2016-17	2017-18	2016-17	2017-18	2016-17	2017-18	2016-17	2017-18
Main plots: Nutrient Management								
M_1	29157	29157	66929	71823	37772	42667	2.25	2.42
M_2	35780	35780	83602	89204	47822	53424	2.30	2.45
M_3	31746	31746	78507	83922	46761	52176	2.42	2.59
SEm±			1993	2169	1993	2169	0.07	0.08
CD (*P=0.05*)			7827	8516	7827	8516	NS	NS
Sub plots: Weed Management								
S_1	28285	28285	37906	41091	9621	12806	1.34	1.45
S_2	31021	31021	76795	81777	45774	50756	2.48	2.64
S_3	33986	33986	93783	100229	59797	66243	2.76	2.95
S_4	35618	35618	96900	103504	61282	67886	2.72	2.90
SEm±			3137	3324	3137	3324	0.10	0.11
CD (*P=0.05*)			9321	9877	9321	9877	0.29	0.31
Interaction								
M × S								
SEm±			5434	5758	5434	5758	0.17	0.18
CD (*P=0.05*)			NS	NS	NS	NS	NS	NS
S × M								
SEm±			5901	6279	5901	6279	0.18	0.20
CD (*P=0.05*)			NS	NS	NS	NS	NS	NS

NS = Non Significant, Stover cost = 1.00 0 kg^{-1}, Grain cost = 14.25 0 kg^{-1}

Nutrient Management

M_1 : 100% RDF

M_2 : 75% RDF + 25% N through Vermicompost

M_3 : 75% RDF + 25% N through FYM

Weed Management

S_1 : Control

S_2 : Atrazine 50 WP 500 g ha^{-1}+Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2,4-D 0.5 kg ha^{-1} at 25 DAS

S_3 : Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 gha^{-1}) at 25 DAS

S_4 : Topramezone 0.03 kg ha^{-1}+ Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS

Net returns (₹ ha^{-1})

Net returns of maize were significantly influenced by various nutrient and weed management practices while no significance was observed with interaction effect during both the years of study. Nutrient treatments reported that highest net returns were fetched with M_2 [75% RDF + 25% N through Vermicompost] (47822, 53424 ₹ ha^{-1}), which was however, comparable with M_3 [75% RDF + 25% N through FYM] (46761, 52176 ₹ ha^{-1}) and M_1 [100%

RDF] (37772, 42667 ₹ ha^{-1}) in the order of descent over two years.

With regard to weed management treatments, S_4 [Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS] realized significantly higher net returns of 61282, 67886 ₹ ha^{-1} than S_3 [Atrazine 50 W P 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS] (59797, 66243 ₹ ha^{-1}), which in turn were at par among themselves and significantly higher than S_2 [Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2, 4 - D 0.5 kg ha^{-1} at 25 DAS] (45774, 50756 ₹ ha^{-1}). The net returns were lowest with control during *rabi* 2016-17 and 2017-18.

Higher yields might be due to constant availability of nutrients throughout the crop growth period might have resulted in higher net returns. Results are in line with Kailash Raman Bhatt *et al*. (2020) and Yadav *et al*. (2016). Higher net returns could be probably due to increased yields of grain and stover as a result of less weed infestation. These results were substantiating with Pene Botlhe (2019).

B:C ratio

B:C ratio of zero till maize did not vary significantly due to different nutrient management practices imposed in maize while a significant effect was found with weed treatments. Interaction of B:C ratio was also not significant during *rabi* 2016-17 and 2017-18. M_3 [75% RDF + 25% N through FYM] (2.30, 2.45) had realized highest B:C ratio as compared to M_2 [75% RDF + 25% N through Vermicompost] (2.42, 2.59) and lowest was noticed in the treatment 100% RDF (2.25, 2.42) across two years.

B:C ratio of 2.76, 2.95 was obtained highest with S_3 [Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS], which was on par with the S_4 [Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS] (2.72, 2.90), but significantly superior over S_2 [Atrazine 50 WP 500 g ha^{-1} + Paraquat 24 SL 0.6 kg ha^{-1} *fb* 2, 4 - D 0.5 kg ha^{-1} at 25 DAS] (2.48, 2.64) in both the years of study. Lowest B:C ratio of 1.34, 1.45 was realized with control treatment according to weed treatments.

Chemical fertilizers in combination with organic manures enhanced constant nutrient supply, which may have improved yield components such as the number of grains row^{-1}, number of grains cob^{-1} and test weight, resulting in enhanced grain and stover output and a higher benefit-to-cost ratio. Amandeep Kaur and Mahesh Kumar (2019) and Shah and Kumar (2014) found similar results.

The highest benefit-to-cost ratio was likely achieved as a result of excellent weed control at critical phases, which led to greater stature, yield components and yield, which resulted in a higher B:C ratio. These findings were agree with Mitra *et al*. (2018) and Rajbir Singh *et al*. (2018).

CONCLUSION

The results of current investigation clearly indicated that, significantly higher number of grains cob^{-1}, test weight, grain yield, gross returns, net returns and B:C were observed with integrated nutrient management 75% RDF + 25% N through Vermicompost and 75% RDF + 25% N through FYM in *rabi* 2016-17 and 2017-18 respectively compared to application of inorganic fertilizers *i.e.* 100% RDF alone. Similarly, Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1} at 15 DAS *fb* HW at 35 DAS {S_4} and {S_3} Atrazine 50 WP 500 g ha^{-1} *fb* (Topramezone 0.03 kg ha^{-1} + Atrazine 50 WP 500 g ha^{-1}) at 25 DAS were found to be better weed control option for maize respectively during two consecutive *rabi* seasons to obtain maximum yields and higher returns.

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Research Article
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STUDIES ON HETEROSIS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN HYBRID RICE

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ABSTRACT

Forty hybrids of rice were developed by crossing four CMS lines and ten restorers in line x tester mating design for estimation of heterosis for various yield and yield contributing traits and to identify best hybrid combinations. Heterosis in desirable direction was recorded for important yield and its attributes *viz.,* days to 50% flowering, plant height, panicle length, number of productive tillers per plant, spikelet fertility (%), 1000 grain weight and grain yield per plant (g). The analysis of variance (line x tester) revealed that parents and hybrids differed significantly for all the characters, indicating considerable amount of genetic variability in the material studied. Parents vs hybrids comparison was found significant for all the characters except panicle length. Some of these heterotic crossings have turned out to be the best specific crosses and exhibited desirable *per se.* Among the heterotic crosses, JMS 13A x RNR 2354 (Grain yield per plant), JMS 13A x JGL 35126 (Duration of fifty percent flowering), CMS 23A x RNR 2354 (Plant height), CMS 59A x RNR 26085 (Panicle length), CMS 13A x RNR 21571 (Number of productive tillers per plant), CMS 59A x ZGY 1 (Spikelet fertility) and CMS 23A x RNR 28411(1000 grain weight) were found to be superior expressing heterosis, heterobeltiosis and standard heterosis in desirable direction. The results of the present study indicated the potential of these parental lines in the improvement of grain yield of rice hybrids.

Keywords: CMS lines, heterosis, heterobeltiosis, hybrid rice, yield

Rice has been one of the world's most important food crops, feeding more than half of the world's population (Khush, 1997). In Asia and Pacific region, rice is the main staple food and the most important source of employment and income for rural people. The rice productivity has reached a plateau, so it is therefore imperative to find other way to increase the yield potential of rice cultivars in a sustainable manner. Of the various approaches contemplated to break the existing yield barriers in rice, hybrid rice technology offers an opportunity to boost the yield of rice under fragile conditions since hybrid rice varieties have a yield advantage of 15- 20% over the conventional high yielding varieties (Virmani *et al.,* 1996). Breeding strategies for developing hybrids with high yield potential and better grain quality require the expected level of heterosis and combining ability. Heterosis or hybrid vigour is a genetic phenomenon initially reported in maize and now being used in many commercial crops including rice. Heterosis breeding is an important tool which can facilitate yield enhancement and helps enrich many other desirable quantitative traits in rice. In short, the study of heterosis helps the plant breeder in eliminating the less productive crosses in early generations. Now a days, it has been mandatory to exploit heterosis in self-pollinated crops like rice for enhancing crop productivity. Selection of parental cross combinations should be exploited on the basis of manifestation of heterosis for varietal improvement (Satheesh kumar *et al.,* 2016). The objective of this experiment was to estimate the magnitude of heterosis for grain yield and its component characters.

MATERIAL AND METHODS

The present study was carried out during two seasons *viz., Kharif* 2020 and *Rabi* 2020-21 at Regional Agricultural Research Station, Polasa, Jagtial, Professor Jayashankar Telangana State Agricultural University, Telangana. The research material consists of four WA cytoplasmic male sterile (CMS) lines (JMS 13A, CMS 23A, CMS 46A and CMS 59A) and ten testers (RNR 26085, ZGY 1, RNR 2354, RNR 28359, RNR 21571, IR 72, JGL 35126, JGL 35047, JGL 34551 and RNR 28411) identified as fertility restorers for the respective CMS lines. All the 14 genotypes were obtained from Regional Agricultural Research Station, Polasa and Rice Research Center, Rajendranagar, Professor Jayashankar Telangana State Agricultural University, Hyderabad. During *Kharif*-2020, all the genotypes were seeded in nursery at three dates,

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10 days apart and transplanted in crossing block at 25 days after sowing. Ten genotypes were crossed with all the four CMS lines in Line x Tester fashion (Kempthorne, 1957). Thus, the set of 40 rice hybrids were generated.

In *Rabi* 2020-21, fourteen parents, 40 F_1 hybrids along with two checks were planted in randomized block design with three replications at Regional Agricultural Research station, Polasa, Jagtial. All the parents, F_1s and checks were planted in 2 rows of 3 m length with 20 x 15 cm spacing. Recommended agronomic, cultural and plant protection practices were followed. Five competitive plants for each parent, F_1 and check per replication were randomly selected for data generation.

Duration of fifty percent flowering was taken from the date of sowing to complete exertion of the panicle in 50 per cent of the total plants in the net plot. Plant height was measured from base of the plant to last grain of the main panicle. The length of panicles from each plant was measured in centimeters from neck node to the tip of top most grain in a panicle and was expressed in cm. Number of productive tillers per plant at maturity were counted and recorded. Spikelet fertility was calculated as the ratio of fertile grains per panicle to the total number of grains in a panicle and was expressed as percentage. Thousand well filled grains were counted from a random sample of each entry in each replication and weighed with the help of electronic top pan balance in grams. The matured panicles were harvested, threshed, cleaned and dried to 12-14% moisture level. The grain yield plant^{-1} was recorded in grams. Data obtained was subjected to analysis of variance and heterosis, heterobeltiosis, standard heterosis over high yielding checks were computed as given by Liang *et al.* (1971) and expressed in percentage as follows:

Heterosis over mid parent: Heterosis was expressed as per cent increase or decrease observed in the F_1 over the mid-parent as per the following formula.

$$\text{Heterosis (\%) } (h_1) = \frac{\overline{F1} - \overline{MP}}{\overline{MP}} \times 100$$

Where, $\overline{F1}$ = Mean of F_1

$\overline{MP}$ = Mean of mid parents

Heterobeltiosis: Heterobeltiosis was expressed as per cent increase or decrease observed in F_1 over the better parent as per the following formula.

$$\text{Heterosis (\%) } (h_2) = \frac{\overline{F1} - \overline{BP}}{\overline{BP}} \times 100$$

Where, $\overline{BP}$ = Mean of better parent (for the characters like days to 50% flowering, earliness are desirable so the early parents are taken as better parents).

Standard heterosis: Standard heterosis was expressed as per cent increase or decrease observed in F_1 over standard checks.

$$\text{Standard heterosis \% } (h_3) = \frac{\overline{F1} - \text{Mean of check}}{\text{Mean of check}} \times 100$$

Test of significance of heterosis: To test the significance for different types of heterosis needs computation of standard error (SEm). For relative heterosis and heterobeltiosis, SEm were calculated based on error mean squares (EMS) from the ANOVA table consisting of parents and crosses, whereas, EMS from the RBD ANOVA (s^2e) table based on all the treatments (parents, crosses and check) were used for standard heterosis.

The significance of heterosis *viz.,* heterosis over mid parent , heterobeltiosis and standard heterosis was then tested by comparing the calculated 't' value with the tabulated 't'-value for appropriate error degrees of freedom at 5 per cent and 1 per cent level of significance (0.05 and 0.01 level of probability), respectively.

$$\text{'t'}_{cal} \text{ for heterosis and heterobeltiosis} = \frac{\overline{F1} - \text{Mean of mid parents or better parent}}{SEM}$$

Where, SEm = $\sqrt{2EMS/r}$, EMS = Error mean of squares and r = Number of replications

$$\text{t'}_{cal} \text{ for Standard heterosis} = \frac{\overline{F1} - \text{Mean of check}}{SEM\overline{SC}}$$

Where, SEm $\overline{SC} = \sqrt{2\sigma\sigma^2/r}$

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences for all the treatments. It indicates presence of sufficient variability among the genotypes studied. So, further heterotic studies were carried out. The exploitation of heterosis can enhance yield from 30 to 40 per cent and can also enrich the domesticated crops with the most important traits of qualitative and quantitative nature. In the present study, heterosis over

mid parent (relative heterosis), over better parent (heterobeltiosis) and over the standard check (standard heterosis) were estimated in 40 hybrids for seven characters to search out the best combination of parents giving a high degree of useful heterosis and characterization of parents for their prospects for future use in breeding programs. For plant height and days to 50% flowering, negative heterosis is desirable but for rest of the characters, positive heterosis is desirable.

For days to 50 per cent flowering, negative heterosis is considered important as induction of earliness is one of the desirable characters for hybrid rice genotypes. Among the forty hybrids tested, 33 hybrids exhibited significant negative heterobeltiosis ranging from -18.13 (JMS 13A × JGL 35126) to 4.73 (CMS 23A × RNR 21571) (Table 2). Four hybrids were significantly earlier than the early flowering check, Tellahamsa recorded maximum standard heterosis, of -5.79 (JMS 13A × JGL 35126). Six hybrids recorded significantly negative standard heterosis over hybrid check, US 314 ranging from -6.80 (JMS 13A x JGL 35126) to -2.85 (JMS 13A x RNR 21571). Both negative and positive heterosis resulted over mid parent, better parent and standard checks. Chouhan *et al.,* (2016), Dilruba *et al.,* (2018) and Gokulakrishnan *et al.,* (2018) reported significant heterobeltiosis and standard heterosis in desirable direction.

Short stature is one important trait in rice to withstand lodging especially under high input management, hail storm and high rainfall areas. Negative heterosis is treated as desirable, the negative standard heterosis was observed in 19 hybrids over

Table 1. Analysis of variance (Mean sum of squares) for combining ability for yield and yield components in rice at Jagtial

Source of Variation	DF	DFF	PH	PL	NPT	SF %	TW	GYP (g)
Replicates	2	4.71	2.28	5.87 **	0.67	2.40	0.43	4.59
Treatments	53	64.100 ***	163.07**	10.93 **	8.26**	37.07**	25.48**	79.28**
Parents	13	106.08 ***	209.37**	10.41 **	14.70**	35.01**	44.58**	18.55**
Parent vs. Crosses	1	475.51 ***	662.50**	1.46	16.73**	352.80**	72.68**	945.27**
Crosses	39	39.56 ***	134.84**	11.34 **	5.90**	29.66**	17.90**	77.32**
Line effect	3	30.87	425.95**	32.95 **	7.49	33.23	15.75	111.29
Tester effect	9	45.05	245.83**	17.08 *	10.42*	23.59	43.77**	84.61
Line* Tester effect	27	38.69 ***	65.50**	7.03 **	4.22**	31.29**	9.52**	71.12**
Error	106	2.55	2.309	0.70	0.65	4.13	0.91	4.818

*Significant at P=0.05 level** Significant at P=0.01 level

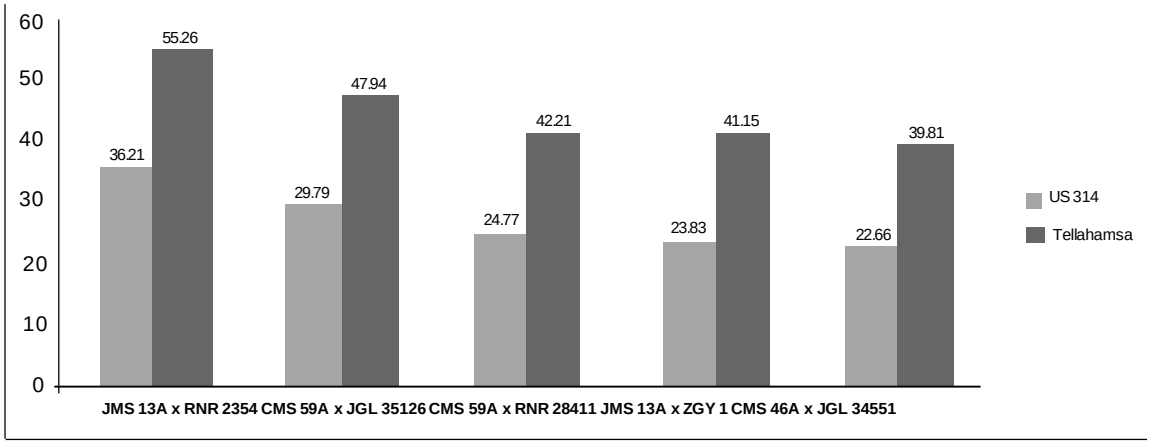

Fig 1. Top five hybrids identified based on standard heterosis percentage over checks US 314 and Tellahamsa

Table 2. Estimates of heterosis, heterobeltiosis and standard heterosis for days to 50 percent flowering and plant height

Crosses	Days to 50 percent flowering				Plant height			
	Heterosis		Standard		Heterosis		Standard	
	MP	BP	US 314	Tella hamsa	MP	BP	US 314	Tella hamsa
JMS 13A x RNR 26085	-11.01 **	-11.56**	0.67	1.76	-7.49**	-12.93**	-6.63**	-1.46
JMS 13A x ZGY 1	-11.46 **	-13.13**	-1.07	0.00	-2.12	-3.44*	-6.11**	-0.91
JMS 13A x RNR 2354	-0.65	-3.75**	9.61**	10.79**	1.25	-1.02	-6.73**	-1.56
JMS 13A x RNR 28359	-2.89 **	-5.63**	7.47**	8.63**	-11.31**	-13.09**	-14.32**	-9.58 **
JMS 13A x RNR 21571	-8.57 **	-15.00**	-2.85**	-1.80*	-12.88**	-13.02**	-17.70**	-13.15 **
JMS 13A x IR 72	-10.72 **	-12.81**	-0.71	0.36	-16.37**	-17.32**	-19.94**	-15.51 **
JMS 13A x JGL 35126	-12.96 **	-18.13**	-6.80**	-5.79**	-4.14**	-5.37**	-8.11**	-3.02 *
JMS 13A x JGL 35047	-7.79 **	-13.13**	-1.07	0.00	-8.93**	-16.08**	-20.60**	-16.21 **
JMS 13A x JGL 34551	-6.89 **	-11.25**	1.10	2.19	-3.18**	-5.08**	-6.52**	-1.35
JMS 13A x RNR 28411	-0.83	-6.88**	6.05**	7.19**	-2.00	-10.87**	2.97*	8.67 **
CMS 23A x RNR 26085	-6.55 **	-14.24**	-3.56*	-2.52	2.37*	-8.24**	-1.59	3.86 **
CMS 23A x ZGY 1	-3.15 **	-10.06**	-1.42	-0.36	-6.93**	-12.78**	-15.18**	-10.49 **
CMS 23A x RNR 2354	-4.96 **	-10.67**	-4.63**	-3.60*	-10.64**	-13.29**	-21.64**	-17.30 **
CMS 23A x RNR 28359	1.06	-5.30**	1.78	2.88*	-4.19**	-10.78**	-12.04**	-7.17 **
CMS 23A x RNR 21571	6.86 **	4.73**	2.49	3.60*	0.29	-4.65**	-10.08**	-5.10 **
CMS 23A x IR 72	1.58	-5.25**	2.85*	3.96**	0.65	-5.49**	-8.49**	-3.42 *
CMS 23A x JGL 35126	1.47 -	1.77	-1.42	-0.36	-13.79**	-19.15**	-21.50**	-17.15 **
CMS 23A x JGL 35047	6.76 **	3.18*	3.77*	4.89**	6.39**	3.08*	-12.35**	-7.50 **
CMS 23A x JGL 34551	2.17	-2.41	0.71	1.80	6.24**	-1.02	-2.52	2.88 *
CMS 23A x RNR 28411	-1.65	-4.63**	-4.63**	-3.60*	-3.65**	-16.37**	-3.62*	1.72
CMS 46A x RNR 26085	2.46 *	-1.27	11.03**	12.23**	-3.67**	-9.56**	-3.00*	2.37
CMS 46A x ZGY 1	-6.16 **	-8.44**	0.36	1.44	-12.66**	-14.05**	-16.43**	-11.80 **
CMS 46A x RNR 2354	-1.18	-2.33	4.27**	5.40**	-3.46**	-5.39**	-10.94**	-6.01 **
CMS 46A x RNR 28359	-5.55 **	-6.95**	0.00	1.08	-11.19**	-13.20**	-14.42**	-9.69 **
CMS 46 A X RNR 21571	2.11	-1.02	3.20*	4.32**	-7.05**	-7.14**	-12.42**	-7.57 **
CMS 46A x IR 72	-6.02 **	-7.87**	0.00	1.08	-11.06**	-12.30**	-15.08**	-10.38 **
CMS 46A x JGL 35126	-2.61 *	-4.44**	-0.36	0.72	-6.89**	-8.32**	-10.97**	-6.05 **
CMS 46A x JGL 35047	-2.08	-3.75**	0.35	1.44	2.04	-5.76**	-11.28**	-6.37 **
CMS 46A x JGL 34551	-1.54	-2.05	2.14	3.24*	7.02**	4.66**	3.07*	8.78 **
CMS 46A x RNR 28411	-2.09	-4.10**	0.00	1.08	-8.53**	-17.00**	-4.11**	1.20
CMS 59A x RNR 26085	-6.25 **	-7.41**	6.76**	7.91**	-0.25	-3.09*	3.93**	9.69 **
CMS 59A x ZGY 1	-7.59 **	-9.88**	3.91**	5.04**	-2.49*	-4.37**	-3.28*	2.08
CMS 59A x RNR 2354	-5.13 **	-8.64**	5.34**	6.47**	0.40	-4.95**	-3.83**	1.50
CMS 59A x RNR 28359	-7.03 **	-10.19**	3.66*	4.78**	-2.28*	-3.51**	-2.42	2.99 *
CMS 59A x RNR 21571	-7.85 **	-14.81**	-1.78	-0.72	-4.45**	-7.68**	-6.63**	-1.46
CMS 59A x IR 72	-10.02 **	-12.65**	0.46	1.54	-1.93	-4.03**	3.11*	2.26
CMS 59A x JGL 35126	-10.23 **	-16.05**	-3.20*	-2.16	-0.40	-2.39	-1.24	4.23 **
CMS 59A x JGL 35047	-9.72 **	-15.43**	-2.49	-1.44	2.67*	-8.19**	-7.14**	-2.00
CMS 59A x JGL 34551	-4.23 **	-9.26**	4.63**	5.76**	0.50	-0.82	0.31	5.87 **
CMS 59A x RNR 28411	-8.10 **	-14.20**	-1.07	0.00	-9.54**	-15.17**	-2.00	3.42 *
SEm (±)	1.12	1.30	1.26	1.26	1.07	1.24	1.25	1.25
CD (5%)	2.25	2.59	2.59	2.59	2.14	2.47	2.47	2.47

Tellahamsa and 31 hybrids over US 314. Maximum standard heterosis was recorded in hybrid CMS 23A × RNR 2354 over Tellahamsa (-17.30) and US 314 (-21.64). Maximum negative heterosis was registered by hybrid JMS 13A × IR 72 over mid-parent (-16.37) and CMS 23A × JGL 335126 over better parent (-19.15). Several rice researchers *viz*., Priyanka *et al.* (2014), Srijan (2015), Parimala (2016), Ramesh (2016) and Gokulakrishnan *et al.* (2018) reported negative standard heterosis for this trait.

Hybrids generally are characterized by having larger panicles indicating their efficiency in partitioning of assimilates to reproductive parts. In the present study, CMS 46A × IR 72 exhibited highest positive and significant average heterosis (14.92) and heterobeltiosis (12.11). Only one hybrid exhibited significant positive standard heterosis with a range from -23.78 (JMS 13A × IR 72) to 10.23 per cent (CMS 59A × RNR 26085) over hybrid check, US 314 and 25 hybrids exhibited significant positive standard heterosis over Tellahamsa and maximum heterosis was recorded in CMS 59A × RNR 26085 (34.15) for this trait. Significant positive and negative heterosis was exhibited over mid-parent, better parent and checks in hybrids. Standard heterosis of both positive and negative nature was observed in their studies by Priyanka *et al*. (2014), Nayak *et al*., (2015), Chouhan *et al.,* (2016), Parimala (2016), Ramesh (2016), Thorat *et al.* (2017) and Dilruba *et al.* (2018).

