

Research Application Summary

Analysis of drought tolerance in selected upland rice genotypes in Uganda

Namazzi, B.S.¹, Okori, P.¹, Baguma, Y.² & Lamo, J.²

¹Department of Crop Science, Faculty of Agriculture, Makerere University,
P. O. Box 7062, Kampala, Uganda

²National Crops Resources Research Institute, P. O. Box 7084, Kampala, Uganda
Corresponding author: bira8000@gmail.com

Abstract

Breeding for drought tolerance requires a clear understanding of the mode of gene action for this trait. To understand the action of drought tolerance genes in upland rice varieties in Uganda, a study was carried out to establish the general and specific combining ability of the new rice lines acquired in the breeding programme as well as validate QTLs from previous studies in our own population and environment. F₂ populations from five susceptible and five resistant parents were generated. Drought was simulated in the screenhouse by restricted watering at 50% tillering. Vegetative stage data were taken on leaf rolling, leaf drying, tiller number, plant height flag leaf length and width. Reproductive stage data were taken on days to flowering, grain filling and yield per plant. Molecular analysis to identify known quantitative trait loci (QTL) for drought tolerance in F₂s was performed using 27 SSR markers. Seven markers have been found polymorphic on four parents. Results on general and specific combining ability of the tolerance genes are expected from comparative studies on parents, and F₂ populations. Candidate QTLs are expected from a screening of one F₂ population.

Key words: Combining ability, QTLs, SSR markers

Résumé

La multiplication pour la tolérance sous la sécheresse exige une compréhension claire du mode d'action de gène pour ce trait caractéristique. Pour comprendre l'action des gènes de tolérance sous la sécheresse dans des variétés de riz de montagne en Ouganda, une étude a été effectuée pour établir la capacité de combinaison générale et spécifique de nouvelles lignées de riz acquises dans le programme de multiplication aussi bien que valider les positions des traits quantitatifs QTLs des études précédentes dans notre propre population et notre propre environnement. Les populations F₂ de cinq parents susceptibles et cinq parents résistants ont été produites. La sécheresse a été simulée dans le milieu d'observation par l'arrosage restreint au tallage 50%. Des données de l'étape

végétative ont été prises sur l'enroulement des feuilles, le séchage des feuilles, le nombre des talles la longueur et la largeur des feuilles. Des données sur le stade de la reproduction ont été prises chaque jour à la fleuraison, au remplissage de grain et au rendement par plante. L'analyse moléculaire pour identifier la localisation de caractère quantitatif connu (QTL) pour la tolérance sous la sécheresse dans F_2 s a été exécutée en utilisant 27 marqueurs SSR. Sept marqueurs ont été trouvés polymorphes sur quatre parents. Les résultats généraux et spécifiques sur la capacité de combinaison des gènes de tolérance sont attendus à partir d'études comparatives sur les parents et les populations F_2 . Les QTL candidats sont attendus à partir d'un dépistage d'une population F_2 .

Mots clés: Capacité de combinaison, QTLs, Marqueurs SSR

Background

Rice (*Oryza sativa* L.) is a major food crop for the world's majority. It is mainly produced in Asia with over 90% of the total production. The total global land area covered by rice is 156 Mha with 7.62 Mha in Africa and 105,000 ha in Uganda. The world consumption of rice is increasing on average by 1% per annum yet productivity is only going up by 0.5% (NARO, 2008). In Uganda rice is grown by farmers in almost all regions, mainly for cash. Since the launching of upland rice, rice production in Uganda has grown from 4000 farmers in 2004 to over 35000 in 2007. However, the production of rice is constrained by pests and diseases, low soil fertility, poor agronomic practices and drought.

Drought is one of the main constraints in upland rice production with an annual loss of 18 Mt. Uganda has a very young rice programme, and one of the priorities of this programme is developing drought resistant varieties. This requires drought resistance parental lines that can be used in the breeding. These lines will, however need to be characterized for combining ability if they are to be employed. The heritability of these lines for the various agronomic traits also needs to be determined. Marker assisted selection (MAS) has become a popular tool in breeding especially for difficult traits such as drought tolerance. MAS to be employed in the programme, a number of QTLs for drought tolerance have to be validated. These QTLs together with their markers will aid in the breeding process for drought tolerance.

