

Evaluation of Half -Sib Families Derived from Maize Variety Sarhad White for Grain Yield and Agronomic Traits

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Abstract: This study was undertaken at the Research Farm of KP Agricultural University, Peshawar during 2012 to evaluate half-sib maize families for grain yield and agronomic traits. Forty nine half-sib families derived from maize variety Sarhad White were used in the study. The experiment was laid out in 7×7 partial balance lattice design with two replications. Results indicated that the half-sib families were significantly different from one another for all the traits studied. Among the 49 half-sib families minimum days to 50% tasseling (50.0) were recorded for HS-32 while HS-48 showed maximum days to 50% tasseling (60.0). Minimum days to 50% silking (51.0) were observed for HS-08 while HS-48 showed maximum days to mid tasseling. Minimum plant height of 110.50 cm was recorded for HS-41 while HS-08 showed maximum plant height (160.60 cm), minimum ear height (40.70 cm) was recorded for HS-41 and maximum ear height (79.60 cm) for HS-48. Minimum grain moisture (14.0%) was recorded for HS-03 while maximum (30.60%) for HS-12. Minimum ear length (9.20 cm) was recorded for HS-41 while maximum (14.80 cm) was for HS-04. Minimum grain yield (3133.0 kg ha⁻¹) was recorded for HS-43 while HS-06 showed maximum (7423.0 kg ha⁻¹) grain yield. Maximum heritability estimate (0.84) was observed 100-kernal weight, while minimum (0.42) was observed for yield. Maximum correlation of yield was recorded with plant height and ear height. These results suggest that these half-sib families could be used as source of improved maize germplasm for developing maize genotypes with superior attributes.

Key words: *Zea mays* L. • Sarhad White • Heritability • Correlation

INTRODUCTION

Medicinal plants are an significant source of manufacturing valuable bioactive compounds which is great importance for the health of individuals and communities. The medicinal importance of the plants is due to the secondary metabolites that produce a definite physiological action on human body [1-4]. Maize (*Zea mays* L.) is one of the most important cereal crops of the world grown in the irrigated and rainfed areas. It is a cross pollinated, annual and short day crop that can be grown in tropical and sub-tropical regions with high temperature and enough sunshine. It can be grown on all types of soils ranging from sandy to clay; however, medium textured soil of pH 6.5 to 7.5 is more suitable for maize. Maize plant is protandrous in which

pollen shedding normally begins 1-3 days before the silks have emerged from the husks of the same plant and usually continues for a period of several days after the silks are ready to be pollinated. Hot dry weather tends to hasten the pollen shedding [5]. Maize is a multipurpose crop used for food, feed, fodder and several industrial products. About two third of the total world production of maize is used for livestock feed or for commercial starch and oil production. It has a great nutritional value as it contains about 66.7% starch, 10% protein, 4.8% oil, 8.5% fiber, 3% sugar and 7% ash [6]. Maize ranks 3rd most grown crop in the world with an area of 161 million hectares with total production tons 840 million tons, having an average yield of 519461.1 kg hac⁻¹ [7]. In Pakistan maize is the 4th largest grown crop after wheat, cotton and rice. In Pakistan during the year 2011-12, maize

Heterotic response of three-way cross maize hybrids for grain yield and yield components

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Abstract: The present study was performed to determine the extent of heterosis in three way cross maize hybrids for yield and yield contributing traits at Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera, Pakistan, in 2012. In spring season, 18 three way cross hybrids were developed by crossing 18 elite inbred lines with three single cross hybrids in different combinations. In summer season, the crosses were evaluated along with commercial check hybrids. The experiment was conducted in a randomized complete block design with three replications. Data were recorded on plant height, ear height, cob length, kernel rows cob-1, 100-seed weight and grain yield. Hybrids showed highly significant differences for all traits studied except kernel rows cob-1. Maximum plant height was recorded for Ev3-157-5-4-2×P-30k08, while minimum plant height was attained by Pop 9804×Bemisal. Maximum ear height was recorded for Swajk-4-9×P-3025. Pop 9804×Bemisal exhibited minimum ear height. Percent heterosis for plant and ear height over checks showed positive and negative differences. Among the hybrids, maximum ear length was observed for Ev3-157-5-1-7-3-9-5×Bemisal, while minimum was recorded for Ev3-157-5-1-1-9-1×P-3025. Maximum number of kernel rows ear-1 was detected for Ev3-157-5-1-1-9-1×P-30k08 and Pop9804×Bemisal, while minimum number of kernel rows ear-1 was exhibited for Ev3-157-5-4-2×P-30k08 and Ev3-45-4-3-7-2-3-2×P-30k08. Maximum 100-kernel weight was recorded for Ev3-120-2-3-2-1-2-1×P-30k08, while minimum 100-kernel weight was observed for Ev3-157-5-4-2×P-30k08. Highest yielding cross was Swajk-6-6-3-5-1×P-30k08, while lowest grain yield was observed for Ev3-157-5-4-2×P-30k08. The magnitude of heterosis for yield and yield contributing traits varied and showed significant as well as non significant estimates for various traits studied during investigation.

Keywords: Genetic variability; Heterotic performance; Hybrid evaluation; Zea mays

1 Introduction

Maize (*Zea mays* L.; 2n=20) is an important cereal, which belongs to grass family Poaceae. It is an annual, herbaceous, and monoecious plant, which is grown over a wider range of agro climatic conditions of the world. Maize is a multipurpose crop, used by humans as well as a fodder crop for animals feeding purposes. Millions of people from developed and developing countries use maize as a staple food for protein and calories requirements (Bjarnason and Vassal, 1992). Globally maize considered as the second most important creal crop while in Pakistan it is a third. In Pakistan during 2010-2011, maize was cultivated over area of 974.1 thousand hectare with average production of 3707 tones (FBS 2010-2011). The productivity figures are low compared to other countries of similar agro climatic conditions because of lack of breeding interest in maize.

Heterosis or hybrid vigor refers to the superior performance of an hybrid relative to its parents. Shull (1908) suggested the concept of increase in performance of hybrids over mean of its two homozygous parents for growth and physiological characters in maize. Heterosis is being studied in many cross pollinated crops, especially in maize where it shows highly significant and positive heterosis for yield and yield components. Plant breeders from all over the world used heterosis as a tool for high

productivity in maize. The uses of heterosis boosted the development of seed industry and altered the landscape of professional plant breeding (Janick, 1998).

For high productivity in maize, different types of hybrids are grown commercially. Among hybrids, three way cross hybrids are regularly used since they are cheap in seed production. Three way crosses are intermediate between single and double cross hybrids with respect to uniformity, yield, stability and the relative simplicity of selecting and testing (Weatherspoon, 1970). The present study was carried out to estimate extent of heterosis with respect to grain yield and other yield contributing traits among three way cross hybrids and to identify the best hybrid combinations for future maize breeding programs.

