**GENOTYPE × YEAR INTERACTION FOR YIELD AND YIELD RELATED TRAITS IN RICE (*Oryza sativa* L.)**

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**ABSTRACT**

This study was conducted to assess the performance of 18 rice genotypes across years for yield and yield related traits among rice genotypes. The experiments were planted in randomized complete block design with three replications during 2017 and 2018 rice crop growing seasons. The pooled analysis of variance depicted significant (P≤0.01) differences among the genotypes, years and genotype by year interaction for yield and yield associated traits. Across years both the years, DR-92 showed the highest number of spikelets panicle-1 (228.50) while Dokri-Basmati manifested the maximum number of grains panicle-1 (219). Genotype IR-8 exhibited maximum 1000-grain weight (34.70 g). DR-92 produced the highest grain yield (7223 kg ha-1) across both the years followed by Dokri-Basmati (6474 kg ha-1), Pakhal (6214 kg ha-1) and IR-8 (5086 kg ha-1). Grain yield showed significantly positive phenotypic and genotypic associations with spikelets panicle-1, grains panicle-1 and 1000-grain weight. Overall, the study indicated the differential behavior of genotypes for the studied traits across years. Rice genotypes DR-92, Dokri-Basmati and IR-8 showed superior performance for yield and yield related traits across the years and could be recommended for commercial cultivation in the region. Moreover, the genetic potential of these genotypes as parents could be exploited in rice breeding program.

**Keywords: Rice, Genotypes by Year Interaction (GYI), Genetic Variation, Correlation, Grain Yield, Yield Associated Traits.**

1. **INTRODUCTION**

 Rice is one of the most important food crops worldwide. It is considered as a major staple food crop for more than half of the world’s human population. On the basis of its nutritional status it has better nutritional profile value as it contains 75 to 80% starches, 12% water and 7% proteins (Oko *et al*., 2012; Hossain *et al*., 2015).

Rice is the second major cereal crop in Pakistan after wheat. It is grown not only for the purpose of local consumptions but also in view of larger exports. Besides its importance as a food crop, about 23% of the total foreign exchange earnings is shared by rice and is called as “Golden grain of Pakistan”. In Pakistan rice crop is grown on an area of 2.78 million hectares that is 11% of the total cultivated area with a production of 6.80 million tones and with an average yield of 2.52 tones ha-1 (FAOSTAT, 2017).

 According to recent report of United Nation it is predicted that the world population would reach to eight billion mark by 2030 while 9.6 billion by the year 2050. Rice production, thus needs to be enhanced by 50% to ensure food security for this increasing population (Konate *et al*., 2016). Identification and development of new high yielding rice cultivars is therefore the need of hour.

The performance of the particular genotypes for different traits is the combined result of the genetic potential (G), the environment (E) and the interaction between the genotype and environment (GE). Genotypes by environment interaction can be defined as the differential response of various different genotypes across different environments. Genotypes with low G x E interaction and high stable yields are considered desirable by crop breeders. A good and efficient genotype should have stable performance for yield and yield attributing traits across years ([Hill, 1975](https://www.sciencedirect.com/science/article/pii/S1672630817300227#bib0085)) because it indicates that the environments have relatively less influence on the performance of genotypes. The development of rice genotypes with high yield and stable in performance over a wide range of environments is therefore, an important consideration in rice breeding (Tai, 1971). To evaluate the consistency of rice [grain yield](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/grain-yield) and develop genotypes that respond optimally and consistently across years, it is necessary to study genotype by environment interactions ([Blanche et al., 2009](https://www.sciencedirect.com/science/article/pii/S1672630817300227%22%20%5Cl%20%22bib0020)).

