

EVALUATION OF SOME RICE GENETIC RESOURCES FOR DROUGHT TOLERANCE

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Introduction

About 70% of the rice eaten in Ghana is imported and the state of self-insufficiency in rice production can be attributed to lack of adequate/continuous water supply. Rice, being a water loving plant, has drought as the most disturbing abiotic factor causing as much as 64% reduction in yield. Therefore, a study was conducted to identify drought tolerance genotypes among 24 rice collections and to estimate heritability in the broad sense. A total of 24 traits were scored in this study, and three treatments were applied including stress free, mild stress and severe stress with three replications. The results showed that most of the parameters studied including panicle length, fertile panicle rate, shoot and root dry weight, maximum root depth decreased considerably as the level of drought stress increased. In addition, five of the accessions showed considerable tolerance to drought, eight accessions were high yielding and eight accessions combined high yields and drought tolerance. The study concluded that 80% of the rice accessions present promising lines to be used as parents in the development of drought tolerant varieties hence may be used in genetic improvement programs aimed at such a purpose. The study recommended that molecular studies, as well as morphological characterization should be done on the collections to understand their genetic makeup, similarities and differences.

Rice is a major food staple in Africa including Ghana and has become part of Ghana's local delicacies (Quaye et al., 2010). However, 70% of the rice eaten in Ghana is imported, constituting a huge drain on Ghana's scarce foreign exchange reserves (Sam-Amoah, 2004). The state of self-insufficiency in rice production in the country can be attributed to lack of adequate/continuous water supply. Rice, being a water loving plant, has drought as the most disturbing abiotic factor causing as much as 64% reduction in yield (Shaibu et al., 2018). Rice susceptibility to drought is more pronounced at the reproductive stage (Anupam et al., 2020). Depending on the severity and timing of drought incidence, low yields are recorded.

The possibility of huge losses due to drought deters farmers from investing in yield-enhancing inputs such as fertilizer, trapping them in a cycle of low productivity (Shaibu et al., 2018). Therefore, developing a variety with more efficient water use will decrease cost associated with irrigation while boosting food production and livelihood of farmers in drought prone areas (Asante et al., 2013). Success in breeding for a drought tolerant cultivar largely depends on the identification of diverse yet promising parents. Phenotypic studies that involves proper screening of germplasm for drought tolerance presents an opportunity for achieving such parents. Hence, the importance of screening rice genetic resources for drought tolerance cannot be overemphasized.

Therefore, the objectives of the study were to (1) identify drought tolerant genotypes among the collections and (2) estimate heritability of characters such as spikelet fertility, fertile panicle rate,

Twenty four genetic resources of rice were used in the study including Vandana, Moroberikan, NERICA 6, NERICA 8, NERICA 5, 1592, 1581, 1579, 1552, 1586, 1514, 1539, 1593, 1520, 1596, 1526, 1580, 1582, 1575, 1541, 1521, 1598, IR64 and CG14. Seventeen were assembled from the Plant Genetic Resource Research Institute, PGRRI-Ghana, five from African Rice Centre, ARC-Benin, two from the International Rice Research Institute, IRRI-Philippines.

Screening and drought treatment of the rice accessions were carried out in a greenhouse following a modification of a protocol used by Yue et al. (2006). Pre-germinated rice seeds were sown directly in PVC pipes arranged in a completely randomized design (CRD) with three water regimes viz. stress free, mild stress and severe stress as treatments. The pipes contained 9.6 kg of thoroughly mixed soil composed of one part heavy clay and one part loose sandy soil. A total of 24 traits were scored in this study; 14 of which were traits collected from above ground part of the plants and the other 10 were root traits.

Conclusion

The differences in mean performance between accessions for all traits were significant showing that performance measured in this study is accession specific. This indicates the scope of genetic improvement of these characters through selection of promising lines from the present gene pool for crop improvement programmes. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence acting on the phenotypes. These findings are compatible with the findings of Tiwari et al. (2011), Singh et al. (2011) and Sabar and Arif (2014) who also observed significant variability for yield and its components in rice. There were also significant differences among treatments as well as accessions by treatment interaction for all measured parameters.

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