2 Material and methods

This study was carried out at the Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera, Pakistan during spring and summer seasons of 2012. Breeding material comprised eighteen elite inbred lines crossed with three single cross hybrids in various combinations to develop three way cross hybrids during spring season, 2012. At maturity all the crosses were manually harvested, shelled and labelled separately. The resulting hybrids were evaluated in a randomized complete block design with three replications along with two commercial checks (Babar and 30k08), during summer season 2012. Each

COLONY COLOUR AND TEXTURE OF DIFFERENT ISOLATES OF *FUSARIUM SOLANI*, THE CAUSE OF ROOT ROT DISEASE OF OKRA (*ABELMOSCHUS ESCULENTUS* L) IN PESHAWAR

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ABSTRACT

The research work was conducted at department of plant pathology, University of Agriculture, Peshawar, Pakistan during 2012. The objective was to determine the fungal colony texture and colour of five different isolates of *Fusarium solani*, causing root rot of okra (*Abelmoschus esculentus* L) plant, in Peshawar. In this study, five isolates of *Fusarium solani* collected from different places of (Chamkani, Budhni, Palosi, Achinipayan and Jogian) were investigated for colony colour and texture. They were flat to cottony or woolly densely and densely floccose to fluffy. The colony colour was white to off white, creamy and chocolate colour or bright or silver coloured.

Keywords: *Abelmoschus esculentus* L, Colony texture and Colour, *Fusarium solani*

INTRODUCTION

Okra (*Abelmoschus esculentus* L.Moench) is one of the most widely known and utilized species of the family Malvaceae (Bayer and Kubitzki, 2003; Naveed *et al.*, 2009). Okra is a tropical and subtropical crop, is widely distributed from Africa to Asia, in Southern European, the Mediterranean and all of the America (Oyelade *et al.*, 2003; Andras *et al.* 2005). Okra commonly known as “lady finger” is primarily a vegetable crop sown for its immature pods that can be consumed as a fried or boiled vegetable or may be added to salads, soups and stews (Kashif *et al.*, 2008). The crop grows well in hot weather, especially in the region with warm night (Ndungurn and Rajabu, 2004).

A number of fungi bacteria, viruses, mycoplasma, nematode and insect attack okra crop. The total loss of vegetable on this account has been estimated up to 20-30% but if the pathogen is allowed to develop, This loss may increase up to 80-90% (Hamer and Thompson, 1957). Okra plant is attacked by a number of diseases caused by fungi such as *Macrophomina phaseolina*, *Rhizoctonia solani*, *Rhizoctonia bataticola*, *Fusarium solani*, *Pythium butteri*, *Cercospora abelmoschii*, *Phytophthora palmivora* and *Erysiphe cichoracearum* (Mital, 2006). *Fusarium* root rot are known to decrease the quantity and quality of major world crops including tomato

(Parveen *et al.*, 1993; Stephen *et al.*, 1996), other vegetables (Ghaffar, 1995) and soybean (Mousa, 1994). This disease is caused by *Fusarium solani* (Rahim *et al.*, 1992).

Greater variability exists in colony colour and texture of different isolates of *Fusarium solani*. Variations in coloris white to pale white (Dong *et al.*, 2012), white, cream, tan, salmon, pink, purple (Hoog *et al.*, 2000) and pink, light pink, yellowish with orange pigmentation and white (Sreedevi, 2007). Variability also reported in colony texture of various isolates of *Fusarium solani*. These are fluffy growth and wool to cottony and flat (Dong *et al.*, 2012; Hoog *et al.*, 2000; Sreedevi, 2007). Current research project was initiated with the objective to find out variability in colony colour and texture of different isolates of *Fusarium solani*, collected from different locations of district Peshawar.

MATERIALS AND METHODS

A survey was conducted in okra growing regions (Achini Payan, Palosi, Chamkani, Jogian and Budhni) of Peshawar district during 2012. Infected seedlings were collected from each location and brought to the laboratory of Plant Pathology Department, The University of Agriculture, Peshawar for further studies.

Isolation and identification of the pathogen from diseased okra seedlings

Infected okra seedlings were collected from five different areas of Peshawar district and it was washed with distilled water. Then it was

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Full Length Research Paper

Evaluation of Wheat Advance Lines under Rainfed Conditions

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Abstract. Development of high yielding and drought tolerant cultivars is one of the prime objectives of all wheat breeding programs. An experiment was performed at Malakandher Research Farm, The University of Agriculture, Peshawar during 2011-12 to evaluate 14 wheat advance lines with four cultivars i.e. Atta-Habib, Siren, Pirsabak-2005 and Pirsabak-2008 used as checks under rainfed conditions. The experiment was not irrigated throughout the whole growing season. The experiment was laid out in a randomized complete block design (RCBD) with 3 replications. Each entry was planted in 03 rows, 03 meter long and 30 cm apart. To minimize environmental effects on the genotypes recommended cultural practices were applied same for all the treatments. Data were recorded on 6 parameters viz, days to maturity, spike length, spikelets spike⁻¹, grains spike⁻¹, spike weight and spike density. Highly significant differences were observed for all the parameters. Mean values for genotypes ranged between 161.3 to 167.3 for days to maturity, 9.57 to 12.86 cm for spike length, 15.13 to 19.93 for no. of spikelets per spike, 41.05 to 60.80 grains spike⁻¹, 2.47 to 3.61g for spike weight and 0.531 to 0.675 for spike density. Spike density was positive and highly significantly correlated with spike length, positive significant correlated with days to maturity, negative highly significantly correlated with spikelets spike⁻¹. Based on the results of this study MPT7 can be recommended to be used in further breeding programs as it has high spike length, spikelets spike⁻¹, grains spike⁻¹, spike weight and spike density.

Keywords: Evaluation, wheat, advance lines, rainfed

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is most important staple food of about 36% of the world population (two billion people) but also core part of animals feed as straw in most of the countries. It is staple food for the people of Pakistan occupying 70% of Rabi and 37% of the total cropped area of the country. In KPK, wheat is grown on 40% of the total cropped area (Khan, 2011). Wheat takes more than 21.7 million acreage agricultural lands in Pakistan during 2011-12 producing approximately 23.5 million tones grains. The current average production is approximately 1133 kilograms per acre (Economic survey of Pakistan, 2011-12). Although the total production of wheat in Pakistan has increased manifolds over the past few decades and we have touched the level of self sufficiency in the recent past, but we are far behind in per unit production compared to the other wheat producing countries. World food security is dependent on continuous crop improvement particularly in the development of crops with increased tolerance to abiotic stresses especially drought and salinity (Denby and Gehring, 2005). Selection for grain yield can only

be effective if desired genetic variability is present in the genetic stock. Plant breeders are interested in development of new varieties which are having high yield potential. Genetic increase in yield under stress environments has been recognized to be a difficult challenge for plant breeders while progress has been much higher in favorable environments (Richards et al., 2002).