Grain yield improvement is a primary trait of concern in rice crop breeding program. However, this is quantitative in nature and is greatly influence by environment. In such a scenario, indirect selection for secondary traits like grains panicle-1 and 1000-grain weight is used to improve the primary character. For effective application of indirect selection, strong correlation of secondary traits with primary trait is crucial (Gallais., 1960). The analysis of correlation offers an opportunity to get an idea about causal relationship between the two characters. Genotypic and phenotypic associations of yield with yield attributing traits is therefore, of immense importance to crop breeders for identification and development of high yielding rice cultivars (Agarwal *et al*, 1978, Amin, 1979, Ragarathiram *et al*., 1992). The present study was conducted to, i) assess the performance of rice genotypes across two years, ii) figure out genotype by year interaction for yield and yield related traits and to, iii) estimate phenotypic and genotypic correlation for yield and yield related traits.

**II. Materials and Methods**

The experiments were conducted at the Plant breeding and Genetics Research Farm, The University of Agriculture-Peshawar, Pakistan across two years 2017 and 2018 rice growing seasons. The experimental materials comprised of 18 rice genotypes (cultivars/advance lines) which were evaluated in randomized complete block design with three replications across both the years. The list of rice genotypes used in the study is given in Table 1. In each rice crop growing season, first nursery was raised during the 1st week of May while transplantation of seedlings into well-paddled field was done during 3rd week of June. Each rice genotype was planted in four-row plot with row length of three meters and row-row distance of 30 cm. Data were recorded on spikelets panicle-1, grains plant-1, 1000-grain weight and grain yield.

Data were subjected to analysis of variance separately for each year and across years using Statistical Analysis System (SAS) package. Means were separated using least significant difference (LSD) Test to discriminate the genotypes at 5% level of probability.

**Table 1: List of the rice genotypes used in the study.**

|  |
| --- |
| **Rice genotypes** |
|  |
| 1. | Pakhal | 10. | Bas-100 |
| 2. | IR-8 | 11. | Bas-370 |
| 3. | Kashmir-Basmati | 12. | Bas-6129 |
| 4. | DR-92 | 13. | Dilrosh |
| 5. | DR-83 | 14. | Sadahayat |
| 6. | Dokri-Basmati | 15. | Mathra |
| 7. | Bas-2008 | 16. | Sathra |
| 8. | Kangni-27 | 17. | Kkhushboo |
| 9. | TN-1 | 18. | Shadab |
|  |

**III. Results and Discussion**

**Spikelets panicle-1**

The pooled analysis of variance manifested highly significant (P≤0.01) differences among the genotypes, years and genotypes by year interaction for spikelets panicle-1 (Table 2). During 2017 rice growing season spikelets panicle-1 among the genotypesranged from 174 to 233. Sadahayat showed minimum number of spikelets panicle-1(174) while Dokri-Bas displayed maximum number of spikelets panicle-1 (233). During 2018, the spikelets panicle-1 among the genotypes varied from 164 to 237. The lowest number of spikelets panicle-1 (164) were observed for genotype Kangni-27 while the highest number of spikelets panicle-1 (237) were recorded for the genotype DR-92. Across the years, spikelets panicle-1ranged from 174 to 228. Kangni-27 produced minimum numbers of spikelets panicle-1 (174) while maximum panicle-1 spikelets panicle-1(228.50) were recorded for genotype DR-92 (Table 3). These results are similar to the findings of Rashmi *et al*. (2017); Ajmera *et al*. (2017). Rashmi *et al*. (2017) assessed 22 rice breeding lines over three various experimental sites and observed significant genotype x environment interaction for spikelets panicle-1. In their study, rice genotype JK2 15-1 produced maximum spikelets panicle-1 (143). Similarly, Ajmera *et al*. (2017) studied thirty seven rice genotypes including two checks at three different locations and observed that spikelets panicle-1 is having significant differences among environments, genotypes and genotype × environment interaction for spikelets panicle-1. They reported that the rice genotype RPHP 107 had maximum number of spikelets panicle-1 (181).

Spikelets panicle-1 exhibited significantly positive phenotypic association with 1000-grain weight and grain yield while manifested positive association with grain yield at genotypic level (Table 5). Singh and Verma (2018) conducted a study to assess correlation and path coefficient studies for grain yield and associated traits in rice. They also observed significantly positive phenotypic and genotypic correlation of spikelets panicle-1 with grain yield.

