Advances in Crop Science and Technology

Musyoki et al., Adv Crop Sci Tech 2015, 3:5
http://dx.doi.org/10.4172/2329-8863.1000193

Research Article

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Genetic Diversity Studies on Selected Rice (*Oryza Sativa*) Genotypes Based on Amylose Content and Gelatinization Temperature

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Abstract

Oryza sativa

of 0.4697. Pair-wise genetic dissimilarity coefficients ranged from 0.9003 to 0.2251 with an average of 0.5627. *R 2793* *BS 17, Supa* *IR 64, R 2793* *ITA 310, Saro 5* *ITA 310, Saro 5* *R 2794* *Wahiwahi* *BW 196, IR 64* *BW 196.*

Keywords: *Oryza sativa; Oryza glaberrima;* Heterozygosity; Germplasm; Genotypes

Introduction

Rice (*Oryza spices)* is a monocotyledonous plant belonging to the family Granineae and subfamily Oryzoidea. It is cultivated under diverse eco-geographical conditions in various tropical and subtropical countries [1]. Due to its importance as a food crop, rice is being planted on approximately 11% of the Earth's cultivated land area [2]. It is the grain with the third highest production globally after sugarcane and maize (FAOSTAT, 2012). *Oryza sativa* and *Oryza glaberrima* are the only two cultivated species of rice while the other species are wild. *Oryza sativa* is commonly grown in Asia, North and South America, Europe and Africa. *Oryza glaberrima* is highly grown in West African but due to higher yields of *O.sativa* and *O. glaberrima-sativa* varieties; it is being replaced in most parts of Africa [3].

There are two classes of rice based on starch content, that is, waxy and non waxy rice. Glutinous or waxy rice in which endosperm starch lacks or has very little amylose content consists mainly of amylopectin starch [4]. The ratio of amylose to amylopectin has a major effect on the physical properties of starch. When cooked, the semi-crystalline structure of rice starch is disrupted thus transforming the starch into a softer, edible, and gel-like material [5]. Generally, the amylose content of milled rice is classified into five classes: waxy (0-2%), very low amylose (3-9%), low amylose (10-19%), intermediate amylose (20-24%) and high amylose (above 24%) [6]. The cooking temperature at which water is absorbed and the endosperm starch granule swell irreversibly with subsequent loss of crystalline structure is referred to as gelatinization temperature (GT) [7].Gelatinization temperature is an important component of rice cooking quality. Rice grain with low gelatinization temperature takes shorter cooking times leading to significant potential savings in fuel costs [8]. Three classes of GT are recognized in rice breeding programs: high (>74°C), intermediate (70-74°C), and low (<70°C) [9,10]. Besides waxy and alk genes that controls amylose content and gelatinization temperature in rice, there are other several QTLs within the rice genome that are linked to these two genes.

There is a wide range of rice varieties grown both in Kenya and Tanzania. These rice cultivars are either local landraces or improved varieties and they express different levels of amylose and amylopectin that influences amylose content and gelatinization temperature in rice respectively. Since these two traits are key determinant in cooking and eating qualities of rice, unscrupulous traders often blend rice grains which have good cooking and eating quality traits with grains which have poor cooking and eating quality traits based on amylose content and gelatinization temperature to make more profit from their trade. This causes a negative impact on rice trade and consumption. Accurate evaluation of these two traits is difficult and has hindered development of better varieties with good eating and cooking qualities by rice breeders both in Kenya and Tanzania. The various physicochemical methods commonly used to determine amylose content and gelatinization temperature in rice are often inaccurate and time consuming. However, genetic diversity analysis on these selected rice genotypes from Kenya and Tanzania based on amylose content and gelatinization temperature using microsatellite markers has not yet been studied.

Molecular markers can have a number of applications in agriculture, and their application in rice improvement has been reviewed [11]. Simple Sequence Repeat (SSR) markers are easily available for any

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Received **Accepted** **Published**

Citation: *Oryza Sativa L*

could be due to different group of rice genotypes used. The high level of similarity recorded by this author could be due to the intra specific variation in the germplasm used.

On comparing Kenyan and Tanzanian rice genotypes, it was found that Kenyan genotypes were closely related compared to Tanzanian genotypes, with a mean genetic dissimilarity coefficient of 0.3939 against that of 0.5064 for the Tanzanian genotypes. The genetic closeness of Kenyan rice varieties could be as a result of high intra specific variation, evolution from a common ancestry and introgression of similar traits during the time of genetic improvement. On the other hand, the relatively high genetic dissimilarity witnessed among the Tanzanian varieties could be as a result of having diverse ancestral origins, high gene flow caused by cross pollination among these varieties and chromosomal mutations in their genome.

Clustering of these genotypes together, for example, *BW 196* and *BS 370* could be as a result of sharing common ancestry or similar genes were introgressed into their genome during their breeding. Surprisingly, group I genotypes which were all improved varieties were genetically distinct when compared with the *IR 64* that was used as a check variety. Therefore, based on these results, it is evident that the six improved varieties studied have different levels of amylose content and gelatinization temperature. Thus further breeding on these genotypes should be carried out so as to introgress favorable genes conferring intermediate amylose content and gelatinization temperature in their genome so as to make them highly competitive in rice market.

Supa, a local landrace from Tanzania and *IR 54*, an improved cultivar with low amylose content from Philippine clustered together. Based on these results, these two genotypes share common alleles for *waxy* gene responsible for high amylose content and *alk* alleles associated with low gelatinization temperature. Therefore, *Supa* genotype does not have good cooking and eating quality characteristics. Genes expressing good quality traits should be introgressed into genome of this genotype. *Kilombero, Wahiwahi* and *IR 64* were clustered together. Factors such as sharing of common ancestry and gene flow caused by interspecific gene transfer could be reason behind clustering together. Clustering of *Kilombero* and *Wahiwahi* together with *IR 64* is an indication that these two Tanzanian local landraces have good cooking and eating qualities like those of *IR 64*.

Principle coordinate analysis is a method that visualizes similar and dissimilar data. It assigns similar or dissimilar matrix a location in a three dimensional space. It was chosen to complement the UPGMA cluster analysis by visualizing the relationship between the sample genotypes using genetic distances. The Kenyan improved genotypes were clearly separated from Tanzanian local landraces. Genotypes that grouped together were interpreted to have similar characteristics (closely related) while those apart interpreted to be different or distantly related.

Analysis of molecular variance revealed percentage variation between and among the Kenyan and Tanzanian rice genotypes used in this study. The high genetic variation within the sample populations could be due to increased gene flow or mutations of a number of repeats of a given genotype for a given SSR. In addition, natural selection mechanism could be another source of this high genetic variation within the rice genotypes studied. On the other hand, the relatively low genetic variation among these rice genotypes could be attributed by sharing of same SSR profiles among themselves. The low genetic variation among these genotypes could explain the probability of sharing a common ancestry despite the fact that they are grown in different countries. Similar huge differences in percentage variation between and among a group of rice genotypes studied using SSR markers.

Conclusion

The present study provided an overview of genetic diversity based on amylose content and gelatinization temperature among the rice genotypes studied. The UPGMA cluster analysis showed that all 13 rice genotypes could be easily distinguished based on the information generated by the 8 polymorphic SSR markers. The PIC values revealed that RM 141, RM 225, and RM 434 might be the best markers for identification and diversity estimation of rice genotypes. The genetic distance revealed that the Kenyan genotypes had relatively narrow genetic base compared to the Tanzanian genotypes. Therefore, it is highly important not only to conserve these genotypes, but also to reveal their gene pool and unlock other valuable genes for breeding purposes.

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