Number of productive tillers per plant plays a crucial role for higher gains on total biomass. Heterosis in positive direction was considered highly desirable for this character, out of 40 hybrids evaluated, two hybrids registered significant positive values over the better check US 314 with respective standard heterosis ranging from -39.29 (JMS 13A × RNR 26085) to 28.57 % (JMS 13A × IR 72). The maximum heterosis was recorded in CMS 23A × ZGY 1 (36.59) over mid parent and (21.74) over better parent heterosis (Table 3). This indicates a great scope for genetic improvement of this trait through adopting an appropriate method of breeding. In the present study, both positive and negative standard heterosis are reported by Nayak *et al.* (2015), Srijan (2015), Chouhan *et al.,* (2016), Parimala *et al*., (2016), Ramesh (2016), Dilruba *et al.,* (2017), Thorat *et al*., (2017) and Gokulakrishnan *et al.,* (2018) in their studies which were in similarity with present study suggesting methods of exploiting both additive and non-additive gene effects.

For spikelet fertility percentage, the range of standard heterosis of the crosses varied from -7.30 (CMS 23A × RNR 2354) to 7.94 per cent (CMS 59A × ZGY 1) over hybrid check, US 314 and 3 cross combinations exhibited significant positive standard heterosis. Maximum heterosis recorded in CMS 59A × RNR 2354 (4.92) over mid parent and CMS 59A × RNR 2354 (4.75) over heterobeltiosis (Table 4). Similar results were reported by Srijan (2015), Parimala (2016), Thorat *et al*., (2017) and Gokulakrishnan *et al.,* (2018) whereas negative heterosis for this trait was observed by Pandya and Tripathi (2006) and Singh *et al.* (2006b).

Test weight is also one of the important yield contributing character in rice crop. The standard heterosis was recorded in 31 hybrids with a range from -11.68 (JMS 13A × RNR 2354) to 39.76 per cent (CMS 23A × RNR 28411) over the check US 314 and 3 hybrids recorded significant standard heterosis over varietal check, Tellahamsa (Table 4). Highest heterosis was recorded in JMS 13A × JGL 35047 over mid parent (39.61) and JMS 13A × JGL 35047 (30.12) over better parent. Both positive and negative heterosis was resulted in case of test weight. Positive standard heterosis was reported by Nayak *et al.* (2015), Samrath Bedi and Deepak Sharma (2016), Thorat *et al*. (2017) and Gokulakrishnan *et al.* (2018).

Grain yield is a complex quantitative trait governed by many genes interacting with the environment and is the product of various factors called yield components. Selecting the parents based on yield alone is often misleading. Hence thorough knowledge about relationship between yield and its contributing characters is needed for efficient selection and development of high yielding variety. Nine crosses *viz.,* JMS 13A x RNR 2354, CMS 59A x JGL 35126, CMS 59A x RNR 28411, JMS 13A x ZGY 1, CMS 46A x JGL 34551, CMS 59A x ZGY1, CMS 13A x JGL 35126, CMS 13A x JGL 35047 and CMS 46A x RNR 2354 were exhibited significant positive standard heterosis over the hybrid check, US 314 for grain yield. Overall heterosis ranging from -27.45 (CMS 46A × JGL 35047) to 36.21 per cent (JMS 13A × RNR 2354). The highest average heterosis and heterobeltiosis were recorded in JMS 13A × RNR 2354 (73.00) and CMS

Table 3. Estimates of heterosis, heterobeltiosis and standard heterosis for panicle length and number of productive tillers per plant

Crosses	Panicle length				Number of productive tillers per plant			
	Heterosis		Standard		Heterosis		Standard	
	MP	BP	US 314	Tella hamsa	MP	BP	US 314	Tella hamsa
JMS 13A x RNR 26085	-11.33 **	-19.56**	-12.96**	5.93*	-46.03**	-52.78**	-39.29**	-37.04 **
JMS 13A x ZGY 1	-2.90	-4.99	-16.29**	1.88	0.00	-25.00**	-3.57	0.00
JMS 13A x RNR 2354	0.70	-2.29	-13.91**	4.78	-13.33*	-27.78**	-7.14	-3.70
JMS 13A x RNR 28359	0.53	-1.80	-9.27**	10.42**	-28.13**	-36.11**	-17.86*	-14.81 *
JMS 13A x RNR 21571	-8.65 **	-9.20**	-19.02**	-1.45	6.25	-5.56	21.43**	25.93 **
JMS 13A x IR 72	-13.14 **	-13.50**	-23.78**	-7.24*	-12.20**	-21.74**	28.57**	33.33 **
JMS 13A x JGL 35126	6.09 **	1.99	-2.62	18.52**	-6.25	-16.67**	7.14	11.11
JMS 13A x JGL 35047	0.56	-2.56	-14.15**	4.49	-11.48*	-25.00**	-3.57	0.00
JMS 13A x JGL 34551	3.89	1.55	-6.30*	14.04**	-40.63**	-47.22**	-32.14**	-29.63 **
JMS 13A x RNR 28411	12.31 **	11.93**	-0.71	20.84**	-19.35**	-30.56**	-10.71	-7.41
CMS 23A x RNR 26085	-7.71 **	-16.48**	-9.63**	9.99**	20.00**	11.11	7.14	11.11
CMS 23A x ZGY 1	-0.97	-2.85	-14.86**	3.62	36.59**	21.74*	0.00	3.70
CMS 23A x RNR 2354	-2.79	-5.43	-17.12**	0.87	10.64	8.33	-7.14	-3.70
CMS 23A x RNR 28359	-1.06	-3.60	-10.94**	8.39**	-1.96	-10.71	-10.71	-7.41
CMS 23A x RNR 21571	-3.03	-3.87	-14.27**	4.34	5.88	-3.57	-3.57	0.00
CMS 23A x IR 72	-5.71 *	-5.83*	-17.48**	0.43	-10.14*	-32.61**	10.71	14.81 *
CMS 23A x JGL 35126	-5.32 *	-9.22**	-13.32**	5.50	-1.96	-10.71	-10.71	-7.41
CMS 23A x JGL 35047	0.70	-2.17	-14.27**	4.34	-8.33	-12.00	-21.43**	-18.52 *
CMS 23A x JGL 34551	-0.46	-2.96	-10.46**	8.97**	-17.65*	-25.00**	-25.00**	-22.22 **
CMS 23A x RNR 28411	-2.09	-2.68	-13.67**	5.07	22.45**	15.38*	7.14	11.11
CMS 46A x RNR 26085	4.29	-7.80**	-0.24	21.42**	-12.00	-18.52*	-21.43**	-18.52 *
CMS 46A x ZGY 1	0.00	-0.71	-16.29**	1.88	7.32	-4.35	-21.43**	-18.52 *
CMS 46A x RNR 2354	10.03 **	9.87**	-8.68**	11.14**	-14.89*	-16.67*	-28.57**	-25.93 **
CMS 46A x RNR 28359	4.07	-1.16	-8.68**	11.14**	-21.57**	-28.57**	-28.57**	-25.93 **
CMS 46 A X RNR 21571	1.59	-1.87	-12.49**	6.51*	-1.96	-10.71	-10.71	-7.41
CMS 46A x IR 72	14.92 **	12.11**	-2.02	19.25**	-30.43**	-47.83**	-14.29*	-11.11
CMS 46A x JGL 35126	6.92 **	0.00	-4.52	16.21**	5.88	-3.57	-3.57	0.00
CMS 46A x JGL 35047	9.04 **	8.73**	-9.63**	9.99**	0.00	-4.00	-14.29*	-11.11
CMS 46A x JGL 34551	8.75 **	3.35	-4.64	16.06**	1.96	-7.14	-7.14	-3.70
CMS 46A x RNR 28411	3.94	0.67	-10.70**	8.68**	-6.12	-11.54	-17.86*	-14.81 *
CMS 59A x RNR 26085	10.49 **	1.87	10.23**	34.15**	-11.54	-14.81*	-17.86*	-14.81 *
CMS 59A x ZGY 1	-5.35 *	-8.98**	-16.88**	1.16	-6.98	-20.00*	-28.57**	-25.93 **
CMS 59A x RNR 2354	-7.44 **	-11.72**	-19.38**	-1.88	-18.37*	-20.00*	-28.57**	-25.93 **
CMS 59A x RNR 28359	7.44 **	6.82*	-1.31	20.12**	-5.66	-10.71	-10.71	-7.41
CMS 59A x RNR 21571	2.24	1.04	-7.73**	12.30**	5.66	0.00	0.00	3.70
CMS 59A x IR 72	10.98 **	8.59**	-0.83	20.69**	-15.49**	-34.78**	7.14	11.11
CMS 59A x JGL 35126	5.03 *	2.74	-1.90	19.39**	5.66	0.00	0.00	3.70
CMS 59A x JGL 35047	8.41 **	3.26	-5.71*	14.76**	-16.00*	-16.00*	-25.00**	-22.22 **
CMS 59A x JGL 34551	-3.76	-4.25	-11.65**	7.53*	-9.43	-14.29*	-14.29*	-11.11
CMS 59A x RNR 28411	12.02 **	10.42**	0.83	22.72**	21.57**	19.23*	10.71	14.81 *
SEm (±)	0.59	0.68	0.68	0.68	0.56	0.65	0.65	0.65
CD (5%)	1.18	1.36	1.36	1.36	1.13	1.30	1.30	1.30

Table 4. Estimates of heterosis, heterobeltiosis and standard heterosis for spikelet fertility (%) and 1000 grain weight

Crosses	Spikelet fertility (%)				1000 grain weight			
	Heterosis		Standard		Heterosis		Standard	
	MP	BP	US 314	Tella hamsa	MP	BP	US 314	Tella hamsa
JMS 13A x RNR 26085	-5.69 **	-6.30**	-1.69	-11.86**	9.49**	-9.19**	17.09**	-7.49 *
JMS 13A x ZGY 1	-11.05 **	-14.47**	-2.78	-12.83**	22.62**	3.13	28.43**	1.47
JMS 13A x RNR 2354	-7.04 **	-9.65**	-5.20*	-15.00**	4.50	3.98	-11.68**	-30.21 **
JMS 13A x RNR 28359	-5.09 **	-7.88**	-3.35	-13.34**	15.94**	-2.70	21.83**	-3.74
JMS 13A x RNR 21571	-2.82	-3.77*	2.98	-7.66**	17.71**	-3.79	28.76**	1.74
JMS 13A x IR 72	-1.86	-3.69	1.05	-9.40**	24.05**	7.61*	24.37**	-1.74
JMS 13A x JGL 35126	-1.99	-2.38	2.42	-8.17**	-6.60*	-22.86**	0.51	-20.59 **
JMS 13A x JGL 35047	-7.92 **	-10.15**	-5.73**	-15.47**	39.61**	30.12**	27.92**	1.07
JMS 13A x JGL 34551	-2.73	-2.73	2.06	-8.50**	18.01**	13.55**	-3.55	-23.80 **
JMS 13A x RNR 28411	-9.37 **	-10.18**	-5.77**	-15.51**	6.63*	-13.07**	17.09**	-7.49 *
CMS 23A x RNR 26085	0.04	-0.70	2.82	-7.81**	9.00**	-3.02	25.04**	-1.20
CMS 23A x ZGY 1	-13.67 **	-18.09**	-6.90**	-16.52**	19.25**	7.74*	34.18**	6.02
CMS 23A x RNR 2354	-7.78 **	-9.13**	-7.30**	-16.88**	31.44**	20.71**	21.32**	-4.14
CMS 23A x RNR 28359	0.34	-1.26	0.73	-9.69**	2.10	-7.97*	15.23**	-8.96 **
CMS 23A x RNR 21571	-10.03 **	-12.13**	-5.97**	-15.69**	1.52	-11.13**	18.95**	-6.02
CMS 23A x IR 72	-1.69	-2.17	-0.20	-10.52**	8.54**	1.46	17.26**	-7.35 *
CMS 23A x JGL 35126	-1.31	-2.29	1.69	-8.82**	2.93	-8.83**	18.78**	-6.15
CMS 23A x JGL 35047	-2.80	-3.83	-1.90	-12.04**	8.09*	6.90	7.45	-15.11 **
CMS 23A x JGL 34551	-5.53 **	-6.84**	-2.26	-12.36**	17.77**	4.88	5.41	-16.71 **
CMS 23A x RNR 28411	-2.54	-3.01	-0.08	-10.41**	18.85**	3.77	39.76**	10.43 **
CMS 46A x RNR 26085	-5.17 **	-7.55**	-4.27*	-14.17**	5.06	0.79	29.95**	2.67
CMS 46A x ZGY 1	-7.68 **	-13.91**	-2.14	-12.26**	-4.46	-6.79*	16.07**	-8.29 **
CMS 46A x RNR 2354	-4.80 **	-5.13*	-6.05**	-15.76**	2.76	-12.14**	4.06	-17.78 **
CMS 46A x RNR 28359	-1.80	-2.00	-3.23	-13.23**	9.03**	6.08	32.83**	4.95
CMS 46 A X RNR 21571	-5.83 **	-9.65**	-3.31	-13.30**	2.75	-3.16	29.61**	2.41
CMS 46A x IR 72	-5.34 **	-6.59**	-5.65**	-15.40**	9.33**	8.00*	27.92**	1.07
CMS 46A x JGL 35126	0.88	-1.90	2.10	-8.46**	6.26*	1.43	32.15**	4.41
CMS 46A x JGL 35047	2.75	1.98	1.81	-8.71**	17.56**	7.57*	27.41**	0.67
CMS 46A x JGL 34551	1.65	-1.54	3.31	-7.38**	9.11*	-9.29**	7.45	-15.11 **
CMS 46A x RNR 28411	-4.25 *	-6.42**	-3.59	-13.56**	-3.61	-9.42**	22.00**	-3.61
CMS 59A x RNR 26085	3.86 *	1.75	5.36**	-5.53**	10.09**	5.25	35.70**	7.22 *
CMS 59A x ZGY 1	1.34	-5.04**	7.94**	-3.22	11.25**	8.15*	34.69**	6.42 *
CMS 59A x RNR 2354	4.92 **	4.75*	4.07*	-6.69**	-5.70	-19.14**	-4.91	-24.87 **
CMS 59A x RNR 28359	4.91 **	4.59*	3.91	-6.83**	5.78*	2.57	28.43**	1.47
CMS 59A x RNR 21571	-6.60 **	-9.95**	-3.63	-13.59**	-4.71	-10.49**	19.80**	-5.35
CMS 59A x IR 72	-1.59	-2.40	-1.41	-11.61**	13.35**	12.37**	32.15**	4.41
CMS 59A x JGL 35126	-4.42 *	-6.59**	-2.78	-12.83**	0.75	-4.16	24.87**	-1.34
CMS 59A x JGL 35047	-6.11 **	-6.34**	-6.49**	-16.16**	16.14**	6.62	25.38**	-0.94
CMS 59A x JGL 34551	-1.38	-4.00*	0.73	-9.69**	4.75	-12.66**	2.71	-18.85 **
CMS 59A x RNR 28411	-2.53	-4.27*	-1.37	-11.57**	2.48	-4.02	29.27**	2.14
SEm (±)	1.43	1.66	1.66	1.66	0.67	0.78	0.78	0.78
CD (5%)	2.86	3.30	3.30	3.30	1.34	1.55	1.55	1.55

46A × RNR 2354 (60.52) respectively (Table 5). Earlier rice workers viz., Priyanka *et al.* (2014), Bhati *et al.* (2015), Dar *et al.* (2015), Srijan (2015), Chouhan *et al.* (2016), Parimala (2016), Ramesh (2016), Samrath Bedi and Deepak Sharma (2016), Srivastava and Jaiswal (2016), Galal *et al.* (2017), Premkumar *et al.* (2017), Thorat *et al.* (2017), Gokulakrishnan *et al.* (2018) and Manjunath *et al.* (2019) reported positive heterobeltiosis and standard heterosis values for this trait.

CONCLUSION

Based on *per se* performance and positive standard heterosis 9 superior combinations for grain yield were identified, they are JMS 13A x RNR 2354, CMS 59A x JGL 35126, CMS 59A x RNR 28411, JMS 13A x ZGY 1, CMS 46A x JGL 34551, CMS 59A x ZGY1, CMS 13A x JGL 35126, CMS 13A x JGL 35047 and CMS 46A x RNR 2354. These hybrids also excelled in mean performance and heterosis for

Table 5. Estimates of heterosis, heterobeltiosis and standard heterosis for grain yield per plant (g)

Crosses	Grain yield per plant (g)			
	Heterosis		Standard Heterosis	
	MP	BP	US 314	Tellahamsa
JMS 13A x RNR 26085	-9.64	-13.71	-22.78 **	-11.98
JMS 13A x ZGY 1	44.41 **	38.38 **	23.83 **	41.15 **
JMS 13A x RNR 2354	73.00 **	52.22 **	36.21 **	55.26 **
JMS 13A x RNR 28359	4.89	-6.14	-16.00 *	-4.26
JMS 13A x RNR 21571	-6.63	-14.49 *	-23.48 **	-12.78
JMS 13A x IR 72	-7.99	-12.01	-21.26 **	-10.25
JMS 13A x JGL 35126	36.16 **	32.25 **	18.34 **	34.89 **
JMS 13A x JGL 35047	54.71 **	29.77 **	16.12 *	32.36 **
JMS 13A x JGL 34551	-11.69	-13.19	-22.31 **	-11.45
JMS 13A x RNR 28411	12.04	11.67	0.58	14.65 *
CMS 23A x RNR 26085	5.65	3.30	-15.89 *	-4.13
CMS 23A x ZGY 1	15.06 *	12.11	-8.06	4.79
CMS 23A x RNR 2354	3.04	-3.45	-24.88 **	-14.38 *
CMS 23A x RNR 28359	46.03 **	39.34 **	8.41	23.57 **
CMS 23A x RNR 21571	8.06	5.71	-17.76 **	-6.26
CMS 23A x IR 72	-1.68	-4.01	-21.61 **	-10.65
CMS 23A x JGL 35126	5.48	1.39	-14.49 *	-2.53
CMS 23A x JGL 35047	15.27	2.55	-20.21 **	-9.05
CMS 23A x JGL 34551	28.17 **	21.76 **	5.26	19.97 **
CMS 23A x RNR 28411	4.11	-2.98	-12.62 *	-0.40
CMS 46A x RNR 26085	23.19 **	16.21 *	-5.37	7.86
CMS 46A x ZGY 1	28.79 **	21.08 **	-0.70	13.18
CMS 46A x RNR 2354	65.33 **	60.52 **	15.89 *	32.09 **
CMS 46A x RNR 28359	55.85 **	54.21 **	11.33	26.90 **
CMS 46 A X RNR 21571	12.51	10.83	-17.52 **	-5.99
CMS 46A x IR 72	16.02 *	9.30	-10.75	1.73
CMS 46A x JGL 35126	34.18 **	24.52 **	5.02	19.71 **
CMS 46A x JGL 35047	9.23	0.49	-27.45 **	-17.31 *

Crosses	Grain yield per plant (g)			
	Heterosis		Standard Heterosis	
	MP	BP	US 314	Tellahamsa
CMS 46A x JGL 34551	54.64 **	41.89 **	22.66 **	39.81 **
CMS 46A x RNR 28411	6.70	-3.89	-13.43 *	-1.33
CMS 59A x RNR 26085	6.84	-0.29	-18.81 **	-7.46
CMS 59A x ZGY 1	56.05 **	45.16 **	19.04 **	35.69 **
CMS 59A x RNR 2354	21.25 **	19.04 *	-16.00 *	-4.26
CMS 59A x RNR 28359	45.74 **	45.62 **	2.92	17.31 *
CMS 59A x RNR 21571	47.14 **	43.33 **	6.66	21.57 **
CMS 59A x IR 72	46.89 **	36.91 **	11.80	27.43 **
CMS 59A x JGL 35126	67.57 **	53.88 **	29.79 **	47.94 **
CMS 59A x JGL 35047	24.13 **	15.40	-18.57 **	-7.19
CMS 59A x JGL 34551	24.26 **	12.84	-2.45	11.19
CMS 59A x RNR 28411	55.35 **	38.52 **	24.77 **	42.21 **
SEm (±)	1.55	1.79	1.79	1.79
CD (5%)	3.08	3.56	3.56	3.56

important yield deciding traits like plant height and 1000 grain weight. This also indicated that these yield attributes played great role in expression of high heterosis for grain yield per plant.

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Research Article
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SOIL CHARACTERISTICS, MICROBIAL BIOMASS CARBON AND NITROGEN UNDER DIFFERENT LAND USE PATTERNS IN RED SOILS OF VIKARABAD DISTRICT

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ABSTRACT

The microbial biomass of soil is being increasingly recognized as a sensitive indicator of soil quality. Its knowledge is fundamental for sustainable environment management. This study is aimed to determine the impact of different land use patterns *i.e.,* forest land,100% cropping intensity (redgram-fallow), 200% cropping intensity (rice-rice) and fallow land on soil microbial biomass carbon and nitrogen. A survey was conducted for two successive years (2019-20 and 2020-21) in red soils of Vikarabad district of Telangana state covering eight mandals and soil samples were collected from four different land use patterns at two depths (0-15 and 15-30 cm). Soil characteristics like bulk density, pH, EC, organic carbon, total nitrogen varied significantly with land use patterns and soil depth and were significantly higher in forest soils compared to other land use patterns. The mean microbial biomass carbon found to be 242.8 mg kg^{-1}, 128.1 mg kg^{-1}, 119.0 mg kg^{-1}, 69.0 mg kg^{-1} and the mean soil microbial nitrogen was found to be 35.6 mg kg^{-1}, 21.9 mg kg^{-1}, 17.7 mg kg^{-1} and 11.0 mg kg^{-1} respectively for forest, 100% cropping intensity, 200% cropping intensity and fallow land. There was significant positive correlation of microbial biomass carbon with per cent clay (0.998**), soil organic carbon (0.992**), total nitrogen (0.984**) and microbial biomass nitrogen (0.997**). The results confirm that alterations in soil physical and chemical properties due to deforestation and intense anthropogenic activity at agriculture lands may cause disturbances and ultimately affect the soil microbial biomass.

Keywords: Land use patterns, microbial biomass C, microbial biomass N, red soils, vikarabad

Soil organic matter is an important component of soil quality and productivity. However, its measurement alone does not adequately reflect changes in soil quality and nutrient status. Measurements of biologically active fractions of organic matter, such as microbial biomass carbon (MBC) and nitrogen (MBN) and potential C and N mineralization, could better reflect changes in soil quality and productivity that affect nutrient dynamics. This reflection is based upon rapidly changing capacity of both C and N forms (Bremner and Kessel, 1992). These fractions give an indication of soil organic matter changes induced by management practices.

The importance of microorganisms in ecosystem functioning has led to an increased interest in determining soil microbial biomass. The soil microbial biomass is the active component of the soil organic pool, which is responsible for organic matter decomposition affecting soil nutrient content and consequently, primary productivity in most biogeochemical processes in terrestrial ecosystems (Haney *et al.,* 2001). Therefore, measuring microbial biomass is a valuable tool for understanding and predicting long-term effects under the influence of different land use pattern and associated soil conditions (Sharma *et al.,* 2009). The present study was conducted to assess the impact of different land use patterns on soil characteristics, microbial biomass carbon and nitrogen in red soils of Vikarabad district.

MATERIAL AND METHODS

Vikarabad district is one of the newly carved districts from erstwhile Rangareddy in Telangana state. The geographical area of the district is 3,386 sq.km and is situated between 17°20'11.15"N latitude and 77°54'17.45"E longitude. The net cropped area in the district is about 20.4 lakh ha and has a forest cover of 44,548 ha and fallow land to an extent of 20,769 ha. The main crops cultivated in the district are redgram, maize, rice and vegetables. The main tree species found in the forest were *Tectona grandis, Eucalyptus, Acacia nilotica, Tamarindus indica, Leucaena leucocephala, Dalbergia sissoo, Ficus benghalensis, Pongamia pinnata, Syzygium cumini etc.* Fallow land was not disturbed and unmanaged and they were having mixed grasses other plant species and weeds. The climate in this region is semi-arid and characterized

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by warm summers. According to the climatological data gathered over the past 30 years, the mean maximum and minimum temperatures found to be in the range of 28-45^{0}C and 12-26^{0}C (Directorate of Economics and Statistics, 2021).

Soil sampling

A survey was carried out in eight mandals of Vikarabad district predominantly covered by red soils during the years (2019-20 and 2020-21). Soil samples were collected from at two depths (0-15 and 15-30 cm). From each village, three land use pattern**s** were selected out of which two were from agricultural land use with different cropping intensity *i.e.,*100% cropping intensity (redgram-fallow cropping system), 200% cropping intensity (rice-rice cropping system) and fallow land. The forest samples were collected from mandals where natural forest existed. A total of 320 soil samples were collected at two depths. The microbial biomass carbon and microbial biomass nitrogen were analysed in fresh soil samples within 24h. For determination of other soil properties, the soil samples were air dried, pounded and stored in polythene bags for further analysis.