**Grains panicle-1**

Pooled analysis of variance showed highly significant (P≤0.01) variations among rice genotypes, years and genotype by year interaction for grains panicle-1 (Table 2). During 2017 rice planting season grains panicle-1 among genotypes varied from 155 to 222. Minimum grains panicle-1 (155) were observed for the genotype TN-1 while maximum gains panicle-1 (228) were recorded for genotype Dokri-Basmati. During 2018, grains panicle-1 among genotypes ranged from 154 to 224. Kagni-27 produced lowest number of grains panicle-1 (154) while the highest grains panicle-1 (226) were recorded for genotype DR-92. Across the two years grains panicle-1 among the genotypes varied from 157 to 219. Minimum grains panicle-1 (157) were observed for genotype Kagni-27 while maximum grains panicle-1 (219) were recorded for genotype Dokri-Basmati (Table 3). The results are compatible with findings of Luguterh and Dioggban (2016) and Dewi *et al*. (2014). Luguterh and Dioggban (2016) evaluated 15 rice genotypes in randomized complete block design using three replications across four locations. The combined analysis of variance showed significant genotypes and environment interaction for yield associated traits. Similarly, Dewi et al. (2014) assessed ten advanced rice lines along with two check varieties using six environments for yield and yield related traits. They observed differential response of the genotypes across different environments for grains panicle-1.

Grains panicle-1 displayed significantly positive phenotypic association with 1000-grain weight and grain yield while manifested positive genotypic association with spikelets panicle-1 (Table 4). Karim *et al*. (2014) assessed phenotypic and genotypic correlation for different quantitative traits using aromatic rice genotypes. They observed significantly negative phenotypic association of grains panicle-1 with 1000-grain weight, which is contrast to our findings. The possible reason for this could be due to the differences in the genetic materials of the two studies.

**1000-grain weight**

The pooled analysis of variance showed highly significant (P≤0.01) differences among genotypes, year and genotype by year interaction for 1000-grain weight (Table 2). During 2017 rice growing season, 1000-grain weight among the genotypes ranged from 22.3 to 38.3. Rice cultivars Sathra displayed minimum 1000-grain weight (22.3 g) while maximum 1000-grain weight (38.3 g) was recorded for IR-8. During 2018, 1000-grain weight among the genotypes varied from 22.3 to 32.6. Minimum 1000-grain weight (21.1 g) was observed for genotype Khusboo while maximum 1000-grain weight (32.6 g) was recorded for genotype Pakhal (Table 4). Lakshmi *et al*. (2014) and Kulsum *et al*. (2013) assessed significant differences among the genotypes, environments and genotype by environment interaction for 1000-grain weight. Lakshmi et al. (2014) evaluated 13 rice genotypes across five environments and observed significant differences among genotypes, environments and genotype by environment interaction for 1000-grain weight.

Thousand grains weight exhibited significantly positive phenotypic and genotypic association with grain yield (Table 4). Karim *et al*. (2014) conducted correlation studies among yield and yield attributing traits using aromatic rice genotypes. They also observed significantly positive phenotypic and genotypic correlation of 1000-grain weight with grain yield.

**Grain yield**

Pooled analysis of variance showed highly significant (P≤0.01) differences among the genotypes, years and genotypes by environment interaction(Table 2). During 2017 rice growing season, grain yield among genotypesranged from 3020 to 7562. Minimum grain yield(3020 kg ha-1) was recorded for genotype TN-1 while maximum grain yield(7562 kg ha-1) was observed for Dokri Basmati. During 2018, grain yieldamong the genotypes varied from 2069 to 7602. Kangni-87 produced the lowest grain yield (2069.6 kg ha-1) while highest grain yield (7602 kg ha-1) were recorded for genotype DR-92. Across both years the grain yield ranged among genotypes from 2577 to 7223. Kagni-27 showed minimum grain yield ha-1  (2577 kg ha-1) while DR-92 displayed maximum grain yield(7223 kg ha-1) (Table 4).Ajmera *et al*. (2017) studied genetic variation for yield and yield attributing traits in 37 rice genotypes across various environments. They observed significant differences among the genotypes, years and genotypes by environment interaction for grain yield.