Literature Summary

Drought tolerance is a trait controlled by many genes having different effects. The complexity of drought is explained by the

fact that its tolerance involves an interaction between yield potential and drought tolerance genes (Bernier *et al.*, 2008). Various scholars have studied the number and action of genes responsible for drought tolerance. Several QTLs associated with various traits in rice such as simple root traits (Price and Tomos, 1997), rate of leaf rolling and stomatal closure (Price *et al.*, 1997), leaf rolling and leaf drying and for water content (Price *et al.*, 2002) have been identified. Evidence has been provided that the regions of chromosome 5, 7, 9 and 11 that affect root growth also affect performance under drought. QTLs that increase relative water content and reduce leaf rolling at WARDA were detected on chromosome 5, but also in the same place a QTL in which alleles increased leaf rolling at IRR were revealed (Price *et al.*, 2002). QTLs for drought cell membrane stability have been identified on chromosome 3 using RZ403 markers and on chromosome 9 using RZ698-RM219 markers. Also grain yield-drought QTLs were identified on chromosome 12 using AFLP markers. Up to 299 drought resistant genes have been identified using cDNA microarray (Shinozaki and Yamaguchi, 2005).

Combining ability is the capacity of the parent to produce superior progenies when crossed with another parent (Won *et al.*, 2000). Its analysis gives clues to the gene action, desirable parents and important yield traits (Can *et al.*, 1997). Gravois and McNew (1993) reported that general combining ability (GCA) is more important in rice than specific combining ability (SCA) in the US southern long grain. Studies by Xu and Shen (1991) show that additive effects are more important than dominance effects in determining rice tiller number. Won and Yoshida (2000) in their study on combining ability in rice lines selected for direct seeding in flooded fields indicated the importance of additive effects of the genes for the traits studied.

Study Description

The study was carried out at National Agricultural Crops Resources Research Institute (NaCCRI), Namulonge, central Uganda. Five (5) female and 5 male parents with known drought susceptibility and resistance levels were used in the experiment. Crosses were made in the North Carolina design II to generate F₁s. The F₁ plants were selfed by bagging the panicles before pollen shed to produce pure F₂ seed. The generated F₂ seed was planted in an alpha lattice design with two replications to generate F₂ population. In order to assess the reaction of the plants to drought, irrigation was restricted at 50% tillering of all the plants. Data were taken on leaf rolling

and drying, tiller number, plant height, panicle height, and flag leaf length and width. The soil moisture content was taken using the ECHO soil moisture tester (Decagon Devices, Inc Pullman, Washington USA). The F₂ populations and the parents were assessed for drought tolerance following the standard procedure of IRRI. Data obtained were analyzed using GENSTAT statistical packages. Separation of means using LSD was performed. So far, seven SSR markers for drought tolerance QTL have been found to be polymorphic among four parents. Meanwhile, data is being analysed to determine SCA among the studied parents.

Research Application

The number of tillers, leaf drying and panicle length between parents was significant ($P \leq 0.001$). The growth increase during the stress period was also significantly influenced by parents. From the 10 parental lines on which the study is conducted, WAB 881-10-37-18-3-P1-HB showed the highest level of tolerance to drought, while CT 16333 (1)-CA-15-M the most susceptible.

Recommendation

The line WAB 881-10-37-18-3-P1-HB can be used in further breeding studies for drought tolerance because as in previous studies, it has maintained the same tolerance levels in this study. The F₂ population for molecular screening for QTL has been selected from these two lines.

Acknowledgement

I thank AGRA, RUFORUM, Dr. Okori, Dr. Baguma, Dr. Lamo, Dr. Edema and Dr. Gibson for their contribution to this work. Mrs. Gibson and fellow students are highly appreciated for the moral support.

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