Soil analysis

The soil samples were analysed for salient characteristics like texture, pH, EC, bulk density, soil organic carbon (g kg^{-1}) and total nitrogen (kg ha^{-1}) following standard procedures.

For determination of Soil Microbial Biomass Carbon, field-moist soil samples (10.0 g) were exposed to $CHCl_3$ vapour for 24 h and extracted with 0.5 M K_2SO_4. A second set of non-fumigated samples was also extracted under similar conditions. The difference between C obtained from the fumigated and the non-fumigated ones was taken to represent the microbial C-flush and converted to MBC using the relationship: MBC = (1/0.41) ´ C-flush (Christian *et al.,* 2000). All results are expressed on an oven-dry soil basis (105^{o}C, 24 h).

Microbial biomass nitrogen was also estimated using the same principle of microbial biomass carbon. The K_2SO_4 extractant of both fumigated and unfumigated soil was digested for 3 h with addition of digestion mixture and sulphuric acid. After cooling, distillation was carried out to find the total nitrogen content. The difference between fumigated and unfumigated extracted nitrogen of soil divided by a calibration factor (KEC) 0.38 gives the measure of microbial biomass nitrogen in soil and expressed as micro gram of microbial biomass-N per gram of dry soil (Beck *et al.,* 1997).

The data collected was statistically analysed using SPSS statistical package version 18.0. All the soil parameters were analysed by two-way ANOVA by taking equal replications where depth and land use pattern are the fixed factors and number of mandals were considered as the replicates. The Duncan's multiple range test was used to segregate the significance of difference among the mean values obtained for soil parameters, in each land use pattern at $P< 0.05$ which were considered to be statistically significant at 5% level of significance.

RESULTS AND DISCUSSION

The data on salient soil characteristics *viz;* bulk density (BD), pH, EC, organic carbon and total nitrogen obtained are presented in (Table 1).

The soil samples in general were sandy loam to sandy clay loam in texture with clay percent ranging from 35.96 to 40.28 %.

Bulk density (Mg m^{-3})

Bulk density in Vikarabad district under different land use patterns in red soils was ranging from 1.33 to 1.45 Mg m^{-3}. The values on an average, indicated that 200% cropping intensity (rice-rice) recorded the highest bulk density (1.45 Mg m^{-3}) followed by 100% cropping intensity (1.41 Mg m^{-3}), fallow land (1.39 Mg m^{-3}) and forest land recorded the lowest bulk density (1.33 Mg m^{-3}). The interaction effect between depth and land use pattern for soil bulk density was significant. Across the depth at 15-30 cm the highest BD was obtained by 200% cropping intensity (1.48 Mg m^{-3}) this was followed by 100% cropping intensity (1.44 Mg m^{-3}), fallow land (1.42 Mg m^{-3}) and the lowest were recorded under forest land use (1.36 Mg m^{-3}). It was found that there was an increase in bulk density from 0-15cm (1.37 Mg m^{-3}) to 15-30cm (1.43 Mg m^{-3}). The increase in bulk density with increase in depth in all the land use system may be attributed to lower organic matter content and soil compaction from the pressure of upper soil layer (Devi *et al.,* 2013).

Soil pH and EC

The soil pH under different land use pattern on an average indicated that the soils under forest land

use recorded the lowest soil pH (6.68), followed by fallow land (7.43), 100% cropping intensity (redgram-fallow) (7.59) and the highest was recorded in 200% cropping intensity (rice-rice) (7.72). Among the depths there was increase in soil pH from (7.27) to (7.43). Interaction effect between soil pH and land use pattern was significant with forest soils recording the lowest soil pH (6.56) followed by fallow land (7.38), 100% cropping intensity (7.50), 200% cropping intensity (7.64) at 0-15 cm. Irrespective of land use, the pH of the soil was higher at 15-30 cm soil depth.

The highest soil electrical conductivity was recorded under 200% cropping intensity (rice-rice) (0.28 d Sm^{-1}) this was followed by 100% cropping intensity (redgram-fallow) cropping pattern (0.25 dSm^{-1}), fallow land (0.23 dSm^{-1}) and the lowest was recorded under forest land use (0.18 dSm^{-1}). Under all the land use patterns with increasing in soil depth, the EC of the soil decreased. The interaction between depths and land use pattern for soil EC was significant with highest EC being recorded under rice-rice cropping system with 200% cropping intensity (0.30 dSm^{-1}) at 0-15 depth. A close perusal of the data on soil pH and EC indicates that the soils sites having lower pH shows lower EC values especially in forest and fallow lands. Similar results were obtained by Barros and Chaves, 2014 and Shah *et al.,* 2013. An increase in total soluble salt content has been reflected by an increase in EC under cultivated soils this could be due to the addition of fertilizers and other amendments.

Soil organic carbon (g kg^{-1})

The data pertaining to soil organic carbon is presented in (Table 1). Irrespective of soil depth on an average, the highest soil organic carbon content was recorded under forest land (7.05 g kg^{-1}) which was followed by 200% cropping intensity (rice-rice) (4.14 g kg^{-1}),100% cropping intensity (redgram-fallow)

Table 1. Effect of land use patterns on soil characteristics in red soils of Vikarabad district

Parameters	Bulk density (Mg m^{-3})	pH	EC (dSm^{-1})	Organic carbon(g kg^{-1})	Total nitrogen (kg ha^{-1})
Depth					
D_1 (0-15cm)	1.37 ^{A}	7.27 ^{B}	0.25 ^{A}	4.72 ^{A}	1346.8 ^{A}
D_2 (15-30cm)	1.43 ^{B}	7.43 ^{A}	0.23 ^{B}	3.87 ^{B}	1150.8 ^{B}
Land use pattern					
L_1: 100% cropping intensity (redgram-fallow)	1.41 ^{b}	7.59 ^{b}	0.25 ^{ab}	3.42 ^{c}	1250.5 ^{b}
L_2: 200% cropping intensity (rice-rice)	1.45 ^{a}	7.72 ^{a}	0.28 ^{a}	4.14 ^{b}	1212.5 ^{b}
L_3: Forest land	1.33 ^{d}	6.68 ^{d}	0.18 ^{b}	7.05 ^{a}	1577.1 ^{a}
L_4: Fallow land	1.39 ^{c}	7.43 ^{c}	0.23 ^{c}	2.68 ^{d}	955.0 ^{c}
Interaction					
D_1L_1	1.39±0.01 ^{d}	7.50± 0.05 ^{c}	0.27± 0.04 ^{ab}	3.90± 0.21 ^{d}	1375.0± 96.8 ^{d}
D_1L_2	1.43± 0.02 ^{bc}	7.64±0.07 ^{b}	0.30± 0.03 ^{a}	4.54± 0.18 ^{c}	1320.3± 56.35 ^{c}
D_1L_3	1.30± 0.02 ^{f}	6.56± 0.09 ^{f}	0.19± 0.01 ^{de}	7.30± 0.14 ^{a}	1679.4± 97.53 ^{a}
D_1L_4	1.36± 0.01 ^{e}	7.38±0.09 ^{d}	0.25± 0.02 ^{bc}	3.12± 0.16 ^{e}	1012.5 ± 85.08 ^{f}
D_2L_1	1.44± 0.01 ^{b}	7.66±0.04 ^{b}	0.24± 0.04 ^{bc}	2.94± 0.26 ^{e}	1125.1± 95.69 ^{f}
D_2L_2	1.48 ± 0.02 ^{a}	7.79±0.05 ^{a}	0.26± 0.03 ^{ab}	3.73 ± 0.24 ^{d}	1105.7± 65.04 ^{e}
D_2L_3	1.36± 0.03 ^{ef}	6.80±0.06 ^{e}	0.17±0.01 ^{e}	6.80± 0.15 ^{b}	1474.8± 83.00 ^{b}
D_2L_4	1.42 ± 0.01 ^{b}	7.48±0.03 ^{c}	0.22±0.02 ^{cd}	2.24 ± 0.16 ^{f}	897.6± 90.25 ^{g}

Mean values with different lower case superscript letters indicate significant difference between land use patterns for each soil depth and all land uses. Uppercase superscript letters indicate significant difference between depths for all land use system respectively at ($P<0.05$).± indicates standard deviation of mean

(3.42 g kg^{-1}) and lowest was observed under fallow land (2.68 g kg^{-1}). However, with increase in depth the mean organic carbon decreased from (4.72 g kg^{-1}) to (3.87g kg^{-1}). Interaction effect between soil depth and land use pattern was significant and it varied from (7.30 g kg^{-1}) in forest soils at 0-15 cm to (2.24 g kg^{-1}) in fallow land at 15-30 cm.

Higher amount of organic carbon under forest land could be attributed to leaf litter decomposition at the surface. It was observed that about 60-80% total carbon resources are in oxidisable form due to the presence of higher amount of soluble extractives like fat, waxes and alcohol soluble extractives in forest residues (Lorenz and Lal, 2006). Among the cropping systems, 200% cropping intensity (rice-rice) has shown significantly higher SOC. This might be due to continuous submergence of soils for 8-9 months in a year under rice-rice cropping system, prolonged water logging conditions may reduce the decomposition of added crop residues (Mandal *et al.,* 2008). However the lower values of SOC under fallow lands could be attributed to the very low amount of addition of residues in the form of leaf litter to the soil though the soil was undisturbed for longer period of time.

Total nitrogen (kg ha^{-1})

The results indicated that the mean total nitrogen values varied across the land use patterns and soil depth. Among the land use patterns studied forest land recorded the highest mean total nitrogen (1577.1 kg ha^{-1}) followed by 100% cropping intensity (redgram-fallow) (1250.5 kg ha^{-1}) and 200% cropping intensity (rice-rice) (1212.5 kg ha^{-1}) but were on par with each other and the lowest was recorded under fallow land (955.0 kg ha^{-1}). With increase in depth of soil the total nitrogen content reduced from 1346.8 kg ha^{-1} (0-15cm) to 1150.8 kg ha^{-1} (15-30 cm). Interaction effect between depth and land use pattern was significant with highest total nitrogen content recorded in forest land at 0-15 cm (1679.4 kg ha^{-1}) and lowest was recorded in fallow land at 15-30 cm depth (897.6 kg ha^{-1}).

The higher total nitrogen in the surface soil layers of forest land might be due to lack of disturbance which reduced the mineralization rate which contain plenty of plant litter. Similar results showing higher total nitrogen concentrations in the top soils under forest land than agricultural land use was also been reported by (Bohra and Ghosh, 2013).

Effect of land use pattern on soil Microbial biomass carbon and nitrogen (mg kg^{-1} soil)

The results revealed that land use patterns had a significant impact on soil microbial biomass C and N (Table 2).

Among all the land use patterns studied the highest microbial biomass carbon was recorded in forest land (242.8 mg kg^{-1}) which was followed by 100% cropping intensity (redgram-fallow) (128.1 mg kg^{-1}), 200% cropping intensity (rice-rice) (119.0 mg kg^{-1}) and lowest was recorded in fallow land (69.0 mg kg^{-1}).

While considering the land use pattern across the depths the interaction effect for microbial biomass carbon was significant and forest land use recorded the highest value (262.10 mg kg^{-1}) followed by 100% cropping intensity (149.6 mg kg^{-1}), 200% cropping intensity (138.3 mg kg^{-1}) and lowest was recorded in fallow land (82.8 mg kg^{-1}) at 0-15cm. Similar pattern was observed where forest soils recorded the highest MBC (223.6 mg kg^{-1}) at 15-30 cm and lowest was recorded in fallow land (55.2 mg kg^{-1}).With increase in depth average, microbial biomass carbon decreased from (158.2 mg kg^{-1}) to (121.3 mg kg^{-1}).

The higher content of microbial biomass carbon under forest as compared to other land use could be possibly due to the effect of more addition of litter in the form of fine roots biomass and aerial plant residues. Among the cropping systems comparatively higher MBC under redgram-fallow cropping system could be due to the diversity of organic materials which contained greater concentration of MBC and enzymes under redgram especially under long term experiment in semiarid tropics.

The values of MBC under 200% cropping intensity (rice-rice) were lower than that of 100% cropping intensity (redgram-fallow). The shift in microflora from aerobic to facultative anaerobes and weak microbial metabolism caused by oxygen limitation as a result of continuous water logging resulted in decreased biomass carbon in rice-rice system (Chen and Stark, 2000).

Compared to all the land use patterns the fallow land recorded lower values of biomass carbon which could be attributed to the very little turnover of plant residues to the soil and also partly due to less input of organic matter resulting in lack of substrate of growth of microbes in soil (Kujur and Patel, 2012).

Table 2. Effect of land use patterns on microbial biomass carbon and nitrogen in red soils of Vikarabad district

Parameters	Microbial biomass carbon (mg kg^{-1})	Microbial biomass nitrogen (mg kg^{-1})
Depth		
D_1 (0-15cm)	158.2 ^{A}	24.7 ^{A}
D_2 (15-30cm)	121.3 ^{B}	18.2 ^{B}
Land use pattern		
L_1: 100% cropping intensity (redgram-fallow)	128.1 ^{b}	21.9 ^{b}
L_2: 200% cropping intensity (rice-rice)	119.0 ^{c}	17.7 ^{c}
L_3: Forest land	242.8 ^{a}	35.6 ^{a}
L_4: Fallow land	69.0 ^{d}	11.0 ^{d}
Interaction		
D_1L_1	149.6 ± 2.13 ^{c}	25.6 ± 1.30 ^{c}
D_1L_2	138.3 ± 13.96 ^{d}	20.2 ± 2.45 ^{d}
D_1L_3	262.1 ± 6.78 ^{a}	40.0 ± 1.23 ^{a}
D_1L_4	82.8 ± 2.15 ^{e}	13.9 ± 0.54 ^{f}
D_2L_1	106.6 ± 5.47 ^{e}	18.2 ± 1.49 ^{d}
D_2L_2	99.7 ± 12.06 ^{e}	15.2 ± 0.54 ^{e}
D_2L_3	223.6 ± 9.06 ^{b}	31.2± 0.90 ^{b}
D_2L_4	55.2 ± 4.21 ^{f}	8.2 ± 0.59 ^{f}

Mean values with different lower case superscript letters indicate significant difference between land use patterns for each soil depth and all land uses. Uppercase superscript letters indicate significant difference between depths for all land use system respectively at ($P<0.05$). ± indicates standard deviation of mean

Microbial biomass nitrogen (mg kg^{-1})

Among the land use patterns studied the highest microbial biomass nitrogen (MBN) was recorded in forest land (35.6 mg kg^{-1}) which was followed by 100% cropping intensity (redgram-fallow) (21.9 mg kg^{-1}), 200% cropping intensity (rice-rice) (17.7 mg kg^{-1}) and lowest was seen in fallow land (11.0 mg kg^{-1}).

While considering the land use pattern across the depth the interaction effect for microbial biomass nitrogen was significant and forest land use recorded the highest mean (40.0 mg kg^{-1}) which was followed by 100% cropping intensity (redgram-fallow) (25.6 mg kg^{-1}), 200% cropping intensity (20.2 mg kg^{-1}) (rice-rice) and lowest was recorded in fallow land (13.9 mg kg^{-1}) at 0-15 cm. At 15-30 cm the similar pattern was seen where forest soils recorded the highest MBN (31.2 mg kg^{-1}) and lowest was recorded in fallow land (8.2 mg kg^{-1}).

With increase in depth average, microbial biomass nitrogen decreased from (24.7 mg kg^{-1}) to (18.2 mg kg^{-1}). The results clearly indicated that MBN was much lower in fallow soils as compared to other land use pattern. The higher amount of MBN in 100% cropping intensity than 200% cropping intensity could be attributed to the biological N fixation by rhizobia in root nodules of redgram in addition to the fertilizers addition to the soil which might have been utilized by microbes for their growth. A close perusal of the data indicated that MBN followed the same trend as MBC indicating that the dynamics of nitrogen in soil are closely linked to carbon which is present in the organic form for their energy which in turn influences the microbial activity in soil (Murrieta *et al.,* 2007).

Correlation between different soil properties, microbial biomass carbon and nitrogen at 0-15 cm soil depth

It was observed that per cent clay had a significant positive correlation (Table 3) with organic carbon (r = 0.993*), MBC (r = 0.907*), MBN (r = 0.903*) and total nitrogen (r = 0.884*). Microbial biomass carbon values showed significant positive correlation with MBN (r = 0.963*), organic carbon (r = 0.966**), total nitrogen (r = 0.910**). Significant positive correlations have also been recorded between MBN (Table 4.) and organic carbon (r = 0.923**), total nitrogen(r = 0.986**). It was observed that bulk density had a significant negative correlation with organic carbon(r = -0.825*), MBC (r = -0.672*) and MBN (r = -0.635*).

Correlation between different soil properties, microbial biomass carbon and nitrogen at 15-30 cm soil depth

At 15-30 cm soil depth the per cent clay had a significant positive correlation (Table 4) with organic carbon (r = 0.980*), MBC (r = 0.900*), MBN (r = 0.886*) and total nitrogen (r = 0.812*). The microbial biomass carbon values showed significant positive correlation with MBN (r = 0.950*), organic carbon (r = 0.916*), total nitrogen (r = 0.901*). Significant positive correlations have also been recorded between MBN and organic carbon (r = 0.900*), total nitrogen (r = 0.901*). Among all the soil properties, bulk density had a significant negative correlation with organic carbon (r = -0.756**), MBC (r = - 0.650**) and MBN (r = - 0.621**) and soil EC had an insignificant negative correlation with soil organic carbon, microbial biomass carbon and nitrogen, total nitrogen.

Table 3. Correlation between different soil properties, microbial biomass carbon and nitrogen at 0-15 cm soil depth

Parameters	Clay	pH	EC	Bulk density	Organic carbon	Total nitrogen	MBC	MBN
Clay	1							
pH	0.704	1						
EC	0.895	0.156	1					
Bulk density	0.929	0.265	0.526	1				
Organic carbon	0.993 *	0.320	0.456	-0.825 *	1			
Total nitrogen	0.884 *	0.252	0.543	-0.621	0.910 **	1		
MBC	0.907 *	-0.190	0.591	-0.672 *	0.966 **	0.962 **	1	
MBN	0.903 *	-0.217	0.620	-0.635 *	0.923 **	0.986 **	0.963 **	1

*Correlation is significant at the 0.05 level; **Correlation is significant at 0.01 level

Table 4. Correlation between different soil properties, microbial biomass carbon and nitrogen at 15-30 cm soil depth

Parameters	Clay	pH	EC	Bulk density	Organic carbon	Total nitrogen	MBC	MBN
Clay	1							
pH	0.623	1						
EC	0.805	0.176	1					
Bulk density	0.901	0.296	-0.265	1				
Organic carbon	0.980 *	0.256	-0.367	-0.756 **	1			
Total nitrogen	0.812 *	0.136	-0.423	-0.568 *	0.901 *	1		
MBC	0.900 *	-0.350	-0.536	-0.650 **	0.916 *	0.955 **	1	
MBN	0.886 *	-0.217	-0.520	-0.621 **	0.900 *	0.974 **	0.950 *	1

*Correlation is significant at the 0.05 level; **Correlation is significant at 0.01 level

CONCLUSION

The results of the present study revealed that land use pattern and soil depth significantly influenced soil physical, chemical properties, microbial biomass carbon and nitrogen. Organic matter or litter layer in forest land increased soil carbon thereby helping in the restoration of better soil health and fertility. Land use pattern and soil depth strongly influenced the top soil of all the study sites. Forest had the highest microbial biomass C and N, suggesting better C and N immobilization in the land use. Low SOC and MBC in fallow land confirmed that the lack of organic matter inputs and external factors like erosion, grazing by animals decreased soil fertility and in turn microbial activity in soil. The study suggests that MBC, MBN may be considered as a key indicator of soil fertility, while land uses are a major cause for loss of microbial biomass.

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Research Article
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PERFORMANCE OF SUPER EARLY PIGEONPEA IN DIFFERENT SOWING WINDOWS AND INTEGRATED NUTRIENT MANAGEMENT IN SOUTHERN TELANGANA ZONE

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ABSTRACT

A field experiment was conducted at Regional Agricultural Research Station, Palem, Nagarkurnool, Southern Telangana Agro Climatic Zone of Telangana State during *kharif* 2018-19 and 2019-20 to study the performance of super early pigeonpea in different sowing windows and with integrated nutrient management practices under rainfed situations. The experiment was laid out in strip plot design for pigeonpea in *kharif* 2018 and 2019 with 3 main treatments *i.e.,* M_1 (1st July), M_2 (20th July) and M_3 (10th August) and four integrated nutrient management practices as sub treatments *viz*., S_1: 75% RDF, S_2: 75% RDF + FYM enriched with microbial consortia (1 tonne ha^{-1}), S_3: 100 % RDF and S_4: 100% RDF + FYM enriched with microbial consortia (1 tonne ha^{-1}) and replicated thrice. The performance of the super early pigeonpea in two years of field study revealed that, among the three sowing dates in main treatments, 1st July *i.e.,* M_1 witnessed higher final plant population (per cent) and growth parameters *viz*., plant height (cm), leaf area per plant (cm^2) and dry matter production (g m^2) at 30, 60 and 90 DAS. The highest seed, haulm yield (kg ha^{-1}) and harvest index of pigeonpea were superior with 1st July (M_1) compared to the other sowing dates *i.e.,* 20th July and 10th August. In the sub treatments application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) reported highest plant height at different stages of crop growth that resulted highest dry matter accumulation at 30, 60 and 90 DAS among the sub treatments in the both the years. The seed and stover yield were significantly higher with the above treatment and was followed by the application of 100% RDF (S_3). The interaction between sowing dates and integrated nutrient management was found non significant.

Keywords: Enriched FYM, growth attributes, microbial consortia, seed and stover yield, super early pigeonpea

Pigeonpea (*Cajanus cajan* L.) is the sixth most important grain legume in the world and second most important pulse crop after chickpea in India. 90% of the world's cultivated area of pigeonpea is present in India and it is grown in an area of 4.43 M ha and produces 4.25 MT with average productivity of 960 kg ha^{-1} in India. Maharashtra, Madhya Pradesh, Karnataka, Gujarat, and Telangana account for India's 82.2% of the area and 84.9% of the production, In Telangana state; pigeonpea occupies 0.33 M ha and contribute 0.26 M tonnes with productivity of 797 kg ha^{-1} (Agricultural Statistics at a Glance, 2018).

Though highest (>90%) area is present in India, the productivity is low as pigeonpea is seldom grown as sole crop in India and non availability of fast growing, short duration, high yielding photo insensitive pigeonpea cultivars. The available medium and long duration pigeonpea cultivars grown under rainfed conditions were experiencing terminal drought at flowering due to cessation of the south west monsoon in October leads to lower productivity in India. The photo and thermo sensitivity of existing pigeonpea cultivars is also another drawback restricting the horizontal expansion to different cropping systems in varied agro ecologies. Traditional cultivars of pigeonpea are of early (120 to 140 days), medium (140 to 160 days) and long duration (>160 days) types which cannot fit in preceding or succeeding crop situations of rainfed and irrigated ecology. Super early pigeonpea varieties developed from ICRISAT are of 100 days duration with yield potential of 1.0 to 1.5 tonnes ha^{-1} (Vales *et al*., 2012). Yield maximization of super early pigeonpea and its cropping system depends on optimum time of sowing and its succeeding crop. Hence it is necessary to standardize the optimum date of sowing of super early photo insensitive pigeonpea cultivars.

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Besides, fertilizers are becoming costlier and difficult for the resource - poor farmers to apply recommended dose of fertilizers. Hence, integrated nutrient management with microbial consortia consisting of *Rhizobium, Pseudomonas putida*, *Pseudomonas fluorescens* and *Bacillus cereus* enhanced plant biomass and yields of pigeon pea (Tilak *et al.,* 2006). In addition to that, plant growth promoting mycorrhiza like *Rhizobium* spp., can promote plant growth and productivity as primary effect and their role in reducing disease as secondary effect. Hence judicious use of microbial consortia with inorganic sources of nutrients is essential to minimize the cost of inputs, increase the yield and maintain soil health.

MATERIAL AND METHODS

A field trial was conducted at Regional Agricultural Research Station, Palem, Nagarkurnool, Southern Telangana Agro Climatic Zone of Telangana State during *kharif,* 2018-19 and 2019-20 to study the performance of super early pigeonpea in different sowing windows and with integrated nutrient management practices. The experimental site is situated at about 16Ú 51' N latitude and 78º25' E longitude with an average altitude of 478 m above the mean sea level. The soil of experimental site was sandy clay loam with pH 6.7, electrical conductivity 0.34 dSm^{-1}, low organic carbon (0.52%), low available nitrogen (201.3 kg ha^{-1}) and medium phosphorus (16.7 kg ha^{-1}) and high in potassium (309.4 kg ha^{-1}). In *kharif,* crop was sown with three sowing dates as main treatments *i.e.,* M_1 (1st July), M_2 (20th July) and M_3 (10th August) and four integrated nutrient management practices as sub treatments *viz.,* S_1: 75% RDF, S_2: 75% RDF + FYM enriched with microbial consortia (1 tonne ha^{-1}), S_3: 100% RDF and S_4: 100% RDF + FYM enriched with microbial consortia (1 tonne ha^{-1}) in strip plot design with three replications.