Grain yieldhad significantly positive phenotypic and genotypic association with spikelets panicle-1, grains panicle-1 and 1000-grain. Karim *et al*. (2014) also observed significantly positive phenotypic and genotypic association of grain yield with spikelets panicle-1, grains panicle-1 and 1000-grain weight. The study depicted that enhancement in the grain yield could be possible through improvement in secondary characters like spikelets panicle-1, grains panicle-1 and 1000-grain weight.

**CONCLUSIONS AND RECOMMENDATIONS**

 The pooled analysis of variance indicated highly significant differences among the genotypes, years and genotype by year interaction for spikelets panicle-1, grains panicle-1, 1000-grain weight and grain yield. The study revealed differential behavior of the rice genotypes for different traits across the two years. DR-92 showed superior performance for yield and yield related traits across the two years followed by Dokri-Basmati, Pakhal and Shadab and are recommended for commercial cultivation and use in rice breeding programs. Highly significant positive phenotypic and genotypic correlation were recorded for grain yield with spikelets panicle-1, grains panicle-1 and 1000-grain weight.

**Table 2: Mean squares of rice genotypes for spikelets panicle-1, grains panicle-1, 1000-grain weight and grain yield at Peshawar during 2017 and 2018:**

|  |  |  |
| --- | --- | --- |
| **Source of Variance** | **D*f*** | **Mean squares** |
| **Spikelets panicle-1** | **Grains panicle-1** | **1000-grain weight** | **Grain yield**  |
| Years (Y) | 1 | 104.3 | 720.8 | 635.6 | 22408271.9 |
| Rep within Years | 4 | 419.9 | 58.9 | 77.9 | 175709. 00 |
| Genotypes (G) | 17 | 1458.9\*\* | 1827.5\*\* | 77.1\*\* | 8917073. 6**\*\*** |
| Y x G | 17 | 886.3**\*\*** | 769. 6 **\*\*** | 28.3 **\*\*** | 3528298.7**\*\*** |
| Error | 68 | 46.5 | 60.9 | 19.2 | 727898.2 |

\*\* Significant at 1% level of probability.

**Table 3. Means of rice genotypes for spikelets panicle-1 and grains panicle-1 at Peshawar during 2017 and 2018.**

|  |  |  |
| --- | --- | --- |
| **Gennotypes** | **Spikelets panicle-1** | **Grains panicle-1** |
| **Year-I****(2017)** | **Year-II****(2018)** | **Means** | **Year-I****(2017)** | **Year-II****(2018)** | **Means** |
| **Pakhal** | 231 | 210 | 220 | 222 | 204 | 213 |
| **IR-8** | 212 | 212 | 212 | 205 | 195 | 200 |
| **Kashmir-Basmati** | 218 | 206 | 212 | 200 | 200 | 200 |
| **DR-92** | 220 | 237 | 228 | 211 | 224 | 217 |
| **DR-83** | 186 | 213 | 199 | 179 | 189 | 184 |
| **Dokri-Basmati** | 233 | 223 | 228 | 228 | 210 | 219 |
| **Bas-2008** | 190 | 181 | 185 | 183 | 163 | 173 |
| **Kangni-27** | 185 | 164 | 174 | 160 | 154 | 157 |
| **TN-1** | 175 | 194 | 184 | 155 | 178 | 166 |
| **Bas-100** | 188 | 172 | 180 | 180 | 168 | 174 |
| **Bas-370** | 187 | 221 | 204 | 171 | 195 | 183 |
| **Bas-6129** | 195 | 196 | 195 | 173 | 172 | 172 |
| **Dilrosh** | 215 | 204 | 209 | 190 | 180 | 185 |
| **Sadahayat** | 174 | 221 | 197 | 163 | 201 | 182 |
| **Mathra** | 181 | 198 | 189 | 171 | 172 | 171 |
| **Sathra** | 221 | 181 | 201 | 210 | 167 | 188 |
| **Khushboo** | 200 | 183 | 191 | 187 | 178 | 182 |
| **Shadab** | 217 | 180 | 197 | 212 | 157 | 184 |
| **Means** | 201 | 199 | 176 | 188 | 183 | 186 |
| **LSD(0.05)** | 13 | 8 | 36 | 13 | 12.4 | 33 |
| **LSD(Gen x Yr)** | - | - | 11 | - | - | 12 |