The identification and use of genotypes with better genetic potential is a continuous requirement for synthesis of physiologically efficient and genetically superior genotypes showing potential for increased production per unit area under a particular environment. Grain yield is the most important trait of wheat, which is a considerably complex character and is a final product of several contributing factors and their interactions. Generally yield associated traits have relatively higher heritability and can be used as selection tools. Effective application of indirect selection requires strong genetic association between primary and secondary characters accompanied with higher heritability of secondary characters. The knowledge of association between yield and these factors provides the basis to plan breeding programs



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Evaluation of imidacloprid and entomopathogenic fungi, *Beauveria bassiana* against the red palm weevil *Rhynchophorus ferrugineus* (Coleoptera: Curculionidae)

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Abstract

The Red Palm Weevil is a serious problem of the date palm in Pakistan. The sole and combine application effects of *Beauveria bassiana* (Balsamo) Vuillemin (Hyphomycetes) and sub-lethal dosages of Imidacloprid against the second and fourth instar larvae of *Rhynchophorus ferrugineus* Olivier was investigated in laboratory. Additionally, the *in vitro* hyphal growth of *B. bassiana* amended with three different concentrations (50, 250, 500 $\mu\text{L L}^{-1}$) of Confidor® 200 SL was also assessed. The results showed significantly higher mortality for the second and fourth instar larvae of RPW when *B. bassiana* and Imidacloprid applied together compared to their sole application. The highest mortality level (100%) for the second instar was recorded after 15 days of treatment with *B. bassiana* (1×10^6 conidia/ml) and Imidacloprid ($1 \mu\text{L L}^{-1}$) in combination, while for the fourth instar larvae it was achieved after 20 days of application. However, the presence of Imidacloprid did not significantly affect the hyphal growth of *B. bassiana* on Sabouraud Dextrose Agar (SDA), and greater colony sizes compared to untreated control were recorded in all cases. The maximum number of sporulation (173, 159.83 conidia mL^{-1}) and percentage (89.15, 79.4%) of mycosed *R. ferrugineus* cadavers was observed at lower dose rate (1×10^6 conidia/ml) of *B. bassiana*, exhibited the potential to be exploited for the control of RPW.

Keywords: Entomopathogenic fungi, Imidacloprid, Mortality, Mycosis, Sporulation.

1. Introduction

The invasive Red Palm Weevil (RPW) *Rhynchophorus ferrugineus* Olivier (Curculionidae: Coleoptera), is considered as economically important and destructive pest insect of date palm in Pakistan^[46]. It was first reported in 1992 from Khairpur Sindh^[3], from where the pest spread to other date palm growing areas of Pakistan. At present, the pest has successfully invaded many areas including Asia, Africa, Oceania, and Europe^[18], and more recently it has been reported from California and Australia^[32, 36]. The female RPW lay their eggs singly in the apertures made with their rostrum at the leaf base^[35]. On hatching the larvae made their way into the center of palm and make galleries by feeding inside the trunk, the mature larvae made their cocoons from the chewed fiber and pupate at the leaf base^[22]. The adult emerged from the cocoon, resided on the same tree and reproduced till the death of host^[13].

The existing methods of RPW management largely rely on the IPM strategies, which include: phyto sanitation, use of conventional insecticide, pheromone traps and bio-control agents. The chemical control method against RPW, include repeated fumigation, spraying and injecting of synthetic insecticides into infected palms^[19]. These approaches are not enough as under this category the use of certain chemicals causes the development of resistance in the pest and further have negative environmental and human impacts^[1]. Neonicotinoids, comparatively new group of synthetic insecticides, similar to natural product nicotine present in the insect nervous system, agonists the nicotinic acetylcholine receptors (nAChR)^[30]. The peculiar mode of action and Chemorational ability of the neonicotinoid insecticides make them a better choice in pest management, especially in case of concealed borers. Imidacloprid [1-(6-chloro-3-pyridylmethyl)-2-nitroimino-imidazolidine] possess both systemic and contact mode of action and is compatible with different application methods for example foliar application, seed treatment^[45], soil drench and stem application in different crops and trees^[10].

Genetic Diversity and Traits Association in Parental and F₃ Populations of Chickpea

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ABSTRACT

Genetic diversity is an indicator for a plant breeder to proceed further. Five chickpea populations, i.e. three parental and two F₃ populations (NDC-4-20-4, ICC-19181, NDC-5-S10, ICC-19181 x NDC-4-20-4, ICC-19181 x NDC-5-S-10) were evaluated for variability and interrelationship at Malakandher research farm, The University of Agriculture Peshawar during chickpea growing season 2011-12. Analysis of variance revealed promising differences ($P \leq 0.01$) among populations for pods plant⁻¹, secondary branches plant⁻¹, seed yield plant⁻¹, days to flowering, harvest index, biological yield plant⁻¹ and days to maturity. Furthermore, significant differences were shown for plant height, primary branches plant⁻¹ and seed yield kg ha⁻¹. F₃ population of C₁ revealed maximum values for pod plant⁻¹, secondary branches plant⁻¹ (14.87), seed yield plant⁻¹ (19.66 g), biological yield plant⁻¹ (36.91g) and harvest index (52.78 g). Whereas population of C₂ showed maximum values for days to flowering (141.33) and primary branches plant⁻¹ (5.00). On the other hand, ICC-19181 showed minimum values for days to flowering (132), plant height (32.90 cm) and seed yield plant⁻¹ (14.13 g). Correlation analysis showed highly significant and positive association of grain yield plant⁻¹ with pods plant⁻¹, secondary branches plant⁻¹, biological yield plant⁻¹ and harvest index while significant correlation with days to flowering, days to maturity whereas non-significant correlation was revealed for plant height and primary branches plant⁻¹. This study suggests that pods plant⁻¹, secondary branches plant⁻¹, seed yield plant⁻¹, biological yield plant⁻¹ and harvest index are the key component in grain yield. C₁ (ICC-19181 x NDC-4-20-4) population can be used in future chickpea breeding programs for higher yield.