Super early photo insensitive cultivar ICPL 20325 pigeonpea is non determinate type (NDT) and it comes to maturity in 90-100 days to open the avenue to explore during the off season and in non-traditional eco systems (Shruthi *et al.,* 2020). This photo insensitive crop is being hardy and early fits in rice fallows, wheat-pulses and sugarcane-pulses intercropping system using residual moisture for growth and development (Hingane *et al.,* 2018). The seeds @ 10 kg ha^{-1} was hand dibbled at the rate of 2 seeds per hill by adopting spacing of 45 x 15 cm in *kharif* season. Farm yard manure enriched with microbial consortia @ 1 tonne ha^{-1} was applied and incorporated into soil one week before sowing as per the treatments. The recommended doses of fertilizer (RDF) for pigeonpea *i.e*., 20:50:0 kg NPK ha^{-1} was applied through urea and single super phosphate (SSP) respectively. Entire N and P_2O_5 were applied basally by placement and covered with the soil. Other cultural operations and plant protection measures were followed as per the recommendations. The data on growth parameters *i.e.,* plant height, leaf area $plant^{-1}$, dry matter accumulation was taken at 30, 60 and 90 DAS. The seed and stover yield taken on net plot basis. The replicated data was statistically analysed in strip plot design and the analysis of variance was calculated using ANOVA table. The experiment was conducted under rainfed situations. The rainfall distribution during the crop period of pigeonpea sown on July 1st (M_1) received 326 mm in 24 rainy days in 2018 and 539.4 mm in 43 rainy days in 2019. The pigeonpea crop sown on July 20th (M_2) utilized 263.4 mm rainfall in 18 rainy days in 2018 and 437.2 mm rainfall in 32 rainy days in 2019. Finally, August 10th sown pigeonpea recorded 247.2 mm rainfall in 15 rainy days in 2018 and 330.0 mm in 29 rainy days in 2019. The dry spells recorded were two, three and four for the July 1st (M_1), July 20th (M_2) and August 10th (M_3) sown pigeonpea crop in the 2018. Whereas in 2019, pigeonpea sown on different dates experienced no distinct dry period during the crop growth. Protective irrigation of 50 mm (each irrigation) was given during the dry period occurred during the crop growth period of pigeonpea. In 2018 for July sown pigeonpea (M_1) two protective irrigations of 50 mm each given at active growth stage (30 DAS) and at initiation of flowering (60 DAS), in July 20th sown (M_2) pigeonpea crop saved with three protected irrigations at crop establishment stage (10 DAS), flowering initiation stage (50 DAS) and pod development stage (80 DAS). Similarly, the August 10th sown (M_3) pigeonpea was provided with four life saving irrigations at active growth stage (30 DAS), initiation of flowering (60 DAS) and two irrigations at pod development stages (one at 90 DAS and another at 100 DAS). The crop was harvested on 22nd October, 7th November and 23rd November in 2018 and 29th October, 11th November and 28th November in 2019 for the three different sowing dates *i.e.,* July 1st, July 20th and August 10th respectively.

RESULTS AND DISCUSSION

Growth parameters

Plant population

During both the years of field study the initial plant population (Table 1) of pigeonpea crop was not significantly influenced by different sowing dates and integrated nutrient management and ranged between 97.0 to 98.0 per cent. Significant variation in the final plant population was noticed with the different sowing dates but not with the integrated nutrient management practices in the both the years of study.

In the year 2018-19, significantly highest final plant population was recorded by the July 1st (94.2) sown and it was on par with the July 20th (93.3) sowing and significantly superior over the August 10th (91.7) sown pigeonpea crop. Whereas in 2019-20, final plant population in July 1st (92.8) sowing was significantly superior over the July 20th (90.6) and August 10th (88.9) sowing dates. The pooled results also followed the similar trend recorded in the 2019-20. The variation in the final plant stand in pigeonpea crop might be influenced by the weather parameters like quantity and intensity of rainfall and availability of soil moisture in the experimental plot. The rainy season catches its peaks of precipitation in the late July and August months of the two years. This enables the soil to have continuous availability of soil moisture and even to excessive soil moisture lead to lose plant population through wilt from the sowing stage to 75% pod maturity of pigeonpea. Similar results were confirmed by Dasharath *et al.* (2012) in the chickpea during *rabi* season. The weather parameter like maximum and minimum temperature influenced the plant population with changed sowing dates in the experiment. The insignificant difference in the integrated nutrient management practices might due to the inorganic fertilizers integrated with organic manures increased the availability of nutrients to the crop throughout the crop growth period.

Table 1. Effect of dates of sowing and INM on plant population (per cent) of super early pigeonpea

Treatments	Initial			Final		
	2018	2019	Pooled mean	2018	2019	Pooled mean
Main treatments (Dates of Sowing)						
M_1 - 1st July	99.1	96.9	98.0	94.2	92.8	93.5
M_2 - 20th July	99.0	95.9	97.5	93.3	90.6	92.0
M_3 - 10th August	98.8	95.3	97.0	91.7	88.9	90.3
SE m (±)	0.18	0.63	0.39	0.24	0.36	0.19
CD (P=0.05%)	NS	NS	NS	0.96	1.42	0.74
Sub treatments (INM)						
S_1 - 75 % RDF	98.7	95.8	97.3	93.0	90.6	91.8
S_2 - 75 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	99.3	95.5	97.4	93.2	90.3	91.8
S_3 - 100 % RDF	99.0	96.0	97.5	93.1	90.8	91.9
S_4 - 100 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	98.9	96.9	97.9	93.1	91.4	92.2
SE m (±)	0.34	0.56	0.30	0.57	0.4	0.25
CD (P=0.05%)	NS	NS	NS	NS	NS	NS
Interaction effect						
Main at same level of sub						
SE m (±)	0.47	0.86	0.47	0.69	1.06	0.70
CD (P=0.05%)	NS	NS	NS	NS	NS	NS
Sub at same level of Main						
SE m (±)	0.39	0.87	0.51	0.57	0.88	0.56
CD (P=0.05%)	NS	NS	NS	NS	NS	NS

Plant height (cm)

Plant height is an important growth index for the accumulation of dry matter by the plant and is very important to monitor the overall canopy architecture and also govern the orientation of the leaves that further govern the photosynthetic efficiency of a plant to utilize the natural resources.

The data on plant height recorded at 30, 60 and 90 DAS of pigeonpea as influenced by the different date of sowing and integrated nutrient management practices were presented in Table 2. A perusal of data showed that plant height was comparatively higher in the second year *i.e.,* 2019-20 as compared to the first year (2018-19). It was found that the periodic plant height of the crop went on increasing till maturity and the magnitude of increase was more than double from 30-60 DAS to harvest irrespective of treatments. From the pooled data on plant height of pigeonpea, it was revealed that as the plant growth progressed, the plant height of pigeonpea significantly higher with July 1st sowing date (M_1) from 30 DAS up to harvest stage. Among sub treatments (integrated nutrient management), application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) produced taller plants as the crop aged from 30 DAS up to harvest.

The results revealed that the plant height at 30 DAS, was much higher with July 1st (M_1) sowing date *i.e.,* 34.1 cm, 36.0 cm in 2018 and 2019 over the plant height recorded in August 10th sowing (31.1 and 33.3 cm) and statistically on par with the July 20th sowing date (33.1 and 34.7 cm). As the crop grew at 60 DAS, significantly taller plants were noticed with July 1st (95.4 and 100.4 cm) and was significantly superior over the plant height observed at July 20th (95.9 cm) during 2019 and August 10th (81.6 and 93.5 cm) dates of sowing during the both the years. Likewise, 90 DAS also, significantly greater plant height

Table 2. Effect of dates of sowing and INM on plant height (cm) of super early pigeonpea

Treatments	30 DAS			60 DAS			90 DAS		
	2018	2019	Pooled mean	2018	2019	Pooled mean	2018	2019	Pooled mean
Main treatments (Dates of Sowing)									
M_1 - 1st July	34.1	36.0	35.1	95.4	100.4	97.9	109.3	122.7	116.0
M_2 - 20th July	33.1	34.7	33.9	88.1	95.9	92.0	100.2	117.1	108.7
M_3 - 10th August	31.1	33.3	32.2	81.6	93.5	87.5	98.4	109.0	103.7
SE m (±)	0.6	0.5	0.2	2.5	0.9	1.0	2.1	1.1	0.8
CD (P=0.05%)	2.2	1.9	0.7	9.7	3.4	4.0	8.4	4.3	3.2
Sub treatments (INM)									
S_1 - 75 % RDF	31.0	32.2	31.6	83.9	92.0	87.9	98.2	108.9	103.5
S_2 - 75 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	32.0	33.6	32.8	86.0	94.8	90.4	100.4	114.0	107.2
S_3 - 100 % RDF	33.3	35.5	34.4	88.6	97.7	93.1	104.7	118.1	111.4
S_4 - 100 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	34.7	37.3	36.0	95.1	101.8	98.5	107.4	124.2	115.8
SE m (±)	0.7	0.7	0.5	1.2	1.6	0.6	1.8	2.8	1.0
CD (P=0.05%)	2.4	2.3	1.7	4.2	5.6	2.0	6.4	9.9	3.33
Interaction effect									
Main at same level of sub									
SE m (±)	1.2	1.4	0.9	3.4	2.6	2.0	4.1	3.2	2.3
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS
Sub at same level of Main									
SE m (±)	1.0	1.2	0.7	3.4	2.1	1.8	3.7	2.7	1.9
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS

of pigeonpea of 109.3 and 122.7 cm was recorded with July 1st sowing date (M_1) and was followed by July 20th (M_2) (117.1 and 108.7 cm) and minimum plant height was recorded at August 10th (M_3) (98.4 and 109.0 cm) sowing date during 2018 and 2019 respectively. However, it was at par with July 20th sowing during 2018. Increase in plant height with July 1st sowing date might have represented better weather conditions like prolonged photoperiod, optimum temperatures and sufficient amount of moisture levels at vegetative growth resulting in maximum plant height. These results were in line with those of Singh and Kumar (2014) and Lalitha *et al.* (2018).

Among the integrated nutrient management treatments *i.e.,* 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) had resulted in maximum plant height of 34.7 and 37.3 cm and was at par with application of 100% RDF alone (S_3) with 33.3 and 35.5 cm, during 2018 and 2019. Application of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_3) (32.0 and 33.6 cm) and S_1 *i.e.,* 75% RDF (31.0 cm and 32.2 cm) showed the plant height which was significantly at par.

At 60 DAS, S_4 *i.e.,* 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} registered significantly taller plants (95.1 and 101.8 cm). The plant height obtained with application of 100% RDF (S_3) (88.6 and 97.7 cm) was at par with supplication of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 86.0 and 94.8 cm in 2018 and 2019, respectively. Lower plant height was observed with S_1 (75% RDF) (83.9 and 92.0 cm) during both the years of field study.

With the growth advancement at 90 DAS, administration of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) produced significantly taller plants (107.4 and 124.2 cm) and was at par with 100% RDF (S_3) with 104.7 and 118.1 cm. Distinctly, allocation of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) produced at par plant height (100.4 and 114.0 cm) and was at par with 75% RDF (S_1) with plant height of 98.2 and 108.9 cm during both the years.

A significant effect on the increase on the plant height with the application of NPK may be attributed to nitrogen which is an essential constituent of plant tissue that promotes rapid cell division and its enlargement, which together with the adequate quantity of phosphorus and potassium helps in the rapid cell division and better development of the cell size. Further, the beneficial effect of FYM enriched with microbial consortia may be attributed to the fact that it supplied available plant nutrients and had solubilising effect on fixed forms of nutrients thus making the nutrients available for increased intermodal length thus improving plant height. These results are in conformity with Ade *et al.* (2018).

Interaction effect of plant height of pigeonpea crop as influenced by dates of sowing and integrated nutrient management was found to be non significant in all crop growth stages.

Leaf area $plant^{-1}$ (cm^2)

Perusal of data on leaf area $plant^{-1}$ of pigeonpea at different growth stages as influenced by dates of sowing and different integrated nutrient management were presented in Table 3 during both the years of study.

From the pooled mean (Table 3) of two years it is observed that, in case of sowing dates M_1 (July 1st) sown pigeonpea brought out the maximum leaf area per plant *i.e.,* 99.5, 760.0 and 1031 cm^2 at 30, 60 and 90 DAS of plant growth which was significantly higher compared to other treatments. Sowing on 20th July produced significantly higher leaf area (92.6 cm^2) over 10th August (85.7 cm) sowing at 30 DAS, however, with the advancement of crop growth *i.e.,* at 60 DAS and 90 DAS, 20th July (M_2) sowing (676.0 and 890.0 cm^2) was at par with 10th August (M_3) sowing (655.2 and 880.4 cm^2). Pooled data among the INM treatments recorded that application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) showed significantly higher leaf area at 30 (98.1 cm^2), 60 (767.3 cm^2) and at 90 DAS (1032.4 cm^2) over other treatments. The leaf area (93.8 cm^2) obtained with application of 100% RDF alone (S_3) was at par with leaf area (91.0 cm^2) accrued with 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2). At later stages at 60 and 90 DAS, application of 100% RDF (S_3) showed higher leaf area (719.1 and 968.1 cm^2), that was distinctly followed by S_2 (75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1}) with leaf area of 623.9 and 833.2 cm^2 $plant^{-1}$ was obtained with application of 75% RDF alone (S_1) at 60 DAS and 90 DAS.

Table 3. Effect of dates of sowing and INM on leaf area per plant (cm^2) of super early pigeonpea

Treatments	30 DAS			60 DAS			90 DAS		
	2018	2019	Pooled mean	2018	2019	Pooled mean	2018	2019	Pooled mean
Main treatments (Dates of Sowing)									
M_1 - 1st July	93.2	105.8	99.5	692.4	827.6	760.0	980.0	1082.9	1031.5
M_2 - 20th July	87.6	97.5	92.6	632.6	719.5	676.0	820.4	960.7	890.6
M_3 - 10th August	80.4	91.0	85.7	617.3	693.1	655.2	813.5	947.3	880.4
SE m (±)	1.1	2.5	1.2	14.8	15.6	6.1	30.2	22.0	25.4
CD (P=0.05%)	4.5	9.9	4.7	58.0	61.3	23.8	118.7	86.4	99.9
Sub treatments (INM)									
S_1 - 75 % RDF	82.6	92.4	87.5	577.4	670.4	623.9	735.0	931.5	833.2
S_2 - 75 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	85.6	96.4	91.0	620.1	736.1	678.1	824.1	981.6	902.9
S_3 - 100 % RDF	87.8	99.7	93.8	669.7	768.4	719.1	921.3	1014.9	968.1
S_4 - 100 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	92.3	104.0	98.1	722.6	812.1	767.3	1004.9	1059.9	1032.4
SE m (±)	1.8	2.1	1.0	11.0	22.0	9.7	21.9	31.8	15.9
CD (P=0.05%)	6.3	7.2	3.5	38.1	76.1	33.7	75.7	NS	55.0
Interaction effect									
Main at same level of sub									
SE m (±)	4.0	4.6	2.7	23.7	25.4	15.1	32.6	36.4	21.0
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS
Sub at same level of Main									
SE m (±)	3.3	4.2	2.3	22.5	24.0	12.9	36.8	34.2	27.8
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS

The scrutiny of the data on leaf area per plant of pigeonpea at 30 DAS was significantly influenced by main plots, *i.e.,* sowing dates during 2018 and 2019, the pigeonpea sown on July 1st had produced significantly more leaf area $plant^{-1}$ (93.2 and 105.8 cm^2) and it was at par with leaf area $plant^{-1}$ obtained with July 20th sowing (M_2). With advancement of crop growth stage at 60 DAS and 90 DAS also, leaf area $plant^{-1}$ recorded in early sowing (July 1st) was significantly higher during 2018 (692.4 and 980.0 cm^2 $plant^{-1}$) and 2019 (827.6 and 1082.9 cm^2 $plant^{-1}$). Sowing on 20th July produced leaf area of 632.6, 820.4 cm^2 $plant^{-1}$ during 2018 and 719.5, 960.7 cm^2 $plant^{-1}$ during 60 DAS and 90 DAS respectively which was at par with 10th August sowing (617.3, 813.5 cm^2 $plant^{-1}$ during 2018 and 693.1, 947.3 cm^2 $plant^{-1}$ during 2019 at 60 and 90 DAS respectively). The increase in leaf area could be attributed to significant increase in leaf expansion, high rate of cell division and cell enlargement, rapid vegetative growth due to favourable weather conditions like optimum temperature, rainfall and light *etc*., during crop growing period. These are in line with the results of Kumar *et al.* (2018) and Sharanappa *et al.* (2018).

Among the integrated nutrient treatments at 30 DAS, application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) had produced more leaf spread (92.3 and 104.0 cm^2) and it was on par with 100% RDF (S_3) (87.8 and 99.7 cm^2) during 2018 and 2019. The leaf area obtained with application of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) was at par with the 75% RDF alone during the both the years.

Whereas, 60 DAS, application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) expressed significantly higher leaf area $plant^{-1}$ of 722.6 and 812.1 cm^2 during both the years

but was at par with application of 100% RDF (S_3) during 2019. Application of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 620.1 and 736.1 cm^2 leaf area in the both the years was significantly higher leaf area over 75% RDF alone (S_1) during 2018 but found at par in 2019.

At later stages *i.e.,* during flowering and grain filling (90 DAS), higher leaf area $plant^{-1}$ (1004.9 and 1059.9 cm^2) was attained with the 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) which was significantly higher over other treatments. Other treatments also showed distinct variation with higher leaf area (921.3, 1014.9 cm^2) with 100% RDF (S_3), followed by 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with leaf area of 824.1 and 981.6 cm^2 $plant^{-1}$ during both the years. Notably lower leaf area (735.0, 931.5 cm^2 $plant^{-1}$) was observed with application of 75% RDF alone (S_1) during both the years. Application of recommended dose of NPK results in proper leaf expansion, increases leaf surface area and number of leaves and results in better efficiency of chlorophyll during photosynthesis and this overall improvement gets translocated into better growth of the plant resulting in increased leaf area index. Besides application of FYM enriched microbial consortia, apart from improving soil physico-chemical and biological properties of soil releases adequate quantities of nitrogen and phosphorus to boost up the growth of the crop thereby increasing leaf area. These findings are in conformity with Ade *et al.* (2018).

Interaction of leaf area index of pigeon crop was found non significantly influenced by different dates of sowing (main treatments) and various integrated nutrient management (sub treatments).

Dry matter production (g m^{-2})

Dry matter accumulation is another important character to express the growth and metabolic efficiency of the plant, which ultimately influence the yield. Crop performance and final crop yield depends on total dry matter accumulation at different crop growth stages. To visualize the influence of different treatments, the data pertaining to dry matter accumulation at different growth stages *i.e.,* 30, 60 and 90 DAS were analysed statistically and is presented in Table 4.

The pooled results from 2018 and 2019 showed that, the significantly highest dry matter accumulation at 30, 60 and 90 DAS respectively (47.5, 268.7 and 441.1 g m^{-2}) was the result of early sowing in July 1st due to higher metabolic activity of the plants and solar energy harvesting efficiency of plants in the optimum sowing time coupled with favourable climate conditions especially temperature, rainfall and solar radiation which produced higher dry matter. The variation between dry matter accumulation at 20th July (M_2) and 10th August (M_3) was at 30 DAS not different significantly by accumulating 42.9 and 40.8 g m^{-2}, As the crop advances to flowering and maturity stages *i.e.,* 60 and 90 DAS, the dry matter accumulated at 60 and 90 DAS for July 20th (M_2) sowing was significantly higher over the August 10th (M_3) sowing. In the sub treatment, nitrogen supplied through the inorganic and organic sources like application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} had significantly recorded higher accumulation of dry matter at 30 (49.4 g m^{-2}), 60 (286.3 g m^{-2}) and 90 DAS (457.6 g m^{-2}). Whereas at 30 DAS, there is no significant difference in accumulation of dry matter with application of 100% RDF alone (S_3) and 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4). As the crop growth progress to 60 and 90 days, notable variation was observed in the dry matter accumulation between supplication of 100% RDF (S_3) and 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4). The least dry matter accretion was realized by the administering 75% RDF alone (S_1) at 30, 60 and 90 DAS of the pooled results shown in the Table 4.

During both the years of field study *i.e.,* 2018 and 2019 at 30 days after sowing, pigeonpea crop sown on July 1st (M_1) recorded dry matter accumulation (45.6 and 49.4 g m^{-2}) and was at par with 20th July sowing (42.3 g m^{-2}) in 2018 and significantly higher in 2019 with 43.6 g m^{-2}. The dry matter accumulation in July 20th and August 10th were found significantly indistinct at 30 DAS. At 60 DAS, early sowing of pigeonpea on July 1st (M_1) (246.8 and 290.6 g m^{-2}) was recorded significantly higher dry matter accumulated during 2018 and 2019 compared to late sowing on August 10th sowing (195.6 and 236.4 g m^{-2}). The pigeonpea sown on July 20th (229.5 and 270.9 g m^{-2}) was on par with early sown pigeonpea *i.e.,* July 1st in the first and second year of experiment. Likewise, 90 DAS of pigeonpea also reported almost similar results *i.e.,* July 1st (M_1) sown pigeonpea has recorded highest dry matter accumulation with 402.3 and 480.0 g m^{-2} in 2018 and 2019. This was at par with July 20th (M_2) in

Table 4. Effect of dates of sowing and INM on dry matter production (g m-2) of super early pigeonpea

Treatments	30 DAS			60 DAS			90 DAS		
	2018	2019	Pooled mean	2018	2019	Pooled mean	2018	2019	Pooled mean
Main treatments (Dates of Sowing)									
M_1 - 1st July	45.6	49.4	47.5	246.8	290.6	268.7	402.3	480.0	441.1
M_2 - 20th July	42.3	43.6	42.9	229.5	270.9	250.2	368.7	415.7	392.2
M_3 - 10th August	40.4	41.1	40.8	195.6	236.4	216.0	318.7	367.1	342.9
SE m (±)	0.9	1.0	0.7	5.9	8.8	3.6	11.2	12.9	8.9
CD (P=0.05%)	3.6	3.8	2.8	23.1	34.5	14.0	43.9	50.8	34.8
Sub treatments (INM)									
S_1 - 75 % RDF	40.5	39.3	39.9	177.8	236.3	207.0	303.4	349.6	326.5
S_2 - 75 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	41.0	42.6	41.8	201.8	255.8	228.8	330.6	403.6	367.1
S_3 - 100 % RDF	43.5	44.2	43.9	247.4	268.1	257.8	388.7	445.5	417.1
S_4 - 100 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	46.3	52.7	49.4	269.0	303.6	286.3	430.3	485.0	457.6
SE m (±)	1.0	1.1	0.7	4.7	9.5	6.9	5.2	10.8	6.9
CD (P=0.05%)	3.5	3.7	2.4	16.1	33.0	23.8	17.9	37.2	23.9
Interaction effect									
Main at same level of sub									
SE m (±)	3.3	1.8	2.3	8.9	11.6	8.3	17.5	22.6	14.0
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS
Sub at same level of Main									
SE m (±)	2.7	1.7	1.9	8.6	11.9	7.1	16.8	20.9	13.4
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS

2018 and significantly higher over July 20th (M_2) in 2019. The lowest dry matter accumulation was realized by late sowing of pigeonpea on August 10th (M_3) with accumulation of 318.7 and 367.1 g m^{-2} dry matter during 2018 and 2019 respectively. Among all the dates of sowing, July 1st (M_1) was shown to be superior to other sowing dates in terms of dry matter accumulation which might be due to congenial weather condition like optimum amount and uniform distribution of rainfall and favorable temperature prevailed during vegetative period of pigeopea crop which helped in improvement of dry matter production. These results were in conformity with Patel *et al.* (2000) and Rajesh *et al*. (2020).

The pigeonpea crop fertilized with 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) at 30 DAS had produced dry matter accumulation (46.3 and 52.7 g m^{-2}) which was at par with 100% RDF (S_3) alone in 2018 and significantly higher in 2019. The application of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 41.0 and 42.6 g m^{-2} in 2018 and 2019 was found at par with 75% RDF alone (S_1) with 40.5 g m^{-2} in 2018 and significantly higher over 39.3 g m^{-2} dry matter accumulated in the year 2019. At 60 DAS also, application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) had significantly recorded higher dry matter accumulation (269.0 and 303.6 g m^{-2}) followed by application of 100% RDF alone (S_3) (247.4 and 268.1 g m^{-2}). The INM practice with 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 201.8 and 255.8 g m^{-2} recorded significant results over the 75% RDF (S_1) during 2018 and 2019, respectively.