**Table 4. Means of rice genotypes for 1000-grain weight and grain yield of at Peshawar**

**during 2017 and 2018.**

|  |  |  |
| --- | --- | --- |
| **Genotypes** | **1000-grain weight (g)** | **Grain yield (kg ha-1)** |
| **Year-I****(2017)** | **Year-II****(2018)** | **Means** | **Year-I****(2017)** | **Year-II****(2018)** | **Means** |
| **Pakhal** | 35.3 | 32.6 | 33.9 | 7100 | 5327 | 6214 |
| **IR-8** | 38.3 | 31.1 | 34.7 | 5922 | 4249 | 5086 |
| **Kashmir-Basmati** | 31.7 | 30.8 | 31.2 | 5219 | 4225 | 4722 |
| **DR-92** | 28.2 | 31.9 | 30.0 | 6844 | 7602 | 7223 |
| **DR-83** | 34.7 | 28.5 | 31.5 | 4866 | 4930 | 4898 |
| **Dokri-Basmati** | 35.3 | 29.4 | 32.3 | 7562 | 5387 | 6474 |
| **Bas-2008** | 33.3 | 26.5 | 29.8 | 4998 | 3606 | 4302 |
| **Kangni-27** | 36.3 | 26.3 | 31.3 | 3084 | 2069 | 2577 |
| **TN-1** | 33.7 | 26.6 | 30.1 | 3020 | 3868 | 3444 |
| **Bas-100** | 23.0 | 24.1 | 23.5 | 4186 | 2554 | 3370 |
| **Bas-370** | 31.7 | 27.5 | 29.6 | 4177 | 4618 | 4398 |
| **Bas-6129** | 28.8 | 21.9 | 25.3 | 3515 | 2991 | 3253 |
| **Dilrosh** | 34.7 | 27.0 | 30.8 | 4218 | 2948 | 3583 |
| **Sadahayat** | 30.3 | 27.6 | 28.9 | 3012 | 5486 | 4249 |
| **Mathra** | 23.4 | 22.4 | 22.8 | 3867 | 2935 | 3401 |
| **Sathra** | 22.3 | 22.3 | 22.3 | 6779 | 3069 | 4924 |
| **Khushbo** | 34.3 | 21.1 | 27.7 | 4054 | 3822 | 3938 |
| **Shadab** | 33.7 | 24.2 | 28.9 | 6739 | 3070 | 4905 |
| **Means** | 31.6 | 26.7 | 28.1 | 4953 | 4042 | 2746 |
| **LSD(0.05)** | 2.6 | 9.9 | 6.4 | 74.2 | 2000 | 2288 |
| **LSD(GYI)** | - | - | 7.1 | - | - | 1386 |

**Table 5. Phenotypic and genotypic correlation coefficient among yield and yield attributing traits in rice genotypes at Peshawar during 2017 and 2018.**

|  |  |  |
| --- | --- | --- |
| **Characters** | **Phenotypic correlation** | **Genotypic correlation** |
| Sikelets Spike-1 vs Grains Panicle-1 | 0.92 \*\* | 0.91\*\* |
| Sikelets Spike-1 vs 1000-grain Weight | 0.33\*\* | 0.42 |
| Sikelets Spike-1 vs Grain Yield | 0.68 \*\* | 0.67\*\* |
| Grains Panicle-1 vs 1000-grain Weight  | 0.58\*\* | 0.72\*\* |
| Grains Panicle-1 vs Grain Yield | 0.86\*\* | 0.87\*\* |
|  1000-grain Weight vs Grain Yield | 0.57\*\* | 0.73\*\* |

\*\* Significantly Correlated at 1% level of probability respectively

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