Keywords: Chickpea, diversity, F₃ populations, parental, traits

INTRODUCTION

Genetic variation among traits is important for breeding and in selecting desirable genotypes. On the other hand, an analysis of the correlation between seed yield and yield components is essential in determining selection criteria. Chickpea (*Cicer arietinum* L.) ranks third among the world's pulse crops after dry bean and dry peas. It belongs to family Fabaceae and sub family Faboidae. The genus *Cicer* L. (family Fabaceae) consists of 44 species including 35 perennials, 8 wild species and one domesticated chickpea. Chickpea is an edible legume and is high in proteins and is one of the earliest cultivated grain legumes. Chickpea is the cheapest and readily available source of proteins 22%, 64% carbohydrates, 5% fats, 6% crude fiber and 3% ash (Sattar *et al.*, 1990). It makes up the deficiency of cereals diets and also helps in the replenishment of soil fertility by fixing atmospheric nitrogen through symbiosis. Chickpea is playing a vital role in providing food for the poor people of this country. It is generally cultivated under rainfed agriculture system. The introduction of chickpea in a cereal-based rotation, which is used particularly in developing countries, can break the disease and pest cycle, and thus increase the productivity of the entire rotation (Jodha and Subba Rao, 1987). Correlation is one of the most common and most useful statistics which is a single number that describes the degree of relationship between two variables. It is a statistical technique that can show whether and how strongly pairs of variables are related to each other (Biabani *et al.*, 2011). The information on correlations among various economic traits provides the basis of selection and synthesis of improved cultivars. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes

Research Article

Genetic potential and traits association in desi and kabuli chickpea genotypes

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Abstract

The present experiment was carried out at the experimental area, University of Agriculture, Peshawar, Pakistan during the growing season of 2013-14. The current research work was planned to evaluate the genetic potential and traits association in 20 Desi and Kabuli chickpea genotypes (10 Desi and 10 Kabuli). The genetic materials were grown in a randomized complete block design (RCBD) with three replications. Data were collected on plant height (cm), secondary branches plant⁻¹, pods plant⁻¹, seed yield (kg ha⁻¹), biological yield plot⁻¹ and harvest index. Genotypes revealed significant differences for most of the traits which ranged from 63.66 to 105.28 cm for plant height, 8 to 18 for secondary branches plant⁻¹, 43 to 64 for pods plant⁻¹, 862 to 2481 kg for seed yield (kg ha⁻¹), 1383 to 3576 g for biological yield plot⁻¹ and 20 to 39% for harvest index. Mean squares showed highly significant differences ($P \leq 0.05$) for comparative performance of Kabuli and Desi genotypes. Mean value for seed yield (kg ha⁻¹) of Kabuli genotypes was 1210.10 kg, which was comparatively less than mean value of Desi genotypes which was 1823.90 kg. Among Kabuli genotypes, analysis of variance ($P \leq 0.05$) showed significant differences for most of the traits. Genotype NKC-5-S14 showed minimum (861.60 kg ha⁻¹) seed yield while maximum (1589.30 kg ha⁻¹) seed yield was recorded for NKC-5-S16. Mean squares in Desi genotypes also revealed significant differences ($P \leq 0.05$) for most of the traits. Maximum (2481.3 kg ha⁻¹) seed yield was given by genotype NIFA-2005, while minimum (1002.90 kg ha⁻¹) seed yield was recorded for genotype SL-3-29. Broad sense heritability estimates for yield and yield components were moderate to high that ranged from 54% to 92%. Positively and highly significant association of seed yield was observed with biological yield plot⁻¹ ($r = 0.85^{**}$) and harvest index ($r = 0.42^{**}$), while significantly negative correlation was observed with 100-seed weight ($r = -0.26^{*}$). Biological yield plot⁻¹, harvest index would be the proper choice criteria for better seed yield in chickpea. Results showed that genotypes NIFA-2005, NDC-4-20-5, SL-3-64, NDC-4-20-4 and NKC-5-S16 performed better and could be utilized as a part of future breeding projects for the improvement of high yielding cultivars.

Keywords: *Cicer arietinum*; Genetic variability; Heritability; Correlation

Introduction

Chickpea (*Cicer arietinum* L.), otherwise called bengal gram or garbanzo, is one of the soonest food vegetables developed by man

and assumes a key part in human eating routine and agricultural system. It belongs to family Fabaceae and genus Cicer, approximately all Cicer species have

Research Article

Assessment of genetic variability and heritability for quantitative traits between desi and kabuli chickpea genotypes

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Abstract

Twenty chickpea (*Cicer arietinum* L.) genotypes were evaluated for assessment of genetic variability and heritability for quantitative traits. This experiment was carried out in a randomized complete block (RCB) design with three replications. All chickpea genotypes revealed high significant differences for most of the traits. Analysis of variance showed highly significant differences for comparative performance of kabuli and desi genotypes. Mean value for seed yield (kg ha⁻¹) of kabuli genotypes was 1210.1 kg, which was comparatively less than mean value of desi genotypes which was 1823.9 kg. Among kabuli genotypes, the analysis of variance showed significant differences for most of the traits. Mean square analysis in desi genotypes also revealed significant differences for most of the traits. Broad sense heritability estimates for yield and yield components was moderate to high. Results showed that genotypes NIFA-2005, NDC-4-20-5, SL-3-64, NDC-4-20-4 and NKC-5-S16 performed better and could be used in future breeding programs for the development of high yielding varieties in chickpea.

Keywords: Chickpea; Genetic variability; Heritability and quantitative traits

Introduction

Chickpea (*Cicer arietinum* L.), also known as bengal gram or garbanzo, is one of the earliest food legumes cultivated by man and plays a vital role in human diet and agricultural system. It belongs to family Leguminosae and genus *Cicer*, approximately all *Cicer* species have

2n=2x=16 chromosomes. Two distinct types of chickpea are recognized, i.e. desi and kabuli [1]. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a population. The variability of a

ESTIMATION OF HERITABILITY AND SELECTION RESPONSE FOR SOME YIELD TRAITS IN F₃ POPULATIONS OF WHEAT

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ABSTRACT

Estimation of heritability and selection response were evaluated for some yield traits of twelve (12) F₃ populations of wheat got from mating of six advanced lines and two widely cultivated cultivars (Pirsabak-08 and Janbaz). All wheat genotypes (8 parents and 12 F₃ populations) showed significant differences for all traits. Among parental lines, B-IV(N)12 had more spikes (13.2 plant⁻¹). Cultivar Janbaz had maximum spikelets (23.5 spike⁻¹) and biological yield (78.8 g plant⁻¹). Parental line B-IV(N)5 had maximum grain weight spike⁻¹ (3.5 g) and grain yield (32.0 g plant⁻¹). F₃ population B-RF7 x Janbaz had spike index (78.4%) and grain yield (31.9 g plant⁻¹). Similarly, F₃ population B-RF1 x Janbaz had maximum spikes plant⁻¹ (13.5), more single spike weight (4.1 g), grain weight spike⁻¹ (3.14 g) and biological yield (65.1 g plant⁻¹). Population B-RF3 x Janbaz had maximum spikelet's spike⁻¹ (22.9). F₃ populations B-IV(N)11 x Janbaz, B-RF7 x Janbaz, B-IV(N)5 x Janbaz, B-IV(N)5 x Pirsabak-08, B-IV(N)11 x Pirsabak-08 and B-IV(N)12 x Janbaz had maximum heritability and selection responses for spikes plant⁻¹ (0.83 and 6.00), spikelets spike⁻¹ (0.94 and 1.66), grain weight spike⁻¹ (0.81 and 1.39 g), spike index (0.99 and 30.76%), biological yield plant⁻¹ (0.99 and 20.52 g) and grain yield plant⁻¹ (0.75 and 12.15 g), respectively. On the basis of high heritability coupled with high selection response for yield related traits, F₃ populations B-IV(N)11 x Janbaz, B-IV(N)5 x Pirsabak-08, B-IV(N)5 x Janbaz, B-RF1 x Janbaz and B-RF7 x Janbaz should be advanced further for possible development of high yielding wheat cultivars.