The maximum dry matter production of pigeonpea at 90 DAS was recorded with 100% RDF

+ FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) (430.3 and 485.0 g m^{-2}) which was significantly higher over the dry matter registered with S_3 *i.e.,* 100 % RDF (388.7 and 445.5 g m^{-2}) and 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 330.6 and 403.6 g m^{-2}. The lowest dry matter accumulation was realized with S_1 *i.e.*, 75% RDF (303.4 and 349.3 g m^{-2}) only during 2018 and 2019, respectively. The increase in periodic dry matter accumulation with application of integrated fertilizer management may be attributed to increase in plant height and leaf area index resulting in better light interception by crop which accumulated more photosynthates and thus produced more dry matter. Further, FYM enriched with microbial consortia brought nutrients to available form in gradual process and improved the soil physical characters, which might have increased the availability of nutrients. These results are in line with those of Tilak *et al.* (2006).

Interaction effect between sowing dates and integrated nutrient management was non significant in respective to dry mater production at all the growth stages of pigeonpea crop.

YIELD

Seed yield (kg ha^{-1})

Seed yield of pigeonpea as influenced by dates of sowing and different INM are presented in Table 5. On the basis of pooled analysis, it was observed that the seed yield ranged between 559 to 759 kg ha^{-1} among the different treatments. Significantly the higher seed yield of pigeonpea (759 kg ha^{-1}) was recorded with early sowing on July 1st treatment followed by the July 20th sowing with 626 kg ha^{-1}. Significantly lower seed yield was noticed as pigeonpea crop sown on August 10th (M_3) with 576 kg ha^{-1} seed yield. Similarly, the combined application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1}

Table 5. Effect of dates of sowing and INM on yield of super early pigeonpea

Treatments	Seed Yield (kg ha^{-1})			Stover Yield (kg ha^{-1})			Harvest Index (%)		
	2018	2019	Pooled mean	2018	2019	Pooled mean	2018	2019	Pooled mean
Main treatments (Dates of Sowing)									
M_1 - 1st July	739	779	759	3402.5	3527.4	3464.9	17.8	18.0	17.9
M_2 - 20th July	606	646	626	3146.4	3245.4	3195.9	16.1	16.6	16.3
M_3 - 10th August	545	573	559	3052.3	3121.6	3087.0	15.1	15.5	15.3
SE m (±)	20.0	14.8	17.2	56.8	77.5	62.2	0.4	0.4	0.4
CD (P=0.05%)	78.5	58.0	67.7	223.1	304.1	244.2	1.7	1.6	1.6
Sub treatments (INM)									
S_1 - 75 % RDF	554	594	574	3043.1	3113.4	3078.2	15.4	16.0	15.7
S_2 - 75 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	598	632	615	3138.7	3269.4	3204.0	15.9	16.1	16.0
S_3 - 100 % RDF	645	678	662	3251.5	3356.0	3303.8	16.5	16.8	16.7
S_4 - 100 % RDF + FYM enriched with microbial consortia (1 t ha^{-1})	724	758	741	3368.3	3453.7	3411.0	17.5	17.9	17.7
SE m (±)	14.4	11.7	12.2	36.2	42.8	25.5	0.3	0.3	0.3
CD (P=0.05%)	49.7	40.6	42.2	125.3	148.2	88.4	1.1	1.1	0.9
Interaction effect									
Main at same level of sub									
SE m (±)	27.0	28.0	26.4	83.2	113.8	79.7	0.7	0.8	0.7
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS
Sub at same level of Main									
SE m (±)	27.3	25.1	25.5	81.6	111.5	82.7	0.7	0.7	0.6
CD (P=0.05%)	NS	NS	NS	NS	NS	NS	NS	NS	NS

(S_4) was identified as best INM practice to yield 741 kg ha^{-1} seed. The next best treatment followed significantly with supplication of 100% RDF alone (S_3) with 662 kg ha^{-1} and application of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 615 kg ha^{-1}. Significantly lower seed yield was noticed with administering of 75% RDF (S_1) with 574 kg ha^{-1}.

Seed yield was significantly influenced by dates of sowing during 2018 and 2019. The data on seed yield revealed that, maximum seed yield was (739 and 779 kg ha^{-1}) produced when pigeonpea was sown on July 1st (M_1) and was significantly higher over July 20th (606 and 646 kg ha^{-1}) and August 10th (545 and 573 kg ha^{-1}) sowing dates. The higher seed yield with July 30th sowing was probably due to good seed set favoured by warm weather prevailed during at maturity. Similar results were reported by Chih-Li Yu *et al.* (2014) and Patil *et al.* (2018).

The seed yield of pigeonpea was higher with application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) with 724 and 758 kg ha^{-1} in 2018 and 2019 years respectively. These findings were significantly superior over the provision of 100% RDF alone (S_3) with 645 and 678 kg ha^{-1} and followed by 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) (598 and 632 kg ha^{-1}). The minimum seed yield was obtained with the application of 75% RDF alone (S_1) with 554 and 594 kg ha^{-1} during 2018 and 2019 respectively. Significant increase in seed yield of pigeonpea with fertilizers coupled with organic manures might have supplied nutrients improving crop growth, nutrient uptake and yield attributes. Similar results were reported by Ahmad *et al.* (2017) and Ade *et al.* (2018).

The synergy effect of sowing dates and integrated nutrient management were not statistically significant during both the years of experimentation.

Stover yield (kg ha^{-1})

Stover yield of pigeonpea as influenced by dates of sowing and different INM are presented in Table 5. The pooled analysis of the two years data revealed that, the significantly higher stover yield of pigeonpea was recorded with the timely sowing of pigeonpea *i.e.,* on July 1st (M_1) (3465 kg ha^{-1}) followed by the July 20th (M_2) with 3196 kg ha^{-1} and August 10th (M_3) with 3087 kg ha^{-1} stover yield. Similarly, the combination of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) was identified as best INM practice to produce 3411 kg ha^{-1} stover yield. The next best INM practice was application of 100% RDF (S_3) with 3304 kg ha^{-1} and followed by administering of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 3204 kg ha^{-1}. Significantly lower stover yield was noticed under in the S_1 (75% RDF) treatment with 3078 kg ha^{-1}.

Stover yield was significantly influenced by dates of sowing during 2018 and 2019. The data on stover yield revealed that, maximum stover yield was (3402 and 3527 kg ha^{-1}) produced when pigeonpea was sown on July 1st (M_1) and was significantly higher over July 20th stover yield (3146 kg ha^{-1}) in 2018 and at par in 2019 (3245 kg ha^{-1}). The lower stover yield was administered with August 10th sowing with 3052 and 3122 kg ha^{-1} during 2018 and 2019 years. Stover yield of crop is the outcome of plant through growth attributes like plant height, dry matter accumulation and partitioning of dry matter at grain filling stage. Sowing of pigeonpea on July 1st resulted maximum stover yield due to optimum utilization of solar radiation, temperature, higher assimilates production and its conversion to starch results in higher straw yield. These finding are similar to those reported by Egbe *et al.* (2013) and Malik and Yadav (2014).

The stover yield of pigeonpea was higher with application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) with 3368 and 3454 kg ha^{-1} in first and second years and was on par with supplication of 100% RDF alone (S_3) in 2018 with 3251 kg ha^{-1} and significantly differed in 2019 with 3356 kg ha^{-1} stover yield. The application of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) recorded 3139 and 3269 kg ha^{-1} of stover yield in 2018 and 2019. This was on par with stover yield recorded by supplication of 75% RDF alone (S_1) in 2018 and significantly superior in 2019. Significant increase in stover yield of pigeonpea with fertilizers coupled with organic manures might have supplied nutrients for good crop growth, nutrient uptake and yield attributes. Similar results were reported by Ahmad *et al.* (2017).

The interaction effect of sowing dates and integrated nutrient management were not statistically significant during both the years of experimentation.

Harvest index (%)

The data on harvest index (HI) as influenced by main and sub treatments is presented in Table 5. Harvest index of pigeonpea was influenced by sowing dates in the main treatments and the expressed in pooled results of the 2018 and 2019 revealed that, significantly highest harvest index was recorded by the July 1st (M1) sown pigeonpea (17.9%) and it was on par with July 20th sowing (16.3%) and followed significantly with August 10th date of sowing (15.3%). Similarly in the subplot INM treatments 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) was identified as best INM practice to attain highest harvest index with 17.7% followed by fertilization with 100% RDF (S_3) with 16.7% and application of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) with 16.0%. Significantly lower harvest index was noticed under in the S_1 (75% RDF) treatment with 15.7%.

Sowing of pigeonpea crop on July 1st resulted significantly highest harvest index (17.8 and 18.0%) and it was on par with July 20th in the year 2019 with 16.6%. Minimum harvest index was obtained with August 10th sown (M_3) with 15.1 and 15.5 during both the years. Optimum utilization of solar radiation, temperature, higher assimilates production and its conversion to starch results in higher biomass, seed yield leading to higher harvest index. These observations corroborated with those made by Kumar *et al.* (2008).

Integrated nutrient management treatments during the both the years, application of 100% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_4) was recorded highest harvest index (17.5 and 17.9% respectively) fallowed on par by application of 100% RDF (S_3) with 16.5 and 16.8%. The administration of 75% RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} (S_2) recorded 15.9 and 16.1% of harvest index was significantly on par with application of 75% RDF only (S_1) (15.4 and 16.0%) in the first and second year of study. Balanced nutrition through inorganic fertilizers coupled with organic manures had supplied nutrients for higher biomass, seed yields, partitioning of dry matter between grain and other plant parts leading to higher harvest index, similar results confirmed by Ade *et al.* (2018).

The interaction effects of harvest index of pigeonpea with sowing dates and integrated nutrient management were non significant during both the years of experiment.

CONCLUSION

Based on the research results, it is concluded that the sowing super early pigeonpea in the first fort of July and with 100 RDF + FYM enriched with microbial consortia @ 1 tonne ha^{-1} resulted in relatively higher final plant population, plant height, leaf area per plant and dry matter accumulation and finally responsible to attain maximum seed yield, stover yield and harvest index of super early pigeonpea. It passed the way for super early pigeonpea based double cropping system in semi arid regions of Telangana.

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Research Article
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CHARACTER ASSOCIATION AND PATH COEFFICIENT ANALYSIS FOR GRAIN YIELD AND ITS COMPONENTS IN MAIZE (*Zea mays* L.)

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ABSTRACT

An investigation was carried out with the objective of assessing the magnitude of the association between grain yield and its component characters. Thirty nine genotypes consisting of eight parents, twenty eight crosses obtained by crossing eight inbred lines using Diallel mating design (without reciprocals), and three checks were evaluated in randomized block design with three replications. In the present study the results indicated that the genotypic correlation coefficient is greater than the corresponding phenotypic correlation coefficient for all the traits studied which indicates that though there is strong inherent association between characters studied, its expression is masked due to influence of environment. Correlation coefficient analysis of grain yield per plant showed strong and significant positive association with ear length, number of kernels per row, ear diameter, plant height, 100-kernel weight, ear height and number of kernel rows per ear at genotypic and phenotypic level. However, days to 50% tasseling and days to 50% silking exhibit negative correlation with grain yield, while shelling percentage showed non significant positive. Path coefficient analysis revealed, the number of kernels per row exerted maximum positive direct effect on grain yield per plant followed by ear length, days to maturity, ear diameter, 100-kernel weight and shelling percentage. The high direct effects of number of kernels per row and ear length appeared to be the main factor for their strong association with grain yield per plant. Hence, direct selection for these traits would be effective for grain yield improvement in maize.

Keywords: Correlation coefficient, diallel mating design, grain yield, maize, path coefficient

Maize (*Zea mays* L.) is one of the important cereal crops and occupies a prominent position in global agriculture. Since the centuries maize plant was known for it's multifariously use. Maize is used as human food, livestock feed, producing alcoholic and non-alcoholic drinks, built material, raw material for fuel, medical industries (Bekric and Radosavljevic, 2008). Keeping in view of wide utilization of maize, the main goal of all maize breeding programs is to obtain new inbreds and hybrids that will outperform the existing hybrids with respect to grain yield and yield contributing traits. Grain yield is a complex quantitative trait that depends on a number of factors. Thus, knowledge of interrelationships between grain yield and its contributing components will improve the efficiency of breeding programs through the use of appropriate selection indices (Mohammadi *et al.,* 2003).

Path coefficient analysis has been widely used in crop breeding to determine the nature of relationships between grain yield and its contributing components. The components with significant direct effect on grain yield are potential for selection criteria. Path analysis showed direct and indirect effects of cause variables on effect variables. In path coefficient analysis, the correlation coefficient between two traits is separated into the components which measure the direct and indirect effects. Generally, this method provides more information among variables than do correlation coefficients since this analysis provides the direct effects of specific yield components on yield, and indirect effects via other yield components. Which could be used as target traits for selection and breeding criteria to bring out improvement to maize yields.

MATERIAL AND METHODS

In the present investigation, a total of 39 maize genotypes including eight parents, twenty eight crosses and three checks were evaluated in randomized block design with three replications at Regional Sugarcane and Rice Research Station, Rudrur, Nizamabad. Each entry was sown in two rows of four meters length with a spacing of 75 cm between rows and 20 cm between the plants. The data on twelve quantitative characters namely, plant height (cm), ear height (cm), ear length

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(cm), ear diameter (cm), number of kernel rows per ear, number of kernels per row, 100 kernel weight, shelling percentage and grain yield per plant were recorded on five randomly selected competitive plants in each replication, whereas days to 50 per cent tasseling, days to 50 per cent silking and days to maturity were recorded on plot basis. Ear diameter without husk was measured in centimeters at the middle of the ear at the time of harvest with vernier calipers. Correlation coefficients and path analysis were estimated by following the methods of Al-Jibouri *et al*. (1958) and Dewey and Lu (1959), respectively.

RESULTS AND DISCUSSION

In general, genotypic correlation coefficients were of higher magnitude than the corresponding phenotypic correlation coefficient values which indicates a strong inherent association between characters studied and poor phenotypic expression is due to influence of environment.

In the present study the results indicated that the genotypic correlation coefficient is greater than the corresponding phenotypic correlation coefficient for all the traits studied (Table 1). The similar results were obtained by Ram Reddy and Jabeen (2016) and Chourasia *et al.* (2020). Character association studies indicated that grain yield per plant had highly significant and positive correlation with plant height, ear height, ear length, ear diameter, number of kernel rows per ear, number of kernels per row and 100-kernel weight at genotypic and phenotypic level, suggesting that the importance of these traits for direct selection in any breeding programme designed to increase grain yield in maize. The significant positive association of grain yield with its component traits *viz.,* ear length, ear diameter, number of kernels per row, plant height, ear height, 100 kernel weight, were also reported by Ram reddy and Jabeen (2016), Kandel *et al*. (2017), Prakash *et al*. (2019) and Chaurasia *et al*. (2020).

Among the characters studied, ear length recorded maximum significant positive correlation with grain yield at phenotypic (0.9098) and (0.9430) genotypic level followed by number of kernel rows per plant (0.8985, 0.9410), ear diameter (0.8599, 0.9121), plant height (0.8548, 0.8909) and 100-kernel weight (0.7647, 0.8140). Hence, in the process of selection attention should be given for such traits for improvement of grain yield in maize. Similar results observed by Patil *et al*. (2016). Days to 50 per cent silking and tasseling were shown significant negative correlation with number of rows per ear, number of kernels per row and shelling percentage at genotypic level, while, with grain yield exhibited negative non-significant correlation. Similar results were obtained by Mogesse *et al*. (2021). In the study, grain yield had positive non-significant association with shelling percentage at genotypic (0.1082) and phenotypic level (0.0980), indicating that selection for increased level of these trait may not bring significant change in grain yield. Ear length had maximum significant positive association with grain yield per plant and its other components *viz.,* ear diameter, number of kernel rows per ear, number of kernels per row and 100-kernel weight. Plant height recorded a significant and positive correlation with ear height, ear diameter, ear length, number of kernel rows per ear, number of kernels per row, 100 kernel weight and grain yield per plant at both genotypic and phenotypic level. Prakash *et al.* (2019) also reported a significant positive association of plant height with grain yield in maize.

Path coefficient analysis allows partitioning the correlations into direct and their indirect effects through other attributes by using grain yield as dependent variable (Wright, 1921). The phenotypic and genotypic direct and indirect effects of different characters on grain yield in maize are presented in Table 2.

In the study, number of kernels per row (0.2971) exhibited the largest direct effect on grain yield per plant followed by ear length (0.2661), days to maturity (0.2244), ear diameter (0.1896), 100-kernel weight (0.1630) shelling percentage (0.0920) plant height (0.0668), number of kernel rows per ear (0.0577), ear height (0.0239), days to 50 per cent silking (-0.0170), and days to 50 per cent tasseling (-0.1826) at phenotypic level. Similarly, at genotypic level it found that character number of kernels per row (0.3284) exhibited the largest direct effect on grain yield per plant followed by ear diameter (0.2742), ear length (0.1970), shelling percentage (0.1948), 100-kernel weight (0.1699), ear height (0.0914), Days to 50% tasseling (0.0812), number of kernel rows per ear (0.0730), days to 50 percent silking (0.0718), plant height (-0.0069) and days to maturity (-0.0848).The direct selection in desirable direction for such traits can be effective for yield improvement. The high direct effect of number of kernels per row and ear length appeared to be the

Table 1. Phenotypic (P) and Genotypic (G) correlation coefficient analysis of yield and yield component characters in maize

Source		Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of kernel rows per ear	Number of kernels per row	100 kernel weight (g)	Shelling percent (%)	Grain yield per plant (g)
Days to 50% tasseling	P	**1.0000**	0.9691**	0.9408**	-0.1321	-0.0079	-0.1531	-0.1100	-0.4433 **	-0.2151 *	0.0382	-0.1043	-0.1512
	G	**1.0000**	0.9883**	0.9741**	-0.1569	-0.0158	-0.1614	-0.1401	-0.5208 **	-0.2503 **	0.0226	-0.1847 *	-0.1534
Days to 50% silking	P		**1.0000**	0.9586**	-0.0645	0.0444	-0.1024	-0.0549	-0.3669 **	-0.1638	0.0564	-0.1255	-0.0917
	G		**1.0000**	0.9780**	-0.0852	0.0337	-0.1082	-0.0661	-0.4386 **	-0.1953 *	0.0517	-0.1929 *	-0.0916
Days to maturity	P			**1.0000**	-0.0561	0.0419	-0.0668	-0.0211	-0.3538 **	-0.1333	0.0846	-0.0919	-0.0427
	G			**1.0000**	-0.0615	0.0357	-0.0605	-0.0297	-0.4177 **	-0.1554	0.0793	-0.1174	-0.0427
Plant height (cm)	P				**1.0000**	0.8469**	0.8656**	0.7904 **	0.4545 **	0.7955 **	0.7196 **	-0.0530	0.8548 **
	G				**1.0000**	0.8621**	0.9073**	0.8437 **	0.4939 **	0.8314 **	0.7635 **	-0.0839	0.8909 **
Ear height (cm)	P					**1.0000**	0.7150**	0.7442 **	0.3781 **	0.6292 **	0.6354 **	-0.1748	0.7182 **
	G					**1.0000**	0.7516**	0.7974 **	0.4290 **	0.6686 **	0.6783 **	-0.2984 **	0.7584 **
Ear length (cm)	P						**1.0000**	0.8089 **	0.4044 **	0.8696 **	0.7403 **	-0.0168	0.9098 **
	G						**1.0000**	0.8761 **	0.4392 **	0.9116 **	0.7973 **	-0.0405	0.9430 **
Ear diameter (cm)	P							**1.0000**	0.4686 **	0.7696 **	0.7055 **	-0.0270	0.8599 **
	G							**1.0000**	0.5353 **	0.8335 **	0.7591 **	-0.1541	0.9121 **
Number of kernel rows	P								**1.0000**	0.5354 **	0.0423	0.1083	0.4771 **
	G								**1.0000**	0.5650 **	0.0588	0.0528	0.5096 **
Number of kernels per row	P									**1.0000**	0.6574 **	0.0626	0.8985 **
	G									**1.0000**	0.7030 **	0.0483	0.9410 **
100-kernel weight (g)	P										**1.0000**	-0.0124	0.7647 **
	G										**1.0000**	-0.0614	0.8140 **
Shelling percent (%)	P											**1.0000**	0.0980
	G											**1.0000**	0.1082
Grain yield per plant (g)	P												**1.0000**
	G												**1.0000**

P: Phenotypic correlation coefficient; G: Genotypic correlation coefficient , * Significant at 5 per cent level; ** Significant at 1 per cent level

Table 2. Phenotypic (P) and Genotypic (G) path coefficient analysis of yield and yield component characters in maize

Source		Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of kernel rows per ear	Number of kernels per row	100 kernel weight (g)	Shelling percent (%)	Grain yield per plant (g)
Days to 50% tasseling	P	**-0.1826**	-0.1770	-0.1718	0.0241	0.0014	0.0280	0.0201	0.0810	0.0393	-0.0070	0.0191	-0.1512
	G	**0.0812**	0.0803	0.0791	-0.0127	-0.0013	-0.0131	-0.0114	-0.0423	-0.0203	0.0018	-0.0150	-0.1534
Days to 50% silking	P	-0.0163	**-0.0170**	-0.0162	0.0011	-0.0007	0.0017	0.0009	0.0062	0.0028	-0.0010	0.0021	-0.0917
	G	0.0710	**0.0718**	0.0702	-0.0061	0.0024	-0.0078	-0.0047	-0.0315	-0.0140	0.0037	-0.0139	-0.0916
Days to maturity	P	0.2112	0.2152	**0.2244**	-0.0126	0.0094	-0.0150	-0.0047	-0.0794	-0.0299	0.0190	-0.0206	-0.0427
	G	-0.0826	-0.0830	**-0.0848**	0.0052	-0.0030	0.0051	0.0025	0.0354	0.0132	-0.0067	0.0100	-0.0427
Plant height (cm)	P	-0.0088	-0.0043	-0.0037	**0.0668**	0.0566	0.0578	0.0528	0.0304	0.0531	0.0481	-0.0035	0.8548 * *
	G	0.0011	0.0006	0.0004	**-0.0069**	-0.0060	-0.0063	-0.0058	-0.0034	-0.0057	-0.0053	0.0006	0.8909 * *
Ear height (cm)	P	-0.0002	0.0011	0.0010	0.0202	**0.0239**	0.0171	0.0178	0.0090	0.0150	0.0152	-0.0042	0.7182 * *
	G	-0.0014	0.0031	0.0033	0.0788	**0.0914**	0.0687	0.0729	0.0392	0.0611	0.0620	-0.0273	0.7584 * *
Ear length (cm)	P	-0.0407	-0.0272	-0.0178	0.2303	0.1902	**0.2661**	0.2151	0.1076	0.2313	0.1969	-0.0045	0.9098 * *
	G	-0.0318	-0.0213	-0.0119	0.1788	0.1481	**0.1970**	0.1726	0.0865	0.1796	0.1571	-0.0080	0.943 * *
Ear diameter (cm)	P	-0.0209	-0.0104	-0.0040	0.1499	0.1411	0.1534	**0.1896**	0.0889	0.1459	0.1338	-0.0051	0.8599 * *
	G	-0.0384	-0.0181	-0.0081	0.2314	0.2187	0.2402	**0.2742**	0.1468	0.2286	0.2081	-0.0422	0.9121 * *
Number of kernel rows	P	-0.0256	-0.0212	-0.0204	0.0262	0.0218	0.0233	0.0270	**0.0577**	0.0309	0.0024	0.0062	0.4771 * *
per ear	G	-0.0380	-0.0320	-0.0305	0.0360	0.0313	0.0321	0.0391	**0.0730**	0.0412	0.0043	0.0039	0.5096 * *
Number of kernels	P	-0.0639	-0.0487	-0.0396	0.2364	0.1870	0.2584	0.2287	0.1591	**0.2971**	0.1953	0.0186	0.8985 * *
per row	G	-0.0822	-0.0642	-0.0510	0.2731	0.2196	0.2994	0.2738	0.1856	**0.3284**	0.2309	0.0158	0.9409 * *
100-kernel weight (g)	P	0.0062	0.0092	0.0138	0.1173	0.1036	0.1207	0.1150	0.0069	0.1072	**0.1630**	-0.0020	0.7647 * *
	G	0.0038	0.0088	0.0135	0.1298	0.1153	0.1355	0.1290	0.0100	0.1195	**0.1699**	-0.0104	0.814 * *
Shelling percent (%)	P	-0.0096	-0.0115	-0.0084	-0.0049	-0.0161	-0.0015	-0.0025	0.0100	0.0058	-0.0011	**0.0920**	0.0980
	G	-0.0360	-0.0376	-0.0229	-0.0164	-0.0581	-0.0079	-0.0300	0.0103	0.0094	-0.0120	**0.1948**	0.1082

Phenotypic residual effect = 0.2701, Genotypic residual effect = 0.1034

P represents phenotypic correlation coefficient; G represents genotypic correlation coefficient; Bold values are direct effects

* Significant at 5 per cent level; ** Significant at 1 per cent level

main factors for their strong association with grain yield per plant. Similar results of direct positive effect of number of kernels per row on grain yield was found by earlier workers Kandel *et al*. (2017) and Raghu *et al.* (2011) and Prakash *et al*. (2019). Hence, during selection attention should be given for such traits for improvement of grain yield. Days to 50 percent tasseling (-0.1826) and days to 50 percent silking (-0.0170) had negative direct effect on grain yield at phenotypic level. Plant height had negative direct effect on grain yield at genotypic level. Plant height had negative genotypic direct effect on grain yield per plant. The positive indirect contribution of plant height on grain yield was through days to 50 percent tasseling, days to 50% silking, days to maturity and shelling percentage at genotypic level. It also had indirect negative contribution through plant height, ear height, ear diameter, ear length, number of kernels per ear, number of kernels per row and 100-kernel weight at genotypic level. Similar results of direct negative effects of plant height on grain yield were reported by earlier workers Begum *et al.* (2016) and Shikha *et al*. (2020).

