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## Abstract

Determining the extent and degree of germ plasm diversity and genetic relationships among breeding materials is an important aid in crop improvement research strategies with an understanding that genetic variability is the base for crop improvement providing an opportunity for plant breeders to develop new and improved cultivars with desirable

**Keywords:** Cluster analysis; Upland rice genotype; Variability

## Introduction

Rice (*Oryza sativa* L.,  $2n = 2x = 24$ ) is the staple food for more than half of the world's population and is increasingly important in Ethiopia for ensuring food security of the country though the crop is relatively new to the country, with its introduction in the 1970s [1,2]. Currently, it is estimated that the country is endowed with about 30 million ha of cultivated land, of which 5.6 million hectare is categorized as highly suitable for irrigated rice production but the current rice production area is only 85,288.87 hectares (CSA, 2021) [3]. However, the national rice breeding and genetics research program is introducing and evaluating different rice germ plasms targeting for their environmental adaptability and agronomic performance (high grain yield, tolerant for biotic and abiotic stresses and for other quality traits) aiming at enhancing the rice national productivity with increasing its annual production and area coverage. Determining the extent and degree of germ plasm diversity and genetic relationships among breeding materials is a vital aid in crop improvement strategies with an understanding that genetic variability is the base for crop improvement providing the opportunity for plant breeders to develop new and improved cultivars with desirable characteristics and it is a key to reliable and sustainable production of the food crops through breeding [4]. It has been also confirmed that measuring the available diversity of crops is important for effective evaluation and utilization of germ plasms to explore their variability so as to identify desirable agronomic attributes [5]. Bringing improvements over the existing crop varieties is a continuous process in plant breeding there identifying diverse parents having high genetic variability for combining desirable characters and similarly the effectiveness of any rice improvement program depends on the utilization of different germ plasm from around the world

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program of the country collected and introduced a set of rice germ plasm from different external sources with the objective of characterizing and evaluating their environmental adaptability in lined with their genetic diversity and agronomic potential so as to identifying the promising rice genotypes for further rice improvement research program. With the same trend, 100 upland rice genotypes have been introduced to be involved in the rice germ plasm enhancement research sub component of the national rice research program of the country for being evaluated under the observation nursery trial at Pawe agricultural research center to assess their environmental adaptability and agronomic performances. In addition, this activity was also designed to determine the extent and pattern of the genetic and phenotypic variability of the upland rice genotypes with using cluster analysis bringing them into similarity groups based on important agronomic traits.

## Materials and Methods

### Description of the Experimental site

The trial was implemented at Pawe agricultural research center for one year during 2019/20 main cropping season under rain-fed condition (Figure 1).

The experimental area is located in the north western regions of Ethiopia at about 575km north west of Addis Ababa at a latitude of 11°19'N and longitude of 36°24'E and at an altitude of 1120mas which is characterized by hot to warm moist conditions with mean minimum and maximum temperature of 16 and 32, respectively and has an

maturing (96-110 days), early maturing (111-125 days), medium maturing (126-140 days) and late maturing (141 days and above). Thus, 16 of the tested 97 upland rice genotypes could be classified as an early maturing genotype. 73 of the upland rice genotypes with days to maturity ranging from 126 to 140 days to 85% were identified as a medium maturing and 8 of the genotypes found to be late maturing with a number of 85% days to maturity ranging from 143 to 158 numbers of days to 85% maturity.

While considering their plant height (PH), the genotypes obtained values ranging from 55.80 to 114.40cm with an average panicle length (PL) of 20.96cm. For number of filled grain per a panicle (NFG), the average value of 105 grains (ranged from 67 to 172 grains) was obtained from which 29 upland rice genotypes scored more than the average value of NFG scored by the standard check called 'Adet-1' which scored a better value of 113 NFG ensuring the higher probability of getting the upland rice genotypes with a better expected grain yield. It was also found that almost 61% of the upland rice genotypes had in-determinant number of unfilled grains per a panicle which was less than or equal to the average value of NUG (6 grains per a panicle). These two results for number of filled and unfilled grains per a panicle indicated that these genotypes had a higher predicted yield potential when compared to the best performing genotypes among the checks directing that they will have a greater chance to be subjected to further rice improvement program focusing on grain yield as the trait of interest.

The 1000 seed weight (TSW) of the tested upland rice genotypes were ranged from 18.38gm to 36.10gm with an average value of 26.13gm where 15 of the genotypes scored a better TSW when compared to a standard check called 'Nerica-4' with the higher TSW value of 30.27gm. A high TSW will increase germination percentage, seedling emergence, tillering efficiency, plant population density and grain yield [13]. Therefore, the higher TSW for 15 upland rice genotypes is an indication for the presence of most promising rice genotypes with a better genetic advantage over the best performing standard checks for their population stand, seedling vigor, tillering efficiency and yield potential.

#### Clustering the upland rice genotypes using eight quantitative traits

From the clustering result, the upland rice genotypes were grouped into five main clusters approving that there was a genetic variation among the tested rice genotypes with 86.39% of between cluster variance decomposition and 13.61% of a variance decomposition within each cluster (cluster) (Table 2). Among the reported clusters, Cluster II contained the highest number of genotypes (45 genotypes) and cluster I contained the second large number of genotypes (36

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