Keywords: Wheat; F₃ population; broad-sense heritability; selection response; grain yield

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the world's significant cereal crop and staple food of many nations, is grown both under irrigated and rain-fed environments. Wheat is one of the first cereals known to have been domesticated, and wheat's ability to self-pollinate greatly facilitated selection of many distinct cultivars. Wheat is cultivated on one sixth of the total cultivable land of the world. A 100 g spring wheat grains contain around 15.4% protein, 1.9% fat, 68-72% carbohydrate, 12.2% dietary fiber, and 0.0036 mg iron (United States Department of Agriculture 2013). Wheat is mostly used for making bread, biscuit and bakery products. The raised bread loaf is possible because the wheat seed comprises gluten, an elastic form of protein that traps minute bubbles of carbon dioxide when fermentation occurs in leavened dough, causing the dough to rise (Hanson, Borlaug & Anderson, 1982).

Heritability is the ratio of genetic variance to phenotypic variance. It is an important genetic parameter due to its direct relationship with response to selection. Plant traits which are exceedingly heritable can be chosen in initial filial

generations without sitting tight for late filial generation to accelerate the system of cultivars development. Grain yield mostly has low heritability because it is more effected by the environment than it's genetic. The selection size of genotypes from a population mainly depends on the quantity of heritable difference present and the amount to which it is transmitted from one filial generation to the next. Phenotypic variance of a trait is partitioned into genetic and environmental components to allow the breeders to plan effective selection programs (Dudley & Moll, 1969).

Heritability provides selection response, which help in predicting performance in the next generation for effective breeding programs. Various approaches have been adopted to improve yield potential of wheat (Ahmedi & Bajelan, 2008; Siddiqui, Mustafa, Arain & Jafri, 1991). High heritability associated with high selection response play a major role in selecting high yielding genotypes, because high heritability with high selection response has additive genetic variation for trait(s) of interest (Iqbal & Khan, 2003).

Comparative Analysis of Some Production Traits in F_{5,9} Recombinant Inbred Lines (RILs) of Bread Wheat

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Abstract: The prime objective of wheat breeding program is to increase economic yield. In this regard the current research was conducted during 2013-14 at The University of Agriculture, Peshawar to evaluate the performance of F_{5,9} recombinant inbred lines (RILs) to generate more comprehensive information on inheritance and association of some production traits. Thirty four F_{5,9} RILs and two check cultivars Atta Habib and Janbaz were evaluated in 6x6 alpha lattice design with two replications. Significant differences among recombinant inbred lines indicated the presence of sufficient genetic variability as reflected from its wide range from 25.5 to 53.2 cm² for flag leaf area, 156.0 to 172.0 days for physiological maturity, 84.8 to 121.9 cm for plant height, 2017500 to 3982500 for spikes ha⁻¹, 33.0 to 72.0 for grains spike⁻¹, 1.5 to 3.4 g for grain weight spike⁻¹, 39.8 to 54.5 g for 1000-grain weight and 3745.6 to 6711.4 kg ha⁻¹ for grain yield. Higher magnitude of genetic variances than environmental variances resulted in high heritability (>60%) for flag leaf area (72.8%), physiological maturity (75.1%), plant height (92.6%), spikes ha⁻¹ (60.9%), grains spike⁻¹ (70.01%), grain weight spike⁻¹ (69.17%) and grain yield (70.4%) accompanied by high genetic advance (10.9, 5.3, 15.1, 9924470.5, 10.5, 0.5 and 1054.7, respectively). These results indicated the prevalence of additive gene action in the inheritance of these traits and hence, amenable for simple selection. Furthermore, the study showed that spikes ha⁻¹, grains spike⁻¹ and grain weight spike⁻¹ could be used as most reliable selection index for yield improvement in wheat since they manifested notable contribution towards grain yield.

Key words: Association • Recombinant inbred lines • Alpha lattice • Genetic variability • Production traits

INTRODUCTION

Wheat, the “king of cereals” holds significant importance among cereals and is the major cultivated cereal and most important staple food of Pakistan. It holds significant position in the cropping pattern of the country. Pakistan ranks 8th among top ten leading wheat producing countries in acreage [1]. In 2013-14, the average national yield of Pakistan was 25.6 million tons with an average yield of 2797 kg ha⁻¹ from 9.09 million hectares, in which our province, Khyber Pakhtunkhwa contributes 1.13 million tons from 0.73 million hectares with an average yield 1550 kg ha⁻¹ [2]. Its share in gross domestic products (GDP) is about 2.2% and 10.3% in the total value added in agriculture.

In self-pollinated crops like wheat, the principle breeding aims are to develop cultivars with consistence performance and high economic yield. Countless research work has been done to explore areas of wheat breeding through genetic manipulation, still increasing population in the country necessitate the breeders for additional breakthrough in this food crop. Hence, in this regard plant breeders assess the extent of transmissibility for yield and yield attributes from parents to offspring in order to bring improvement in heritable characters. In addition, it also ascertains breeding stratagem to be pursued while improving a population. The assessments of broad sense heritability facilitate in envisaging the behavior of succeeding generations by planning suitable selection criteria and calculating the level of genetic gain

REGULAR ARTICLE

Genetic variability, correlation and cluster analysis in elite lines of rice

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Abstract

Development of rice cultivars with appreciative performance is one of the prime objectives of rice breeding programs. The aims of the study were to generate scientific information on nature and magnitude of genetic variability and relationship of yield and related attributes and to classify genotypes into distinct clusters on the basis of quantitative traits. Fourteen elite rice genotypes were evaluated following RCB design with three replications. There was significant ($P \leq 0.01$) differences among genotypes for all the studied traits, except physiological maturity. The magnitudes of PCV and GCV were higher ($>20\%$) in all the studied traits, except physiological maturity, reflecting wide spectrum of variability and offering greater opportunities for selection. Similarly, the magnitude of broad-sense heritability and genetic advance as percent of mean was moderate to high for majority of traits, indicating additive gene action in their inheritance hence, amenable for simple selection. Correlation analysis revealed that paddy yield manifested significantly positive correlation with physiological maturity ($r = 0.46^{**}$) and negative correlation with 1000-grain weight ($r = -0.30^*$). The dendrogram grouped 14 into four clusters. Cluster IV incorporated the highest number of genotypes, which also had highest cluster mean for paddy yield. Therefore, prominence should be given to genotypes aggregated in cluster IV that having high yield potentiality. Based on mean performance, Irrigated-04, E-93, E-94 and E-107 showed superiority in respect of paddy yield and some other traits, hence these lines could be recommended for varietal development.