Number of kernels per row had direct positive influence on grain yield, while it had indirect positive influence through plant height, ear height, ear diameter, ear length, number of kernel rows per ear, 100-kernel weight and shelling percentage. It also had indirect negative contribution through days to 50% tasseling, days to 50 percent silking and days to maturity at genotypic and phenotypic level. Similar results of direct positive effect of number of kernels per row on grain yield was found by Kandel *et al*. (2017).

The 100-kernel weight exhibited the direct genotypic positive effect on grain yield per plant. An indirect positive influence through plant height, ear height, ear diameter, ear length, number of kernel rows per ear and number of kernels per row and indirect negative influence through shelling percentage at genotypic and genotypic level. Similar results of direct positive effect of 100- kernel weight on grain yield was found by earlier workers Roy *et al*. (2018) and Yahaya *et al*. (2021).

The residual effect was 0.2701 for phenotypic and 0.1034 for genotypic path coefficient analysis. As residual effect is low, it indicates that all the characters studied contributed for grain yield.

CONCLUSION

According to the research on correlation, selection of promising genotypes for ear length, number of kernels per row, ear diameter, plant height, 100-kernel weight, ear height and number of kernel rows per ear may be associated with increasing grain yield as they had highly significant positive association with grain yield. The path coefficient analysis clearly emphasized the need for selection of ideal genotypes with greater number of kernels per row, ear length, shelling percentage, 100-kernel weight, ear height and number of kernel rows per ear, as these were found to be the important traits with direct effect on grain yield.

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Research Article
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EFFECT OF TILLAGE AND WEED MANAGEMENT PRACTICES ON WEED DYNAMICS, YIELD ATTRIBUTES AND YIELD OF MAIZE IN SOUTHERN TELANGANA ZONE

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ABSTRACT

Conservation Agriculture (CA) is an alternative sustainable production system to the conventional tillage system for resource conservation in rainfed agriculture. Weed management is the major constraint for the adoption of CA in rainfed regions. A two years study was conducted at Agricultural Research Station, Tandur, during two consecutive *kharif* seasons of 2018 and 2019 to investigate the effect of tillage and weed management practices on weed dynamics, yield attributes and yield of maize in the Southern Telangana Zone. The experiment was carried out in strip-plot design with tillage methods assigned to vertical plots and weed management practices allotted to horizontal plots which were replicated thrice. It was observed that there is no significant difference between tillage methods but weed management practices significantly influenced weed density, weed dry weight, yield attributes and yield. The findings revealed that conventional tillage and hand weeding twice at 20 and 40 DAS maintained the weed density and weed dry weight below the economic threshold level and enhanced the yield of maize in clay loam soils under rainfed conditions. The interaction effect of tillage and weed management practices was found to be non-significant.

Keywords: Atrazine, conservation agriculture**,** maize, reduced tillage, tembotrione

Maize (*Zea mays* L.) belongs to the family Poaceae is one of the most important grain crops in the World's agricultural economy as a staple food crop for human beings, feed for animals, and as a basic raw material for the production of starch, oil, proteins, alcoholic beverages, food sweeteners, and more recently as bio-fuel (Das *et al*., 2008). Before the beginning of the twenty-first century, India was a net importer of maize, and the productivity was not enough to meet the growing demand from poultry and other sectors. However, adoption of hybrids, particularly in non-traditional maize growing states like Karnataka and Andhra Pradesh, and to some extent in some of the traditional maize growing states like Bihar and Maharashtra, enhanced the maize productivity and production in the country sharply to higher levels, which assured not only its self-sufficiency but also gave some scope on the export (Commodity online, 2009). In India, it is cultivated in an area of 9.56 M ha with production and productivity of 28.76 MT and 3006 kg ha^{-1}, respectively (Indiastat, 2019-20). Out of the total maize produced in India, about 35% is used for human consumption, 25% each in poultry feed and cattle feed and 15% in food processing and other industries (corn flakes, popcorn, starch, dextrose, corn syrup, corn oil, etc.).

Conventional agriculture is characterized by intense tillage for weed control and an increase in crop productivity but this enhances soil erosion and degradation which has a negative impact on the environment and natural resources. In this context, conservation agriculture (CA) with three key principles of minimum soil disturbance, crop rotations and residue retention has opened a new paradigm to increase resource use efficiency and mitigation of adverse effects of climate change by increasing carbon sequestration and reducing GHGs (Green House Gases) emissions. The major challenges perceived for low adoption of CA in rainfed regions of developing countries by the producers are: non-availability of CA machinery, competing demand for crop residues for alternative uses, crop-weed competition and weed management (Farooq *et al*., 2011). Hence, the benefits of CA systems in irrigated regions in general and rainfed regions in particular, may be offset by heavy weed infestation and shifts in weed communities (increase, decrease or extinction of a weed species) (Zhang and

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Wu, 2021), since weeds are both agronomical and ecologically key variables in crop production.

Weeds reduce maize yields by an average of 12.8% despite weed management measures and 29.2% if no weed control is used (Dogan *et al*., 2004). So, the maize crop must be kept free of weeds for the initial period of 30 days after crop emergence. Wider spacing coupled with increased fertilizer application and slow germination of maize favour the weed growth which results in drastic yield reduction. Repetitive tillage operations may not necessary if weeds are controlled by cultural or chemical methods. Further, various studies have shown that in many cases tillage operations as intensive as practiced are not required. Information on the influence of preparatory tillage and different weed management practices on the weed dynamics and the productivity of crops is meagre. Keeping in view the above backdrop, a field experiment entitled "effect of tillage and weed management practices on weed dynamics, yield attributes and yield of maize in Southern Telangana Zone" is planned.

MATERIAL AND METHODS

A field investigation was conducted during two consecutive *kharif* seasons of 2018 and 2019 at Agricultural Research Station (ARS), Tandur which is geographically situated at an altitude of 461 m above mean sea level (MSL) (17° 15' N latitude and 77° 35' E longitude). During the growth period, total rainfall of 374.70 mm was received in 31 rainy days during *kharif* 2018 and 675.20 mm in 49 rainy days during *kharif* 2019. The crop was grown completely under rainfed conditions. Soil of the experimental field was clay loam in texture, non-saline (0.30 dSm^{-1}), neutral in reaction (pH 7.91), low in organic carbon (0.37%), medium in available nitrogen (228 kg ha^{-1}) and phosphorus (23 kg ha^{-1}) and high in available potassium (405 kg ha^{-1}). The experiment was laid out in a strip plot design with three replications. The treatments comprised of two tillage methods *viz.*, conventional tillage (T_1) and reduced tillage (T_2) assigned to vertical plots (378 m^2) and seven weed management practices *viz.*, Weedy check (W_1), Weed free (W_2), Intercropping with cowpea (W_3), Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (early PoE) *fb* HW at 40 DAS (W_4), Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (PoE) (W_5), Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* paraquat 24% SL @ 1.0 kg *a.i.* ha^{1} (PoE) (W_6) and Sorghum + Parthenium leach @ 15 L ha^{-1} each (PE) *fb* Sorghum + Parthenium leach @ 15 L ha^{-1} each (PoE) (W_7) which were allotted to the horizontal plots (54 m^2). Buffer strips of 1 m width were kept between the plots. Description of the tillage methods is furnished in Table 1.

Maize hybrid DHM-117 was hand-dibbled on a flat bed at a spacing of 60 × 20 cm and grown with all general cultivation practices except for tillage and weed management practices. The required quantities of herbicides and leaches were administered according to treatment *i.e* as pre-emergence at one day after sowing of the crop, as early-post emergence at 15 DAS and as post-emergence at 25 DAS of the crop. Spraying was done using a knapsack sprayer fitted with a flat fan nozzle, and paraquat was applied with a hood. Hand weeding was done in weed free treatment with the help of hand hoe at 20 and 40 DAS. In the intercropping system treatment, two rows of cowpea (*vigna unguiculata* L.) variety TPTC-29 was planted in between two rows of maize. Oven-dried powders of allelopathic plants (Sorghum and Parthenium) were soaked in water in 1:10 (w/v) for 48 hours. Finally, extracts were filtered through muslin cloth to obtain respective water extracts (Cheema and Khaliq, 2000). A uniform dose of 180 kg N, 60 kg P_2O_5 and 50 kg K_2O ha^{-1} was applied to all plots. Entire doses of phosphorus and potassium were applied as basal in the form of DAP and MOP respectively. Nitrogen in the form of urea after calculating the proportion is supplied through DAP was applied in three splits

Table 1. Tillage practices adopted in maize crop

Tillage	No. of tillage operations	Tillage implement	Timing of tillage operations
Conventional tillage (CT)	2	Cultivator	Summer season Before sowing
	1	Rotavator	Before sowing
Reduced tillage (RT)	1	Cultivator	Before sowing

as per schedule *i.e.*, 1/3rd N as basal, 1/3rd N at 30 DAS and remaining 1/3rd N at 60 DAS. At harvest, plant samples from each plot were harvested to record the yield-attributing characteristics such as cob length, cob girth, number of kernels rows cob^{-1}, number of kernels row^{-1}, number of kernels cob^{-1}, weight of grain cob^{-1}, weight of cob and test weight (100 kernel weight). Maize yields were estimated from the net plot by harvesting all plants in the net plot excluding the border plants in the plot. Weed count and biomass were estimated from three randomly selected quadrates (0.25 m^2) in each plot at harvest. Data recorded on different parameters of maize was statistically analyzed following the analysis of variance for strip plot design. Weed data were subjected to square root transformation ($\sqrt{x}$ + 0.5) before subjecting to statistical analysis to make the analysis of variance valid (Gomez and Gomez, 1984).

Maize equivalent yield (MEY) under intercropping with cowpea was calculated by using the following formula (Tripathi and Singh, 1983).

$$\text{MEY (kg ha}^{-1}) = \frac{Y_C \times P_C}{P_M} + \text{Yield of maize in intercropping treatment (kg ha}^{-1})$$

Where, $Y_{C\,=}$ Yield of cowpea in the intercropping treatment (kg ha^{-1}), P_C = Price of cowpea (kg^{-1}) and $P_{M\,=}$ Price of maize (kg^{-1}).

RESULTS AND DISCUSSION

WEED PARAMETERS

Data on weed flora, weed density and weed dry matter was presented in Tables 2 and 3.

Weed flora

Weed flora of the experimental field belongs to nine taxonomic families, including five grass species, nine broadleaved weed species, and only one species of sedge, *Cyperus rotundus*.

The predominant weed species associated with maize are *Acalypha indica, Amaranthus viridis, Brachiaria reptans*, *Cyperus rotundus*, *Dinebra*

Table 2. Weed flora observed in the experimental plot of maize crop

S.No.	Botanical Name	Common Name	Family
Grasses			
1	*Brachiaria reptans L.*	Running grass	Poaceae
2	*Dactyloctenium aegyptium (L) Beauv*	Crow foot grass	Poaceae
3	*Digitaria sanguinalis (L.) Scop*	Crab grass	Poaceae
4	*Dinebra retroflexa (Vahl.) Panzer.*	Viper grass	Poaceae
5	*Echinochloa colona (L.) Link.*	Jungle rice	Poaceae
Sedges			
1	*Cyperus rotundus L.*	Purple nut sedge	Cyperaceae
Broad leaved weeds			
1	*Acalypha indica L.*	Indian copper leaf	Euphorbiaceae
2	*Amaranthus viridis Hook. F.*	Slender amaranthus	Amaranthaceae
3	*Commelina benghalensis L.*	Day flower	Commelinaceae
4	*Corchorus olitorius L.*	Jews mallow	Tiliaceae
5	*Digera arvensis L.*	Kali gandhari	Amaranthaceae
6	*Euphorbia hirta L.*	Pill pad spurge	Euphorbiaceae
7	*Parthenium hysterophorus L.*	Congress grass	Asteraceae
8	*Phyllanthus niruri L.*	Niruri	Euphorbiaceae
9	*Tridax procumbens L.*	Tridax	Compositae

Table 3. Weed density and dry weight at harvest as influenced by tillage and weed management practices in maize

Treatments	Weed density (No. m^{-2})			Weed dry weight (g m^{-2})		
	2018	2019	Pooled	2018	2019	Pooled
Vertical Plots : Tillage (T)						
T_1 - Conventional tillage (CT)	9.20 (101.61)	10.04 (117.52)	9.64 (109.57)	9.22 (99.97)	10.44 (126.93)	9.85 (113.45)
T_2 - Reduced tillage (RT)	11.00 (135.10)	11.81 (153.81)	11.43 (144.45)	10.40 (122.01)	11.54 (149.69)	10.99 (135.85)
SE(m)±	0.30	0.35	0.31	0.21	0.33	0.31
CD (p=0.05)	NS	NS	NS	NS	NS	NS
CV (%)	14.04	14.70	13.77	10.15	14.06	13.82
Horizontal Plots: Weed Management (W)						
W_1 - Weedy check	15.47 (239.33)	16.49 (272.17)	15.99 (255.75)	15.29 (233.50)	16.81 (282.31)	16.07 (257.90)
W_2 - Weed free (HW at 20 and 40 DAS)	5.24 (29.50)	6.06 (37.67)	5.69 (33.55)	5.33 (28.62)	6.15 (37.94)	5.75 (33.28)
W_3 - Intercropping with Cowpea	12.39 (153.47)	13.46 (181.00)	12.93 (167.24)	12.01 (144.23)	13.49 (181.91)	12.78 (163.10)
W_4 - Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS	5.76 (35.50)	6.57 (44.17)	6.20 (39.83)	5.75 (33.13)	6.62 (43.77)	6.20 (38.45)
W_5 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g a.i. ha^{-1} (PoE)	6.86 (49.33)	7.49 (56.50)	7.22 (52.92)	6.31 (39.82)	7.13 (50.76)	6.73 (45.29)
W_6 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Paraquat 24% SL @ 1.0 kg *a.i.* ha^{-1} (PoE)	10.31 (109.00)	11.03 (121.67)	10.73 (115.33)	9.72 (94.05)	10.70 (113.99)	10.22 (104.02)
W_7 - Sorghum + Parthenium leach @ 15 L ha^{-1} (PE) *fb* Sorghum + Parthenium leach @ 15 L ha^{-1} (PoE)	14.57 (212.33)	15.37 (236.50)	14.97 (224.42)	14.27 (203.57)	16.05 (257.42)	15.18 (230.49)
SE(m)±	0.60	0.55	0.60	0.42	0.50	0.55
CD (p=0.05)	1.84	1.70	1.85	1.31	1.54	1.70
CV (%)	14.56	12.40	14.00	10.63	11.17	13.03
Interaction						
T×W						
SE(m)±	0.55	0.72	0.71	0.50	0.61	0.71
CD (p=0.05)	NS	NS	NS	NS	NS	NS
W×T						
SE(m)±	0.69	0.73	0.77	0.54	0.63	0.74
CD (p=0.05)	NS	NS	NS	NS	NS	NS

***Data in parenthesis are original values that were transformed $\sqrt{x+0.5}$ and analyzed statistically**

retroflexa, *Digera arvensis, Echinocloa colona*, *Euphorbia hirta*, *Phyllanthus niruri* and *Tridax procumbens*. A similar type of weed flora was reported by Swetha *et al*. (2015) and Tarundeep *et al*. (2016).

Weed density

Tillage methods did not show any significant influence on the weed density in maize during both the years of study and pooled means. Weed density was reduced with conventional tillage (109.57 No. m^{-2}) in maize crop due to surface soil inversion and weed seed burial by intensive ploughing over reduced tillage (144.45 No. m^{-2}). Clements *et al*. (1996) found that zero tillage and minimum tillage resulted in greater weed seed deposition at the soil surface and its germination than in conventional tillage. Hume (1991) also documented an increase in perennial and some annual weed species due to reduced tillage.

Weed management practices had a significant effect on weed density in maize during both years and pooled basis. Hand weeding twice at 20 and 40 DAS (33.55 No. m^{-2}) was effective in controlling the total weeds in the experimental plots during *kharif* 2018 and 2019. This was followed by Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS (39.83 No. m^{-2}) and Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (52.92 No. m^{-2}) which was on par with hand weeding twice at 20 and 40 DAS and was equally effective by dropping the population of total weeds. The reasons for this might be due to the mechanism of atrazine by binding to the plasto quinone-binding protein in photosynthesis II. These results were led to the inability to fix CO_2 and uptake of nutrients needed for the plant to survive. Subsequently, weed death occurs due to starvation and oxidative damage caused by a breakdown in the electron transport process. The results are in line with those reported by Rasool and Khan (2016). Early post-emergence application of tembotrione for controlling grasses and broad-leaved weeds affected the weeds causing stunted growth and initially leaves became white in an appearance later it turns yellow in colour. The symptoms appeared within one week after spraying. This herbicide inhibits the activity of 4-hydroxy phenyl pyruvate dioxygenase (HPPD) enzyme in target plants and leads to disruption of carotenoid pigment formation, membrane structure and finally photosynthesis. Within one week after treatment, tembotrione caused a strong photobleaching effect on the shoot, followed by the death of sensitive weeds. *Cyperus rotundus* was the only sedge observed during both years of study. Hand weeding twice at 20 and 40 DAS controlled the sedge during both years. Application of Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS and Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} was found to be effective in suppressing the growth of *Cyperus rotundus*. A significantly maximum number of weeds were found under weedy check (255.75 No. m^{-2}) at harvest, where weeds were not controlled by any means. This might have been due to the uninterrupted growth of weeds by utilizing the growth resource like moisture, nutrient, sunlight to the full extent and offering stiff competition to the crop. These results are in accordance with the results indicated by Deshmukh *et al*. (2014) and Madhavi *et al*. (2014).

Weed drymatter (g m^{-2})

Tillage methods did not show any significant influence on weed dry matter in maize during both the years of study and pooled means. Weed dry weight was lower in conventional tillage (113.45 g m^{-2}) because of the reduced total weed density with lesser individual weed biomass as compared with reduced tillage (135.85 g m^{-2}). These results are in accordance with the findings of Legere and Sampson (1999) and Barberi and Blo Cascio (2001) who have observed higher weed dry weight with more than 60% of weed seedlings emerging from the surface soil layers in non-inversion chisel ploughing and no-tillage systems.

Weed management practices had a significant effect on weed dry matter in maize during both years and pooled basis. Hand weeding twice at 20 and 40 DAS (33.28 g m^{-2}) produced lesser weed dry matter at all the growth stages of the crop, this might be due to the periodical removal of weeds at regular intervals accounting for less count of grasses, sedges and broad-leaved weeds. This was followed by Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS (38.45 g m^{-2}) and Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (45.29 g m^{-2}) during both the years of investigation. The application of atrazine and tembotrione effectively controlled all categories of weeds by inhibiting electron transfer at PSII and disrupting the formation of carotenoids,

respectively leading to reduced growth and finally death of the plant. The higher weed dry matter in weedy check may be related to the open soil surface and niches suitable for germination and free development of weeds. These findings are in agreement with Roy *et al*. (2008) and Swetha *et al*. (2015).

Yield Attributes

Data regarding yield attributes of maize was presented in Tables 4, 5 and 6.

Tillage methods did not show any significant influence on the yield attributes of maize during both the years of study and pooled means. However, higher yield attributes *viz*., length of cob, girth of cob, number of kernel rows cob^{-1}, number of kernels row^{-1}, number of kernels cob^{-1}, weight of cob, weight of grain cob^{-1} and test weight were found in conventional tillage than reduced tillage. Improved physico-chemical condition of the soil, less crop weed competition, higher soil moisture, higher root development increased the space

Table 4. Length and girth of cob as influenced by tillage and weed management practices in maize

Treatments	Length of cob (cm)			Girth of cob (cm)		
	2018	2019	Pooled	2018	2019	Pooled
Vertical Plots : Tillage (T)						
T_1 - Conventional tillage (CT)	14.85	15.63	15.24	12.79	13.46	13.12
T_2 - Reduced tillage (RT)	13.87	14.75	14.31	11.94	12.70	12.32
SE(m)±	0.29	0.33	0.31	0.29	0.30	0.29
CD (p=0.05)	NS	NS	NS	NS	NS	NS
CV (%)	9.55	10.09	9.81	10.95	10.51	10.72
Horizontal Plots : Weed Management (W)						
W_1 - Weedy check	11.59	12.25	11.92	9.97	10.55	10.26
W_2 - Weed free (HW at 20 and 40 DAS)	17.27	18.23	17.75	14.84	15.70	15.27
W_3 - Intercropping with Cowpea	12.94	13.67	13.30	11.12	11.77	11.45
W_4 - Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS	16.50	17.42	16.96	14.18	15.00	14.59
W_5 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g a.i. ha^{-1} (PoE)	15.85	16.74	16.29	13.62	14.41	14.02
W_6 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Paraquat 24% SL @ 1.0 kg *a.i.* ha^{-1} (PoE)	14.05	15.02	14.53	12.22	12.93	12.58

Table 5. Kernel rows cob^{-1}, Kernels row^{-1} and Kernels cob^{-1} as influenced by tillage and weed management practices in maize

Treatments	Kernel rows cob^{-1}			Kernels row^{-1}			Kernels cob^{-1}		
	2018	2019	Pooled	2018	2019	Pooled	2018	2019	Pooled
Vertical Plots : Tillage (T)									
T_1 - Conventional tillage (CT)	13.11	13.80	13.46	25.53	26.98	26.30	340.05	373.66	356.85
T_2 - Reduced tillage (RT)	12.58	13.34	12.96	23.89	25.25	24.57	303.92	337.02	320.47
SE(m)±	0.23	0.26	0.27	0.44	0.45	0.45	6.23	8.67	6.77
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS
CV (%)	8.47	8.90	9.55	8.23	8.01	8.18	8.88	11.19	9.16
Horizontal Plots: Weed Management (W)									
W_1 - Weedy check	10.73	11.34	11.03	19.82	20.92	20.37	214.54	238.18	226.36

Treatments	Kernel rows cob^{-1}			Kernels row^{-1}			Kernels cob^{-1}		
	2018	2019	Pooled	2018	2019	Pooled	2018	2019	Pooled
W_2 - Weed free (HW at 20 and 40 DAS)	14.32	15.13	14.72	28.21	29.75	28.98	403.29	447.45	425.37
W_3 - Intercropping with Cowpea	12.08	12.77	12.42	23.53	24.83	24.18	284.13	316.74	300.43
W_4 - Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS	14.19	14.99	14.59	27.47	28.97	28.22	389.94	419.54	404.69
W_5 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g a.i. ha^{-1} (PoE)	14.06	14.85	14.45	26.81	28.28	27.55	377.45	414.62	396.03
W_6 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Paraquat 24% SL @ 1.0 kg *a.i.* ha^{-1} (PoE)	13.09	13.83	13.46	25.08	26.45	25.76	328.71	366.26	347.49
W_7 - Sorghum + Parthenium leach @ 15 L ha^{-1} (PE) *fb* Sorghum + Parthenium leach @ 15 L ha^{-1} (PoE)	11.43	12.07	11.75	22.37	23.60	22.99	255.92	284.59	270.26
SE(m)±	0.41	0.47	0.27	0.74	0.77	0.78	11.27	13.52	11.05
CD (p=0.05)	1.27	1.45	1.54	2.30	2.39	2.41	34.73	41.66	34.05
CV (%)	7.92	8.50	9.32	7.41	7.30	7.54	8.58	9.32	7.99
Interaction									
T×W									
SE(m)±	0.54	0.60	0.58	1.06	1.11	1.08	15.97	18.07	14.90
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS
W×T									
SE(m)±	0.56	0.62	0.64	1.05	1.09	1.08	15.91	18.15	14.99
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS

Table 6. Weight of cob, Weight of grain cob^{-1} and Test weight as influenced by tillage and weed management practices in maize

Treatments	Weight of cob (g)			Weight of grain cob^{-1} (g)			Test weight (g)		
	2018	2019	Polled	2018	2019	Pooled	2018	2019	Pooled
Vertical Plots : Tillage (T)									
T_1 - Conventional tillage (CT)	116.81	129.38	123.09	80.61	89.16	84.89	23.21	24.46	23.84
T_2 - Reduced tillage (RT)	101.80	114.65	108.18	70.10	78.20	74.15	22.56	23.90	23.23
SE(m)±	2.50	2.81	2.61	1.74	2.02	1.83	0.39	0.44	0.50
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS
CV (%)	10.50	10.58	10.37	10.58	11.07	10.56	7.81	8.43	9.80
Horizontal Plots: Weed Management (W)									
W_1 - Weedy check	66.51	74.33	70.26	41.98	46.91	44.45	19.46	20.53	20.00

Treatments	Weight of cob (g)			Weight of grain cob^{-1} (g)			Test weight (g)		
	2018	2019	Pooled	2018	2019	Pooled	2018	2019	Pooled
W_2 - Weed free (HW at 20 and 40 DAS)	141.60	159.44	150.52	103.00	114.76	108.88	25.57	27.07	26.32
W_3 - Intercropping with Cowpea	87.95	98.20	93.07	57.68	64.40	61.04	20.31	21.43	20.87
W_4 - Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS	137.65	153.03	145.34	99.31	108.84	104.07	25.43	26.82	26.12
W_5 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g a.i. ha^{-1} (PoE)	133.81	146.35	140.08	95.27	105.27	100.27	25.19	26.57	25.88
W_6 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Paraquat 24% SL@ 1.0 kg *a.i.* ha^{-1} (PoE)	113.51	127.45	120.48	75.44	84.70	80.07	22.91	24.33	23.62
W_7 - Sorghum + Parthenium leach @ 15 L ha^{-1} (PE) *fb* Sorghum + Parthenium leach @ 15 L ha^{-1} (PoE)	84.09	95.28	89.69	54.81	60.90	57.85	21.34	22.52	21.93
SE(m)±	4.00	5.14	4.16	2.42	3.33	2.82	0.69	0.78	0.85
CD (p=0.05)	12.33	15.84	12.84	7.46	10.28	8.70	2.14	2.41	2.63
CV (%)	8.97	10.33	8.83	7.88	9.77	8.71	7.44	7.95	8.90
Interaction									
T×W									
SE(m)±	4.81	6.75	1.10	3.48	4.73	3.64	0.96	1.01	1.10
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS
W×T									
SE(m)±	5.08	6.95	1.13	3.34	4.67	3.71	0.96	1.05	1.13
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS

of water, air and nutrient transport, which improved leaf area and crop growth rate. These factors were positively reflected in more photosynthates production and their transfer to reproductive parts might be aided in higher yield attributes in conventional tillage. Reduced tilled plots had lower yield attributes due to poorer water and nutrient intake, which could be related to higher soil bulk density, which limits root penetration into deeper soil layers. Higher weed density in reduced tillage also depleted soil nutrients and moisture, leading to a reduction in crop resource availability thus resulting in a lower yield. These findings are also consistent with those of Anjum *et al*. (2019) and Kumar *et al*. (2018).