Key words: Correlation; elite lines; rice

Introduction

After wheat, rice is most important crop in Pakistan, but the improvements in paddy yield is slow due to lack of ample investment to improve varieties. There is a need of modern breeding programs to improve the rice production (Smith and Dilday, 2003). Cultural

practices and genetic improvements are important to upsurge the paddy yield (Augustina *et al.*, 2013). The existence of morpho-genetic variation in various yield attributes of rice is essential in determining best breeding procedures to enhance the paddy

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REGULAR ARTICLE

CORRELATION AND HERITABILITY ESTIMATION OF VARIOUS SEEDLING TRAITS IN *BRASSICA NAPUS* L. UNDER WATER DEFICIT CONDITIONS

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ABSTRACT

Brassica napus L. contains edible oil ensuring safe limits for human health. But farmers prefer to use their fertile land for main crops and only marginal lands for oilseed. Those marginal lands usually face water scarcity and other a-biotic stresses that affect the normal growth and development of plant. Here we tested three levels of water deficit stress (control, medium and high) under controlled conditions. Seedlings were analyzed for various seedling traits to measure the relative effect of different levels water deficit stress. Graphical trends depict that increasing level of water deficit stress causes declines in leaf area, root length, shoot length, fresh and dry weight of roots and shoots. Correlation coefficients exposed positive significant correlation of fresh shoot weight with chlorophyll contents, relative water contents, leaf area and shoot length at both genotypic and phenotypic level. Path coefficient analysis displayed high direct effects on fresh shoot weight were due to relative water content, root to shoot ratio. Chlorophyll contents, relative water content, leaf area, root length and shoot length showed high broad sense heritability (h^2_{BS}) coupled with high genetic advance (GA). These traits could be focused while breeding for water deficit conditions.

Keywords: Water deficit stress, Correlation and path, seedling characters, heritability and genetic advance

INTRODUCTION

Water deficit stress has been a widely affecting the growth and development of crops. Plants growing on marginal lands face water shortage problem for longer or shorter period of time. Many physiological and biochemical changes occur in micro environment and body of plant to tolerate the water deficit stress especially during seedling stage [1]. The extent to which water deficit stress can slow down the growth of plant is determined by intensity and duration of water stress [2]. The water deficiency at seedling stage can majorly affect germination, root and shoot length significantly causing great reduction in vigor of plants [3].

Canola was firstly derived from *Brassica napus* L. and contains glucosinolates and erucic acid within safe limit for human consumption. *Brassica napus* can tolerate water deficit stress and have evolved various mechanisms against high temperature and water shortage [4]. It contains 37-41% protein and 36-41% oil contents in its seed [5]. It is mainly used for cooking, margarine, animal and poultry feed industry. It is considered healthy because of its low saturated and high monounsaturated fatty acids composition. Its profile is considered safe for human consumption as oil containing lower glucosinolates avoids

ulcer in stomach. The meal obtained after extraction of oil is being widely processed into poultry feed [6]. It is mostly utilized in cooking and margarine production.

Some countries like Iran and China have paid their attention in breeding toward the development of varieties that are tolerant to drought and water deficit stress. As their cultivated area for oilseed mostly fail to irrigate with abundant supply of water. The oilseed yield could be boosted by providing potentially high yielding varieties to farmer that can tolerate biotic and a biotic stress especially water deficit stress with minimum inputs. Government policies and marketing system should be established properly to ensure fair price of oilseed. Heterosis is being now widely used in china and few other countries to oil and yield [7]. But still germplasm resources are lacking behind in stress tolerating varieties. To fill the gap between consumption and production of oil stress breeding should be focused wisely to cope future challenges

MATERIALS AND METHODS

The present experiment was conducted in the wire house under three water deficit stress levels (moisture contents were maintained at FC, medium "50% of FC" and high "20% of FC") by using a set of 35 drought tolerant

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REGULAR ARTICLE

YIELD PERFORMANCE WITH HERITABILITY MEASUREMENTS OF HALF SIB FAMILIES OBTAINED FROM MAIZE VARIETY AZAM

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ABSTRACT

This study evaluated the performance of 64 half sib families (HSF) derived from “Azam” variety of maize using partially balanced lattice square design with two replications. Data were recorded on grain yield and other agronomic traits. Observations showed difference in half-sib families for studied traits. Among the 64 half-sib families, minimum days to 50% tasseling (51 d) were observed for HS-49 while maximum (57 d) for HS-63. Minimum days to 50% silking (56 d) were counted for HS-6 while maximum (63 d) for HS-23. Minimum days to 50% anthesis (55 d) were counted for HS-1 and HS-6 while maximum (62 d) for HS-23. Similarly, minimum ASI (-2 d) were observed in HS-1, HS-15, HS-16, HS-28 and HS-63 while maximum (2 d) in HS-48. Minimum (60 cm) ear height was recorded for HS-11 and maximum (93.5 cm) for HS-28. Minimum fresh ear weight (1.3 kg) was weighted for HS-17 while maximum (3.2 kg) for HS-21. Grain moisture was recorded minimum (19.35 %) for HS-19 and maximum (31.25%) for HS-2. HS-42 showed minimum (28 g) 100 kernel weight while HS-5 showed maximum (47 g). Grain yield was minimum (2323 kg ha⁻¹) for HS-17 and maximum (5742 kg ha⁻¹) for HS-21. Maximum heritability estimate (0.92) was recorded for fresh ear weight, while minimum (0.41) was observed for ear height.

Keywords: Azam, Heritability, ASI, Half-sibs, Breeding Material

INTRODUCTION

Maize (*Zea mays* L.) is an important cereal crop grown in many countries. It belongs to family Poaceae, having diploid chromosome as 20. The plant is monoecious and cross pollinated in nature. It is a short duration crop and is grown twice a year i.e. spring and summer [1]. Maize is the third most important cereal crop in Pakistan following wheat and rice. It is a multipurpose crop, used for food, feed as well as fodder and has its place in industries [2].

Worldwide maize cultivation was on area of 161 million hectares with total production of 840 million tons and yield of 519461.1 kg ha⁻¹ [3]. In Pakistan maize is being cultivated in significant portion of total cultivable land [4].