Weed management practices had a significant effect on yield attributes in maize during both years and pooled basis. Higher yield attributes *viz*., length of cob, girth of cob, number of kernel rows cob^{-1}, number of kernels row^{-1}, number of kernels cob^{-1}, weight of cob, grain weight cob^{-1} and test weight were produced in Hand weeding twice at 20 and 40 DAS which was at par with Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (early PoE) *fb* HW at 40 DAS and Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (PoE). The crop's efficient exploitation of nutrients, moisture, light and space during critical stages of might

have boosted the production and translocation of assimilates from source to sink, resulting in an increase in yield attributes in these treatments could be to the lower density and biomass of the weeds. The poor yield attributing traits in weedy check treatment might be due to higher weed density during the entire crop growth period which resulted in lower dry matter production and poor assimilate translocation from source to sink. The results were in conformed with the findings of Prithwiraj *et al*. (2018) and Rana *et al*. (2018).

Yield and Harvest Index

Data pertaining to the yield and harvest index of maize was presented in Table 7.

Grain yield

Because of the higher rainfall, the grain output of the maize crop was higher in 2019 than in 2018. The amount of moisture in the soil affects the forms, solubility, and accessibility of plant nutrients required for crop growth and development. The variation in rainfall

Table 7. Yield and Harvest Index of maize as influenced by tillage and weed management practices

Treatments	Grain yield (kg ha^{-1})			Stover yield (kg ha^{-1})			Harvest Index (%)		
	2018	2019	Pooled	2018	2019	Pooled	2018	2019	Pooled
Vertical Plots : Tillage (T)									
T_1 - Conventional tillage (CT)	5036	5268	5152	7028	7297	7242	40.83	41.05	40.94
T_2 - Reduced tillage (RT)	4555	4855	4705	6540	6842	6712	40.01	40.58	40.30
SE(m)±	84.52	97.72	85.71	110.20	128.90	111.57	0.75	0.79	0.84
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS
CV (%)	8.08	8.85	7.97	7.44	8.36	7.33	8.56	8.96	9.53
Horizontal Plots: Weed Management (W)									
W_1 - Weedy check	2483	2673	2578	5156	5352	5415	32.40	33.09	32.74
W_2 - Weed free (HW at 20 and 40 DAS)	6465	6786	6625	7984	8357	8221	44.79	44.85	44.82
W_3 - Intercropping with Cowpea	4308 (MEY)	4542 (MEY)	4425 (MEY)	6262	6511	6437	40.73	41.07	40.90
W_4 - Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (Early PoE) *fb* HW at 40 DAS	6266	6620	6442	7876	8234	8105	44.33	44.59	44.46
W_5 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g a.i. ha^{-1} (PoE)	6083	6389	6236	7802	8147	8025	43.78	43.95	43.87
W_6 - Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Paraquat 24% SL @ 1.0 kg *a.i.* ha^{-1} (PoE)	5013	5273	5143	6814	7131	7022	42.35	42.65	42.50
W_7 - Sorghum + Parthenium leach @ 15 L ha^{-1} (PE) *fb* Sorghum + Parthenium leach @ 15 L ha^{-1} (PoE)	2955	3145	3050	5493	5755	5614	34.56	35.50	35.03
SE(m)±	156.69	178.71	152.20	203.50	231.09	201.03	1.31	1.35	1.29
CD (p=0.05)	482.83	550.68	468.99	627.05	712.06	619.43	4.04	4.15	3.98

Treatments	Grain yield (kg ha^{-1})			Stover yield (kg ha^{-1})			Harvest Index (%)		
	2018	2019	Pooled	2018	2019	Pooled	2018	2019	Pooled
CV (%)	8.00	8.65	7.56	7.35	8.01	7.06	7.96	8.10	7.80
Interaction									
T×W									
SE(m)±	217.00	225.51	207.00	288.23	323.29	285.30	1.65	1.48	1.78
CD (p=0.05)	NS	NS	NS	NS	NS	NS	NS	NS	NS
W×T									
SE(m)±	218.76	236.71	209.46	287.73	323.54	283.96	1.72	1.65	1.76
CD (p=0.05)	NS	NS	645	NS	NS	NS	NS	NS	NS

Weed Management

W_1 - Weedy check

W_2 - Weed free (Hand weeding at 20 and 40 DAS)

W_3 - Intercropping with cowpea

W_4 - Atrazine 50% WP @ 0.5 kg *a.i.*ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.*ha^{-1} (Early PoE) *fb* H.W at 40 DAS

W_5 - Atrazine 50% WP @ 1.0 kg *a.i.*ha^{-1} (PE) *fb*Tembotrione 42% SC @ 120 g *a.i.*ha^{-1} (PoE)

W_6 - Atrazine 50% WP @ 1.0 kg *a.i.*ha^{-1} (PE) *fb* Paraquat 24% SL @ 1.0 kg *a.i.*ha^{-1} (PoE)

W_7 - Sorghum + Parthenium leach @ 15 lit ha^{-1} (PE) *fb* Sorghum + Parthenium leach @ 15 lit ha^{-1} (PoE)

MEY: Maize Equivalent Yield

distribution during each growing season was the reason for the drop in yields across the seasons. According to Lobell and Asner (2003), weather conditions influence management options and account for around 30% of year-to-year production variability for key crops like maize. These findings are backed up by the findings of Vetsch and Randall (2004) in Minnesota, USA, who reported a significant effect of season on maize grain yields.

Grain yield of maize was not influenced significantly due to the different tillage methods during both years of study and pooled means. However, yields were numerically higher with conventional tillage (5152 kg ha^{-1}) than with reduced tillage (4705 kg ha^{-1}) which resulted in an 8.67% higher grain yield. Increased grain yield in CT is due to deeper root spread and more root activity. Better tillage methods reduce bulk density, weed density, weed dry matter and increase nutrient and water availability, allowing for more effective water and nutrient uptake, which resulted in increased grain output. The findings are also consistent with those of Anjum *et al*. (2019) and Khan *et al*. (2017). The lower seed yield with the reduced tillage in which the soil was less undisturbed could be attributed to the inferior value of plant growth and yield attributing characters. Similar results were obtained by Feng *et al*. (2014).

Weed management practices had a significant effect on grain yield during both years and pooled means. The maximum grain yield was produced by Hand weeding twice at 20 and 40 DAS (6625 kg ha^{-1}) which was on par with Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (early PoE) *fb* HW at 40 DAS (6442 kg ha^{-1}) and Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (6236 kg ha^{-1}). The highest grain yield in these treatments could be due to reduced competition between the crop and weeds for available resources throughout the crop growing period, allowing the crop to make the best use of nutrients, moisture, light and space thus enhancing the crop's vegetative and reproductive potential, which reflected in higher grain yield. The minimum grain yield was recorded with weedy check (2578 kg ha^{-1}) which might be due to increased competition for growth resources between the crop and weeds, as evidenced by lower crop stature, yield attributes, and eventually maize grain yield. The results corroborate the findings of Parameswari *et al*. (2017) and Prithwiraj *et al*. (2018).

Stover yield

The stover yield in the maize crop was not significantly influenced by tillage practices during both years and pooled means. However, conventional tillage had produced higher stover yield (7242 kg ha^{-1}) as compared to reduced tillage (6712 kg ha^{-1}). Conventional tillage can remediate subsoil compaction. This layer is less permeable for roots, water and oxygen, which may limit root growth and subsoil penetration, resulting in delayed plant growth due to limited water and nutrient uptake, resulting in reduced crop growth in reduced tillage. Similar findings were reported by Anjum *et al*. (2019) and Khurshid *et al*. (2009).

Weed management practices exerted a significant influence on the stover yield during both years and pooled means. The stover yield of maize in different weed management practices ranged from 8221 to 5415 kg ha^{-1}. Significantly higher stover yield was recorded with Hand weeding twice at 20 and 40 DAS (8221 kg ha^{-1}) which was at par with Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (early PoE) *fb* HW at 40 DAS (8105 kg ha^{-1}) and Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (8025 kg ha^{-1}). The minimum stover yield was observed under Weedy check (5415 kg ha^{-1}). Effective weed control might have favoured the crop with increased leaf area, allowing more solar radiation interception and resulting in better photosynthesis for higher stover yield. The results conformed to the findings of Sanodiya *et al*. (2013) and Triveni *et al*. (2017).

Harvest index (%)

There is no significant effect of tillage practices on harvest index during both years and pooled means, but conventional tillage had a higher harvest index (40.94%) as compared to reduced tillage (40.30%). The differences in harvest index owing to different tillage practices could be explained by a better growth environment, which would increase the absorption of water and nutrients required for growth by decreasing weed population in conventional tillage. Increasing the absorption causes a variation in the reallocation of dry matter from plant tissue to the cob. Similar findings were reported by Anjum *et al*. (2019) and Khan *et al*. (2017).

Different weed management practices had a significant influence on the harvest index during both years and pooled means. Higher harvest index was observed with Hand weeding twice at 20 and 40 DAS (44.82%) which was followed by Atrazine 50% WP @ 0.5 kg *a.i.* ha^{-1} + Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (early PoE) *fb* HW at 40 DAS (44.46%), Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* Tembotrione 42% SC @ 120 g *a.i.* ha^{-1} (43.87%) and Atrazine 50% WP @ 1.0 kg *a.i.* ha^{-1} (PE) *fb* paraquat 24% SL @ 1.0 kg *a.i.* ha^{1} (PoE) (42.50%). Weedy check registered the lowest harvest index (32.74%) when compared with all the treatments. Increased maize harvest index in the different weed management practices might be ascribed to enhanced weed suppression and increased availability of moisture and nutrients allowing maize to produce higher dry matter and kernel yield, which was reflected in a higher harvest index. The results conformed to the findings of Sandhya Rani *et al*. (2019) and Triveni *et al*. (2017).

Interaction effect of tillage and weed management practices on maize was found to be non-significant.

CONCLUSION

Although conservation agriculture has higher sustainability and lower environmental impact, growers are less likely to adopt it since weed management is a major limitation. Conventional tillage reduced total weed density and weed dry matter to the tune of 24.14 and 16.76% than in reduced tillage and increased yield of maize by 8.67% though they were on par with each other. Among weed management practices, hand weeding twice at 20 and 40 DAS was supposed to be the most promising option in maize production under different tillage methods because of more yield indicating better resource utilization with good weed control measures.

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Research Article
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MANAGEMENT OF WILT DISEASE OF CUMIN CAUSED BY *F. OXYSPORUM* F. SP. *CUMINI* WITH FUNGICIDES *IN VITRO* AND *IN VIVO*

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ABSTRACT

Cumin is an important seed spice crop. It is affected by several diseases among them wilt disease caused by *Fusarium oxysporum* is one of the most important and destructive disease causing heavy losses in the crop production. The present study was conducted at College of Agriculture, Jodhpur during *Rabi* season 2020-21to evaluate the five different fungicides under *in vivo* and seven different fungicides under *in vitro* condition. Lowest disease per cent was recorded in carbendazim (50% WP) (12.39%) followed by carbendazim 12% + mancozeb 63% (14.75 %), thiophanate methyl (70% WP) (20.39%) which was at par with tebuconazole 50% + trifloxystrobin 25% WG (75 WG) (20.45%) when tested under *in vivo* condition. The maximum per cent disease incidence was observed in pyraclostrobin 5% + metiram 55% WG (22.49 %) whereas, 63.59 per cent disease incidence was recorded in control plot. Result of in vitro study indicated that the fungicide carbendazim (50% WP) completely inhibited the mycelial growth of *F. oxysporum* and also found significantly superior over the other fungicides followed by carbendazim 12% + mancozeb 63% (96.80%), tebuconazole 50% + trifloxystrobin 25% WG (75 WG).

Keywords: Cumin, fungicides, *F. Oxysporum, in vivo*, *in vitro*, wilt

Cumin (*Cuminum cyminum* L.) belongs to the family Apiaceae, locally known as Jeera or Zeera in Hindi and is an annual herb. It is believed to be a native of the Mediterranean and Near Eastern regions. It is mainly cultivated in India, Egypt, Libya, Iran, Pakistan and Mexico (Peter and Nybe, 2002).

It is a cross pollinated crop, and bees often help in pollination. Moderate sub-tropical climate is appropriate and requires cool and dry climate for better growth. Temperature up to 25-30^{0}C is suitable for plant growth though it cannot withstand high humidity and heavy rainfall. Nutritional composition of cumin seeds is protein 17.7%, fat (23.8%), carbohydrate (35.5%), and minerals (7.7%). The essential oil content in seed is varies from 2.5 to 4.5% (Pruthi, 1996).

India is the largest producer and consumer of cumin seed in the world and occupied an area of 12.76 lakh hectares with annual production of 9.12 lakh tones, India exported 2.14 lakh tons of cumin worth of Rs. 3328 crore during the year 2019-20 (Annual Report, 2019-20).

Cumin seeds are used to flavour a variety of dishes, including meat casseroles, lentil soup and curry powders and many savoury spice mixtures. The herb is stimulant, carminative, antispasmodic and also diuretic. It is useful for dyspepsia diarrhoea and may relieve flatulence and colic (Malhotra and Vashishtha, 2008). Cumin seeds yield a volatile oil (2.5-4.5%), the chief constituent is cumin aldehyde (20-40%) which is used in perfumery. In addition to this, seeds also contain a fixed oil (10%) with a strong aromatic flavour as carminative. The residue left over after the extraction of volatile oil contains 17.2% protein and 30% fat. (Merah *et al*., 2020). It can also be used for cattle feed. Additionally, The fixed oil could also be used in the oil, fat, and soap industries.

Fusarium wilt of cumin is broadly spread in all the cumin growing countries. Joshi and Agnihotri (1958) observed it to be caused by *Fusarium oxysporum* and reported about 20 per cent crop losses due to this pathogen. The severity of disease occurs in most of the cumin fields in the major cumin growing states of India. Mathur and Mathur (1965) recorded 5-60 per cent losses due to cumin wilt in Rajasthan, while Dange *et al*. (1992) reported 7-30.6 per cent losses in Gujarat. Pathogen is seed as well as soil borne and survive for long period in soil in the form of chlamydospore. Soil borne propagules of *F. oxysporum* f. sp. *cumini* are highly resistant to adverse conditions. The pathogen found to survive on the root surface in the form of macro conidia and chlamydospores (Mathur and Mathur, 1970), and its transmission through seed demonstrated (Singh *et al*., 1972). Mathur and Mathur (1965) reported that the pathogen is capable to producing toxins and causing

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vascular browning and wilting. The pathogen also produces cellulolytic and pectinolytic enzymes (Champawat, 1986). Keeping in view the importance of the disease, the present study was undertaken to identify the most effective fungicides in controlling wilt disease of cumin.

MATERIAL AND METHODS

Testing of fungicides *in vivo* and *in vitro*

The experiment was conducted in Instructional Farm, College of Agriculture, Jodhpur during *Rabi* season 2020-21. Six treatments including control were evaluated for their efficacy by foliar spray (2000 ppm) against the *F. oxysporum* f. sp. *cumini*. The cumin germplasm was sown in plots and replicated thrice in a Randomized Block Design. The first spray was done just after the initiation of the disease and subsequent two sprayings were given at an interval of 15 days. Standard agronomical practices were followed as per recommendations. Observations on disease incidence were recorded after 15 days of last spraying. The per cent disease intensity (PDI) was calculated and recorded.

$$\text{Per cent Disease Incidence (PDI)} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

The efficacy of seven fungicides Carbendazim (50% WP) (Bavastin), Tebuconazole 50% + Trifloxystrobin 25% WG (75 WG) (Nativo), Pyraclostrobin 5% + Metiram 55% WG (Clutch), Cymoxanil 8% + Mancozeb 64% (Duoguard), Captan 70% + hexaconazole 5% (Klinzo), Carbendazim 12% + Mancozeb 63% (Bendaco) and Thiophanate methyl (70% WP) (Topsin M) along with control was studied against mycelial growth of *Fusarium oxysporum* f. sp. *cumini* by Poisoned Food Technique (Nene and Thapliyal, 1979) with two different concentrations (500 and 1000 ppm).

Poison Food Technique

Desired quantity of fungicides under study were mixed thoroughly and replicated thrice in sterilized 100 ml PDA media filled in 250 ml flask separately under aseptic condition. The medium was supplemented with streptomycin sulphate @ 50 ppm to prevent bacterial contamination. The poisoned medium was then poured in sterilized Petri plates (20 ml) and allowed it to solidify. Mycelium discs of 5 mm size from seven days old culture was cut by a sterile cork borer and one such disc was placed at the center of each agar plate. The plate without any fungicide served as control. Three replications were maintained for each concentration. Such plates were incubated at room temperature and the radial growth was measured when fungus attained maximum growth in control plates. The efficacy of the fungicides was expressed as per cent inhibition of mycelial growth over control, which was calculated by using the formula given by Asalmol *et al*. (1990).

$$I = \frac{C - T}{C} X\ 100$$

Where,

I =Inhibition per cent

C = Colony diameter (mm) in control plat

T = Colony diameter (mm) in treated plate

RESULTS AND DISCUSSION

Efficacy of fungicides *in vivo* condition

Five fungicides along with control were evaluated in field condition and the results presented in Table 1 and Fig 1.

The data depicted in Table 1 showed that the disease incidence per cent of all fungicide treatments were significantly lower than untreated control. The disease incidence ranged between 12.39 to 63.59%. The lowest incidence per cent was recorded in carbendazim (50% WP) (12.39%) followed by carbendazim 12% + mancozeb 63% (14.75 %), thiophanate methyl (70% WP) (20.39%) which was at par with tebuconazole 50% + trifloxystrobin 25% WG (75 WG) (20.45%). The maximum per cent disease incidence was observed in pyraclostrobin 5% + metiram 55% WG (22.49 %) whereas, 63.59% disease incidence was recorded in control plot.

Similar results were also reported by Talaviya *et al.* (2018) where soil drenching of carbendazim 0.1% (20 g/10lit water) @ 1 lit/sq. meter after one month of sowing reduced *Fusarium* population in soil up to harvest as well as highest reduction in wilt incidence. Seed treatment of carbendazim 12% + mancozeb 63% @ 3 g/kg seed was also equally effective in disease reduction and better seed yield except *Fusarium* population reduction in soil as compared to the treatment of carbendazim 0.1 per cent drenching. Kushwaha and Arya (2018) tested eight chemicals namely azoxystrobin, propiconazole,

Table 1. Effect of different fungicides against *F. oxysporum* f. sp. *cumini* under field conditions during rabi 2020-21

S.No	Treatments	Dosage (g/kg)	PDI*	Disease Control (%)
1	Carbendazim (50% WP)	2.0	12.39 (20.59) *	80.51
2	Tebuconazole 50% + Trifloxystrobin 25% WG (75 WG)	2.0	20.45(26.87) *	67.84
3	Pyraclostrobin 5% +Metiram 55% WG	2.0	22.49 (28.30) *	64.63
4	Carbendazim 12% +Mancozeb 63%	2.0	14.75 (22.57) *	76.80
5	Thiophanate methyl (70% WP)	2.0	20.39 (26.83) *	67.93
6	Control	2.0	63.59 (52.86) *	0.00
	S.Em ±		0.23	
	CD (P=0.05)		0.75	

Average of three replications
*Figures in parentheses are angular transformed values
PDI = Per cent disease incidence

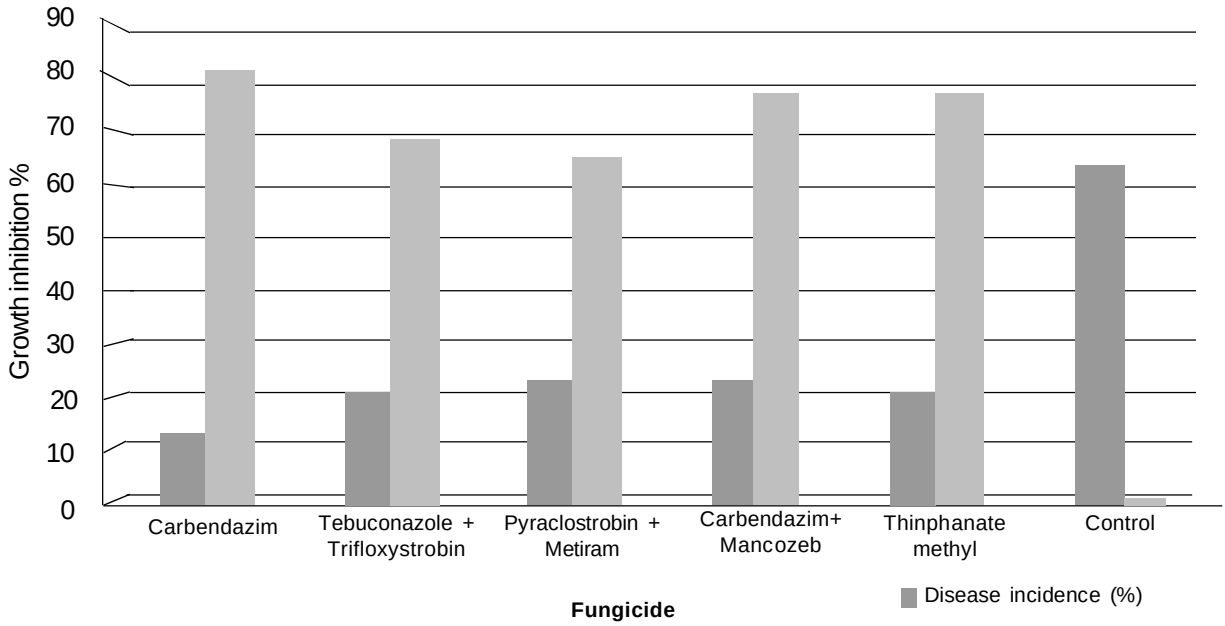

Fig. 1 Efficacy of fungicides against *F. oxysporum* f.sp. *cumini* (*in vivo*)

Provax, captaf, carbendazim, thiram, Raxil and Vitavax Power, were used against the pathogen under *in vitro* and *in vivo* condition. Among all the chemicals evaluated Raxil was found most effective and gave 100 per cent mycelium inhibition and minimum disease incidence. Aslam *et al. (2019)* evaluated thiophanate methyl, acrobat, matalyxal and fosetyl aluminum fungicides and their application methods to inhibit the pathogenic growth and development of *Fusarium oxysporum* f. sp. *pisi* causing wilt disease in pea under *in vitro* and *in vivo* condition.