In Khyber Pakhtunkhwa, maize grown as a main crop in many of the cropping systems and staple food for people in rural areas in most of the province. A considerable area of

approximately 500,000 ha in plains and high mountains is planted with maize [5]. Per hectare production is low in these areas compared with countries of similar climates. Lack of suitable maize varieties with superior attributes is one of these limiting factors.

Maize is the crop with highest per day productivity with a high yield potential. Development of improved varieties with high yield potential can be seen as a possibility to increase production per unit area. Such kind of varieties with improved qualitative and quantitative traits represents one of the most successful aspects of the modern agricultural technology [6]. For developing high yielding varieties to increase yield per unit area a lot of selection processes have been employed by maize breeders particularly mass-selection, modified mass-selection, ear-to-row selection and several methods of recurrent selection including selfed progenies derived from a base population.

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ESTIMATES CORRELATION COEFFICIENT AMONG YIELD AND YIELD ATTRIBUTING TRAITS IN TWENTY CHICKPEA GENOTYPES

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Abstract

An experiment was conducted in The University of Agriculture, Peshawar, Pakistan during growing season 2013 to estimate correlation coefficient among yield and yield attributing traits in twenty chickpea genotypes. Total of (10 desi and 10 kabuli) genotypes were grown in a randomized complete block design with three replications. Plant height showed positive and highly significant correlation with 100-seed weight, while negative and highly significant correlation recorded with seeds pod⁻¹ and harvest index. Secondary branches exhibited positive significant association with pods plant⁻¹ and 100-seed weight while negative significant interrelationship found with seeds pod⁻¹ and harvest index. Pods plant⁻¹ revealed negative significant association with seed yield (kg ha⁻¹), seeds pod⁻¹ and harvest index. Positive correlation of seeds pod⁻¹ presented with harvest index. Highly significant and positive correlation of seed yield (kg ha⁻¹) was observed with harvest index and seeds pod⁻¹, while significantly negative relationship observed with 100-seed weight. Harvest index and seeds pod⁻¹ would be the appropriate selection criteria for better seed yield in chickpea.

Keywords: Chickpea, Correlation, Seed yield and Genotypes.

INTRODUCTION

Chickpea (*Cicer arietinum* L.), also known as gram or chana, is one of the most basic food legumes cultivated by man and acting an energetic role in human nutrition and agricultural organization. It belongs to family Leguminosae and genus Cicer, almost all Cicer species have 2n=2x=16 chromosomes. In worldwide among the yearly seed crops, chickpea grades 14th in terms of area and 16th in production (Knights *et al.*, 2007). Two separate types of chickpea are familiar, i.e. Desi and Kabuli. In Desi chickpea, the seed colours combinations of brown, yellow, green and black. The flowers are usually pink and the plants show various degrees of anthocyanin pigmentation, although some Desi types have white flowers and no anthocyanin pigmentation on the stem. The Kabuli type chickpeas are categorized by white coloured seed, thin seed coat, white flowers, smooth seed surface, and lack of anthocyanin pigmentation on the stem. As compared to Desi types, the Kabuli types have higher levels of sucrose and lower levels of fibre. The Kabuli types mostly have large sized seeds and receive higher market price the Desi types (Gaur *et al.*, 2010). The

correlation between seed yield and yield components is essential in determining selection criteria. Genotypic and phenotypic correlations are of value to indicate the degree to which various quantitative traits of the plant are associated with economic productivity. Correlation study thus provides information on correlate response of important plant traits and therefore leads to a directional model for yield response (Naveed *et al.*, 2012). The methods to make significant improvement in chickpea production to require information on nature and magnitude of genetic variation in quantitative characters and their inter-relationship comprising different genotypes in a population, which are important fundamentals for regular breeding programme (Arshad *et al.*, 2003). Keeping in view the present investigations were planned to estimate correlation coefficient among yield and yield attributing traits in chickpea.

MATERIALS AND METHODS

The experiment to estimate correlation coefficient among yield and yield attributing traits in twenty chickpea genotypes (10 desi and 10 kabuli) was

Research Article



Heritability and Selection Response for Grain Yield and Associated Traits in F_3 Wheat Populations

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Abstract | Broad sense heritability and selection responses were assessed for grain yield and related traits in 12 F_3 populations of wheat got from mating of six advanced lines and two widely cultivated cultivars (Pirsabak-08 and Janbaz) at University of Agriculture, Peshawar during 2013-14. All wheat genotypes (8 parents and 12 F_3 populations) showed significant differences for all traits. Cultivar Janbaz had maximum spike length (13.9 cm) and maximum number of grains spike⁻¹ (89.2). Parental line B-IV(N)5 had maximum single spike weight (4.6 g), 100-grain weight (4.6 g) and grain yield (32.0 g plant⁻¹). F_3 population B-RF7 × Janbaz had 100-grain weight (4.5 g) and grain yield (31.9 g plant⁻¹). Similarly, F_3 population B-RF1 × Janbaz had more single spike weight (4.1 g). Population B-RF3 × Janbaz had maximum spike length (14.5 cm) and number of grains spike⁻¹ (85.1). F_3 populations B-RF7 × Pirsabak-08, B-IV(N)5 × Pirsabak-08, B-RF7 × Janbaz, B-IV(N)5 × Pirsabak-08, B-RF7 × Janbaz, B-RF1 × Janbaz, B-IV(N)12 × Janbaz had maximum heritability and selection responses for plant height (0.76 and 10.96 cm), spike length (0.93 and 4.51 cm), grains spike⁻¹ (0.93 and 25.54), single spike weight (0.89 and 3.08 g), 100 grain weight (0.90 and 1.26 g) and grain yield plant⁻¹ (0.75 and 12.15 g), respectively. On basis of high heritability coupled with high selection response for yield related traits, F_3 populations B-IV(N)5 × Pirsabak-08, B-IV(N)5 × Janbaz, B-RF1 × Janbaz and B-RF7 × Janbaz should be advanced further for possible development of high yielding wheat cultivars.

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Keywords | Heritability, Selection response, F_3 populations, Wheat, Advance lines

Introduction

Wheat has always been under major research to improve its grain production as well as quality. However, there is still broad space for genetic improvement of wheat to meet the developing necessities of the expanding population. Genetic exploitation is the most ideal approach to increase wheat production. In this way, it is essential to study the hereditary changes and mode of inheritance of distinctive parameters for effective wheat breeding projects (Ijaz

and Khan, 2009). Wheat breeders are attempting to grow new cultivars which are high yielding, drought tolerant and have resistance against diseases and insects/pests. Wheat breeders are generally selecting required genotypes in initial filial generations when a trait has high heritability or late selection until advanced filial generations, when the offspring are nearly homozygous. Direct assessment of yield is mostly difficult in initial generation selection. So, plant breeders are selecting those traits which ultimately increase yield. Breeding yield traits to increase grain



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Nitrogen mineralization and microbial activity as influenced by sulfur sources in an alkaline calcareous soil

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ABSTRACT

A study was performed to check the effects of various sources of sulfur on microbial activity, microbial population, N mineralization and organic matter content in an alkaline calcareous soil by using soil samples collected from Malakandher Farm at 0-20 cm depth, and analyzed for microbial activity, total mineral nitrogen, bacterial and fungal population and organic matter content. The results showed that the rate of CO₂ evolution and cumulative CO₂ production were higher in soils amended with elemental sulfur followed by sulfuric acid and gypsum treated soils. The microbial activity decreased with incubation period in all treatments, and the microbial population was greatly affected by sulfur sources. Generally, the bacterial population decreased in soils amended with elemental sulfur, but the population was higher in soils amended with gypsum. Bacterial population was suppressed in soils treated with sulfuric acid. However, the fungal population was higher in soils amended with sulfuric acids was less in soil amended with elemental sulfur. The sulfur amendments promoted immobilization of N. The net N immobilized was higher in soil amended with gypsum followed by soils amended with sulfuric acid and elemental sulfur. The percent organic matter was higher in soils amended with gypsum and was decreased compared with that amended with elemental sulfur or sulfuric acid. These results suggested that soil microbiological properties changed with sulfur amendments during laboratory incubation.

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KEYWORDS: Microbial activity, calcareous soil, N mineralization, microbial population, alkaline

INTRODUCTION

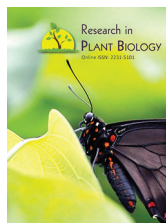
Sulfur is a key nutrient for crop production. However, sulfur deficient soils (>100 million ha) are found in many agricultural areas around the globe. Sulfur plays a crucial role in the formation of chlorophyll and a building block of protein. Without adequate S, crops cannot reach their full potential in terms of yield or protein content [1]. Organic matter is the main sources of total sulfur for the soils in the humid area, while gypsum is the main source for the soils in the drier parts. When S is scarce in the soil, full yield potential of the crop cannot be realized regardless of other nutrients even under good crop husbandry practices. The aftereffects of particulate sulfur supply in soil is of major problem as it creates pollution in agricultural soils.

As there are no minerals containing N in soil, reserves of N depend on the soil organic matter content. Thus, N cycling in soil is closely related to organic matter turnover. Micro-organisms are responsible for soil-N transformations, which play a key role

in determining the availability of N for plant growth and crop production. Therefore, the knowledge of the quality of soil organic matter and understanding of these N-cycling processes are of utmost importance with respect to agricultural systems for the balanced and proper management of external sources of N in the forms of mineral and organic fertilizers and biologically fixed N. Changes in the N cycle associated with excessive soil-N loading can have detrimental effects on terrestrial and aquatic ecosystems, such as eutrophication, algal blooms and dead zones.

Soil micro biota, is involved in the macronutrient cycles [2,3], is negatively affected by the fire. Soil microorganisms are susceptible to the indirect environmental changes caused by heat [4]. Microorganisms are responsible in the formation, stabilization, and degradation of soil aggregates [5,6]. The present study was carried out to study the effects of different sources of sulfur on N mineralization and immobilization, microbial population, organic matter content and microbial activity in alkaline calcareous soil.

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Genetic variability and interrelationship studies in green super rice

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ABSTRACT

Field experiment was executed using 18 advance lines of green super rice (GSR) during Kharif 2015 at Agricultural Research Institute, D.I. Khan, KP, Pakistan. The aims of the study were to screen out genetic variability among GSR lines and to assess heritability and genetic advance and correlation between yield and related attributes. The experiment was laid down in a randomized complete block design with three replications and data on eight production traits were recorded and subjected to various statistical analysis. The results corresponding to analysis of variance revealed significant ($P \leq 0.01$) differences among GSR lines for all the studied traits. The presence of slightly higher phenotypic coefficient of variation than genotypic coefficient of variation indicated the negligible influence of environment on the expression of yield and its component traits. Similarly, the highest heritability ($>60\%$) associated with genetic advance were assessed for all the traits, except panicle length, indicating better scope for improvement of these traits by an effective selection program. Correlation analysis revealed that paddy yield manifested significant correlation with days to panicle emergence ($r=0.57^{**}$), panicle length ($r=0.53^*$) and number of filled grains panicle⁻¹ ($r=0.63^*$) hence, ample importance should be given to these traits during selection.

KEYWORDS: Correlation, genetic variability, GSR lines, heritability

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INTRODUCTION

Rice is the staple food and ranks second in production among cereals in Pakistan. It is also a good source of livelihood for farming community in its growing season as it secures a high proportion of foreign exchange after cotton. Rice accounts for 3.0 percent in the value added in agriculture and 0.6 percent of GDP. During 2016-17, rice crop was sown on area of 2724 thousand hectares showing a decrease of 0.6 percent over the last year's area of 2793 thousand hectares. Rice production stood at 6849 thousand tonnes achieving its targeted production of 6838 thousand tonnes and showing an increase of 0.7 percent over corresponding period of last year's production of 6801 thousand tonnes. Rice area decreased due to decline in domestic prices of rice which reduced the area under the crop and growers shifted to sugarcane and maize crop (Pakistan Economic Survey, 2016-17).

Asian rice, (*Oryza sativa*), is one of the most important and oldest crop species domesticated about 8,000 – 9,000 years ago (Liu *et al.*, 2007). It is a feeding source for more than one half of the world's population (Li *et al.*, 2006). Rice is the combination of several genetically differentiated groups, with the two most important groups being *indica* and *japonica*. *Indica* and *japonica*

are sometimes also described as sub-species. The archeological evidences had showed that it was grown in third millennium BC in Pakistan in the areas of Sindh and Punjab (Paikhomba *et al.*, 2015).

The rapid increase in population of the world demands for improvement in acreage and yield of the crop. It is expected that world population will possibly reach 9-11 billion during 2030-2050. With recent tendency of population growth and agriculture production the requirement of world food will be double in some part of the world. Development of high yielding varieties is the best way to ensure food security of increasing population (Bisne *et al.*, 2009). The challenge, above anything else, is to produce this additional rice with less land, less water, and less labour, in more efficient, environmentally-friendly production systems that are more resilient to climate change, among other factors. The success of fruitful breeding program usually depends upon the extent of genetic variability present in the breeding materials. Thus, knowledge on genetic variability along with heritability and genetic advance is very essential for a breeder to choose good genotypes for crop improvement.

Recognizing the stated importance and existing potentials to boost rice production and productivity to cope up with the

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