Efficacy of fungicides under *in vitro* condition

A total of seven fungicides with two different concentrations 500 and 1000 ppm along with control were tested *in vitro* against *F. oxysporum* f. sp. *cumini,* applying Poisoned Food Technique (Nene and Thapliyal, 1979) and using (PDA) as basal medium. The observations on per cent growth inhibition (PGI) were recorded and the results are presented in Table 2, Plate 1.1, 1.2 and Fig 2.

All the fungicides screened were found significantly superior in inhibiting the mycelial growth of *F. oxysporum* f. sp. *cumini* over the control. The fungicide carbendazim (50% WP) completely inhibited the mycelial growth and also found significantly superior over the other fungicides followed by carbendazim 12% + mancozeb 63% (96.80%), tebuconazole 50% + trifloxystrobin 25% WG (75 WG) (94.50%) and so on (Table 2).

Table 2. Effect of different fungicides against *F. oxysporum* f. sp. *cumini in vitro*

S.No	Treatments	Per cent mycelium inhibition*		
		Concentrations (ppm)		
		500	1000	Mean
1	Carbendazim (50% WP)	100.00 (88.68)	100.00 (88.68)	100.00 (88.68)
2	Tebuconazole 50% + Trifloxystrobin 25% WG (75 WG)	89.05 (70.66)	100.00 (88.68)	94.50 (79.67)
3	Pyraclostrobin 5% + Metiram 55% WG	80.63 (63.87)	98.00 (82.89)	89.30 (73.38)
4	Cymoxanil 8% + Mancozeb 64%	52.84 (46.61)	73.61 (59.06)	63.22 (52.83)
5	Captan 70% + Hexaconazole 5%	47.04 (43.28)	67.75 (55.37)	57.40 (49.33)
6	Carbendazim 12% + Mancozeb 63%	93.66 (75.40)	100.00 (88.68)	96.80 (82.04)
7	Thiophanate methyl (70% WP)	86.83 (68.70)	90.76 (72.28)	88.80 (70.49)
8	Control	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)
	Mean	68.78 (57.52)	78.77 (67.39)	-
	Factor	**S.Em±**	**CD (p = 0.05)**	
	Fungicide (F)	**0.752.18**		
	Concentration (C)	**0.371.09**		
	Inter. (F x C)	**1.073.09**		

* Average of three replications
** Figures in parentheses are angular transformed value]

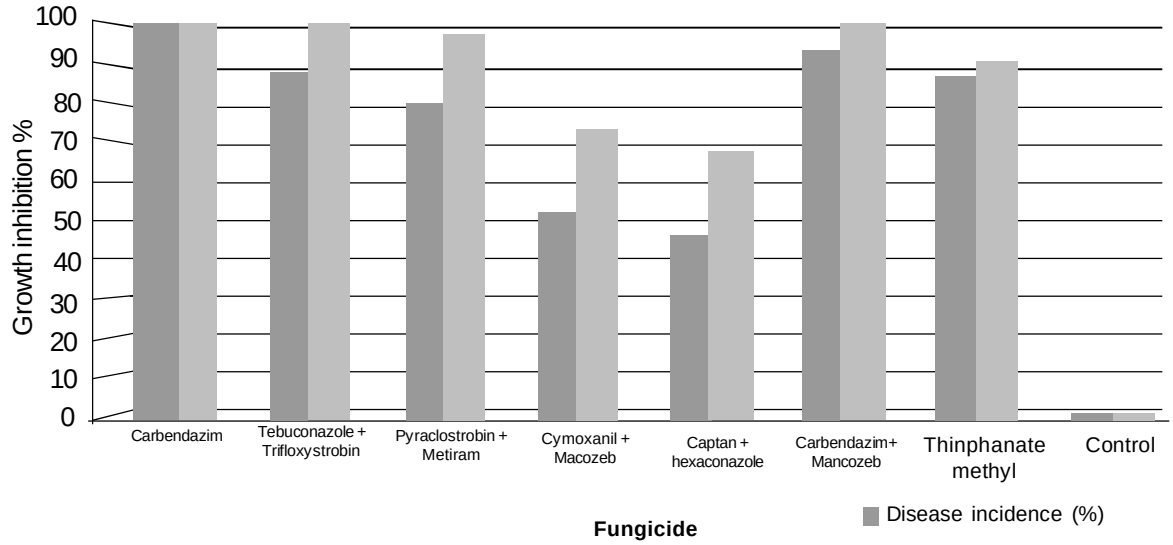

Fig 2. Efficacy of fungicides against *F. oxysporum* f.sp. *cumini* (*in vitro*)

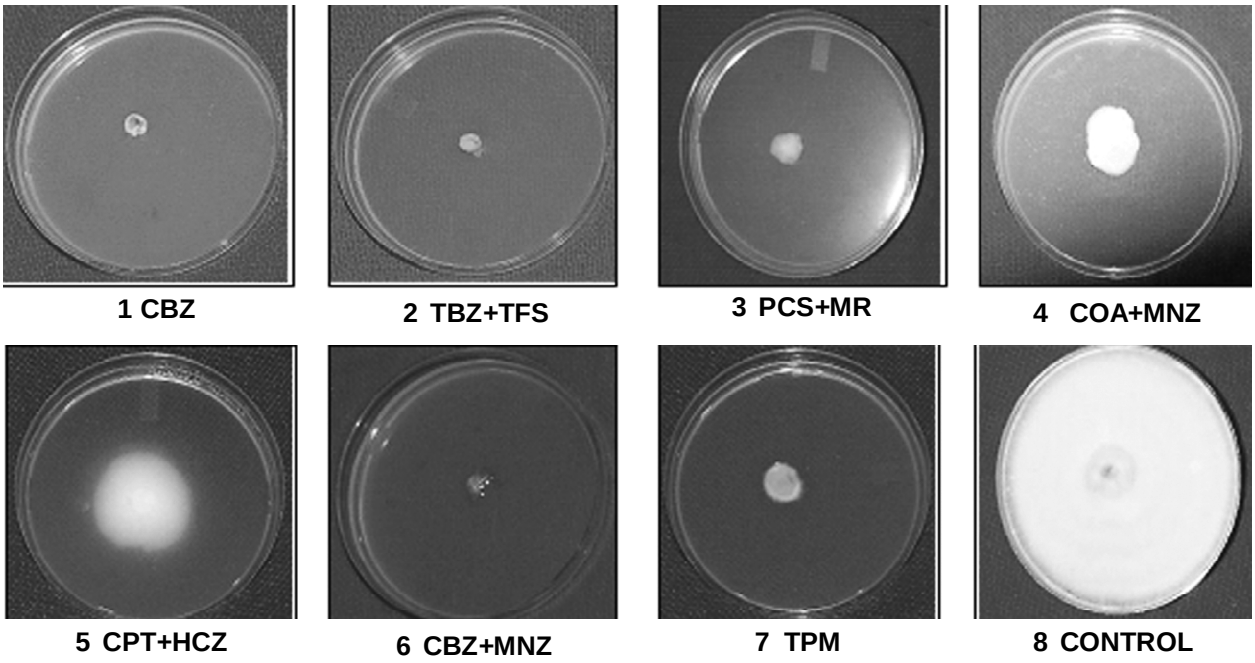

Plate 1. Efficacy of fungicides against *F. oxysporum* f. sp.*cumini in vitro* (500 ppm)

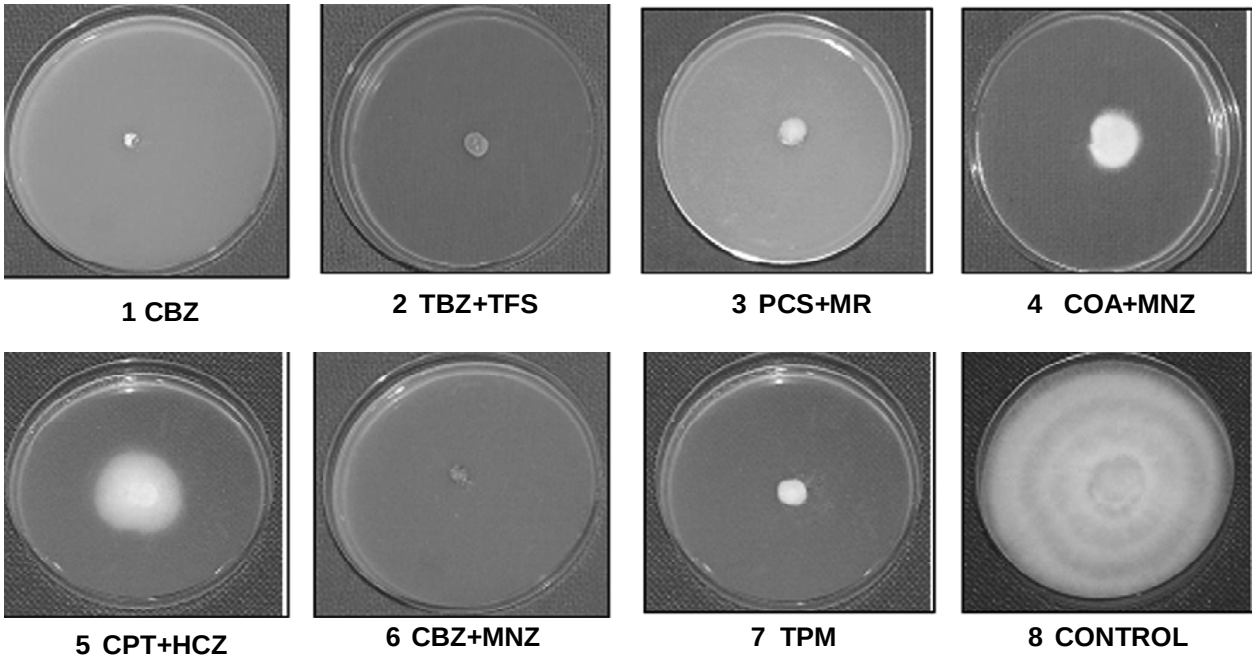

Plate 2. Efficacy of fungicides against *F. oxysporum* f. sp. *cumini in vitro* (1000 ppm)

It was also found that the average mycelium growth inhibition at concentration of 1000 ppm (67.39%) was significantly larger than the fungicide concentration of 500 ppm (57.52%). In case of different fungicides at different concentrations *i.e.,* 500 & 1000 ppm, maximum mycelium growth inhibition was found in carbendazim (50% WP) at all concentrations. Tebuconazole 50% + trifloxystrobin 25% WG (75 WG) and carbendazim 12% + mancozeb 63% were also found completely inhibition at 1000 ppm. The fungicide tebuconazole 50% + trifloxystrobin 25% WG (75 WG), thiophanate methyl (70% WP) at 500 ppm concentration were at par.

Minimum inhibition was observed in captan 70% + hexaconazole 5% followed by cymoxanil 8% + mancozeb 64% at 500 and 1000 ppm concentrations, respectively.

Similar results were also observed by Bardia and Rai (2007) who evaluated the fungal antagonists and fungicides against wilt of cumin (*Cuminum*

cyminum) caused by *Fusarium oxysporum* f. sp. *cumini.* Under *in vitro* studies, *T. harzianum* isolate I6 and carbendazim were the best treatments in inhibiting the growth of the pathogen. This treatment combination resulted in significantly lowest disease incidence (11.7%) and highest yield (6.17 q/ha). Raheja and Patel (2011) tested various fungicides, complete (100%) inhibition of the fungal growth *i.e*., 100% was recorded with Bavistin (carbendazim) followed by Sixer (carbendazim + mancozeb) at all the tested concentrations. The next best fungicides Raxil (tebuconazole), Topsin-M (thiophanate methyl) and Cosko (carboxin + thiram) inhibited the fungal growth by 95, 93 and 91% at 50, 50 and 250 ppm concentrations, respectively and showed complete inhibition (100%) at their highest tested concentration of 500, 500 and 1500 ppm respectively. Chennakesavulu *et al.* (2013) tested efficacy of four systemic fungicides *viz.,* carbendazim, propiconazole, tebuconazole and hexaconazole and two non-systemic fungicides *viz.,* mancozeb and cheshunt compound at 50, 100, 250, 500 and 1000 ppm concentrations *in vitro.* tebuconazole, carbendazim, propiconazole completely inhibited the mycelial growth of the pathogen even at 50 ppm followed by cheshunt compound at 100 ppm. Harshita *et al.* (2019) screened commercially available potential systemic fungicides *viz*. Topsin M and carbendazim against *Fusarium oxysporum* f. sp. *lycopersici* at three different concentrations (50 ppm, 100 ppm and 200 ppm) and revealed that carbendazim at 200 ppm was the strongest anti-mycotic potential followed by carbendazim at 100 ppm.

CONCLUSION

All the fungicide treatments recorded significantly lower disease incidence than untreated control. The disease incidence ranged between 12.39 to 63.59 per cent. The lowest incidence per cent was recorded in carbendazim (50% WP) (12.39%) followed by carbendazim 12% + mancozeb 63% (14.75%), thiophanate methyl (70% WP) (20.39%). The maximum per cent disease incidence was observed in pyraclostrobin 5% + metiram 55% WG (22.49%) whereas, 63.59% disease incidence was recorded in control plot.

Among seven fungicides, carbendazim (50% WP) completely inhibited the mycelial growth and also found significantly superior over the other fungicides followed by carbendazim 12% + mancozeb 63% (96.80%), tebuconazole 50% + trifloxystrobin 25% WG (75 WG) (94.50%). It is also found that the average mycelium growth inhibition at 1000 ppm (67.39%) was significantly larger than the fungicide concentration of 500 ppm (57.52%). In case of different fungicides at different concentrations *i.e.,* 500 & 1000 ppm, maximum mycelium growth inhibition was found in carbendazim (50% WP) at all concentrations. Fungicides Tebuconazole 50% + trifloxystrobin 25% WG (75 WG) and carbendazim 12% + mancozeb 63% also completely inhibited the pathogen at 1000 ppm. Minimum inhibition was observed in captan 70% + hexaconazole 5% followed by cymoxanil 8% + mancozeb 64% at 500 and 1000 ppm concentrations, respectively.

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Research Note
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GENETIC PARAMETERS OF SELECTED RICE (*Oryza Sativa* L.) GERMPLASM FOR YIELD AND YIELD TRAITS

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Food is the most basic requirement for sustaining every kind of living creature on this earth. Green revolution played an important role in reaching self-sufficiency in food production in India. The most important feature of Green revolution which led to the significant gain in the production of food grains was the development of High Yielding Varieties (HYV) (Asfaw *et al*., 2012).

Rice (*Oryza sativa* L.) is the most important food crop in the world, directly feeding more people than any other crop. India's rice production has risen from 69.35 million tonnes in the year 2005-06 to 102.19 M.T in 2018-19. With the current trends of growing population and agricultural production, the demand for food in most parts of the world will nearly triple by the year 2030. Crop yield improvement is of prime importance to full fill the demand. A critical analysis of genetic variability present in a given crop species is a prerequisite for initiating any crop improvement programme and for adoption of appropriate selection techniques. Estimates of heritability will be of immense help to the breeder in selecting for a desired trait from superior individuals for successful utilization in the breeding programme. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection. (Johnson *et al*., 1955).

Present investigation was carried out with the objective of estimating the genetic variability for yield, yield contributing traits, heritability and genetic advance which would help in selection and further improvement of rice genotypes. One hundred and fifty two (152) rice germplasm lines collected from all over India and Philippines were evaluated for yield and component traits during *Kharif* 2019 in Alpha lattice design with two replications at ICAR-Indian Institute of Rice Research (ICAR-IIRR), Rajendranagar, Hyderabad.

Thirty days old seedlings were transplanted by adopting a spacing of 15 cm between plants and 20 cm between rows. Recommended agronomic and plant protection measures for raising a healthy nursery and main crop were taken up during the experiment.

Observations were recorded on five randomly selected plants in each genotype in each replication for ten quantitative traits *viz*., days to fifty per cent flowering (DFF), Total number of tillers per plant (TNT), effective number of tillers (ENT), plant height (PH) (cm), number of filled grains (NFG), number of un filled grains (NUFG), panicle weight (PW) (g), panicle length (PL) (cm), test weight (TW) (g), and yield per plant (YPP) (g). The mean of five plants for each metric trait was considered for statistical analysis using SAS software. The analysis of variance (ANOVA) was done on the basis of model described by Cochran and Cox (1957) for Alpha lattice design. The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton and Devane, 1953. Heritability in broad sense (h^2) was calculated by the formula given by (Lush, 1949) and suggested by Johnson *et al.,* (1955). From the heritability estimates, the genetic advance (GA) was calculated by the formula given by Johnson *et al.,* (1955).

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Table1. Analysis of variance for yield and yield related traits

Source of variation	d.f	DFF	TNT	ENT	PH	NFG	NUFG	PW	PL	TGW	YPP
Replication	1	1.894	1.847	0.39	0.68	0.006	46.89	0.18	2.96	8.45	0.034
Treatment	151	317.73**	11.81**	9.371**	366.9**	2029.0**	360.46**	0.93**	5.90**	27.11**	43.97**
Error	151	0.556	1.257	1.152	6.45	127.07	43.20	0.095	1.34	0.328	2.686

Note: * Indicates significance at 5 per cent probability level

** Indicates significance at 1 per cent probability level

Analysis of variance revealed highly significant differences among the one fifty two (152) genotypes for all the 10 characters indicating the presence of adequate amount of genetic variability among the genotypes assessed. The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated and the details were given in table 2. The graphical representation of variability parameters is depicted in Fig 1 and Fig 2.

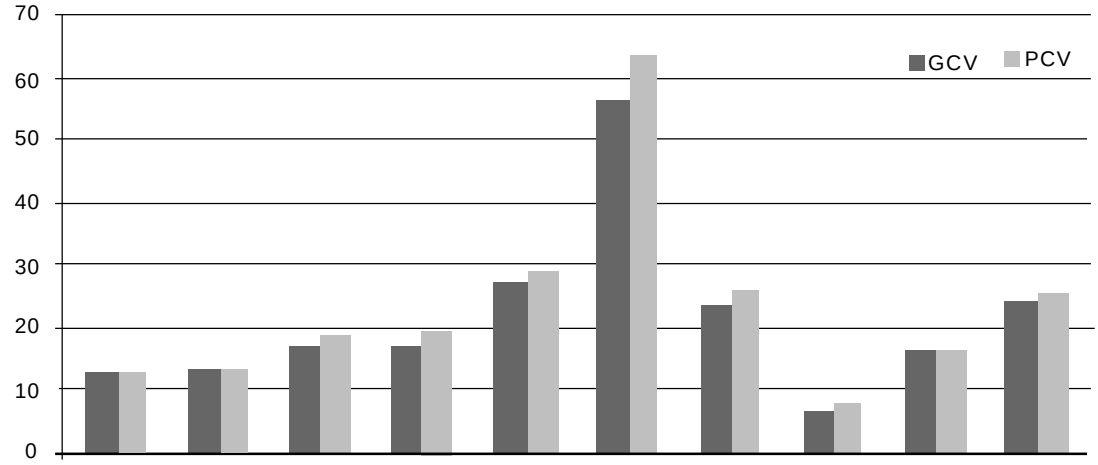

Fig 1. Graphical representation of PCV and GCV in 2019

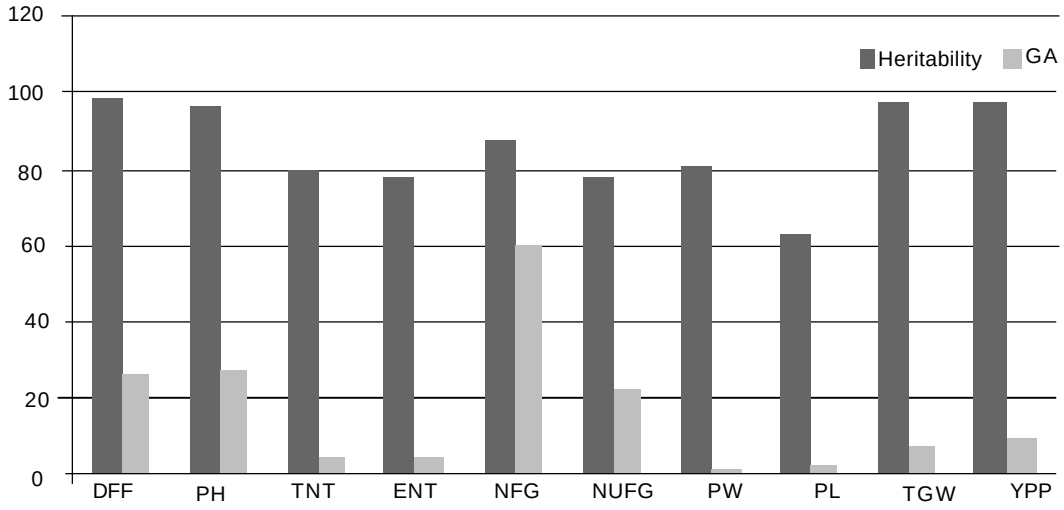

Fig 2. Graphical representation of Heritability and GA in 2019

The present investigation revealed that the estimates of PCV were slightly higher than GCV for all the characters studied indicating less influence of environmental factors on the expression of traits. As the characters were less influenced by the environment, these can be used for selection. The magnitude of PCV and GCV estimates were moderate for five traits *viz.,* days to 50% flowering, plant height, total number of tillers per plant, effective number of tillers per plant and test weight. Similar such observations were made by Mishu *et al.* (2016) for days to 50% flowering in six aromatic rice varieties, Lakshmi *et al.* (2017) for plant height and Devi *et al.* (2016) for test weight.

High estimates of GCV and PCV were observed for panicle weight, number of filled grains, number of unfilled grains and single plant yield. Bagudam *et al.* (2018) for plant height in NPT core rice collections. Parimala *et al.,* 2020 reported similar estimates for number of filled grains and number of unfilled grains per panicle. The above reported observations for high GCV and PCV estimates for important yield component traits, does indicate the possibility for genetic improvement through direct selection for these traits.

Heritability measures the contribution of genetic variability to the phenotypic variability and is a good index of the transmission of characters from parents to their offspring. The estimates of heritability can be utilized for prediction of genetic gain, which indicates the genetic improvement that would result from selection of best individuals. Genetic advance (GA) is the measure of genetic gain under selection. Heritability estimates along with genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

High heritability coupled with high genetic advance indicates the preponderance of additive gene action and such characters could be improved through selection estimates recorded for these traits viz., days to 50% flowering, plant height, number of filled grains per panicle, number of unfilled grains per panicle. These results are in conformity with Tiwari *et al.* (2020) for days to 50% flowering plant height and single plant yield in Swarna x type 3 RIL population. Similar findings were reported by Bagudham *et al.* (2018) for total number of tillers per plant in NPT core rice accessions. This indicates that there was low environmental influence on the expression of these characters and hence one can practice selection. High heritability coupled with high genetic advance for plant height (Das *et al.*, 2005) and 50% flowering (Satyanarayana *et al.,* 2005) was also reported.

CONCLUSION

The genetic architecture of grain yield is based on the overall net effect produced by various yield components interacting with one another. The present investigation revealed that there is adequate genetic variability present in the germplasm lines studied. Among all the characters, days to 50% flowering, plant height, total number of tillers per plant, effective number of tillers per plant, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, test

Table 2. Estimation of Genetic Variability parameters for one fifty two genotypes

Characters	Mean	Range		Coefficient of variability		Heritability h^2 (%) broad sense	Genetic Advance as per cent of Mean (5%)
		Min.	Max.	GCV (%)	PCV (%)		
DFF	100.711	64	130	12.50	12.52	99.65	25.89
TNT	13.874	7	22	16.55	18.42	80.75	4.25
ENT	12.069	7	19	16.79	19.00	78.08	3.69
PH	103.141	75	157	13.01	13.24	96.54	27.17
NFG	113.193	37	248.7	27.24	29.00	88.21	59.66
NUFG	22.265	1	80	56.56	63.80	78.59	23.00
PW	2.755	1.2	5.1	23.44	26.00	81.31	1.20
PL	24.222	18	31.4	6.23	7.85	62.93	2.46
TW	22.419	11.5	30.5	16.32	16.52	97.60	7.44
YPP	19.144	5.8	33.5	23.73	25.23	88.48	8.80

weight and single plant yield recorded high heritability as well as high genetic advance, indicating the presence of considerable variation and additive gene effects. Hence, improvement of these characters could be effective through phenotypic selection.

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