

Unlock the genetic potential of rice from Africa for sustainable agriculture through the Integrated Genotyping Service and Support (IGSS)



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Project summary

Numerous rice accessions have been collected in different African countries and conserved in the AfricaRice genebank. These include the two cultivated species - *Oryza sativa* and *Oryza glaberrima* – with the latter known to possess high phenotypic diversity and to be well adapted to harsh African environments. *O. glaberrima* has also immense genetic value and represent a wide range of genetic stocks for rice improvement. However, to date, less than 1% of *O. glaberrima* germplasm has been successfully used for varietal improvement, as it was the case for the NERICA (New Rice for Africa) varieties. Germplasm characterization for better management and utilization remains central in achieving better exploitation and use in rice improvement. Advances in genotyping technology, such as genotyping by sequencing (GBS), are making genomic information more attractive for precision-breeding. Subsequently, more specific SNP markers can be generated for African cultivated rice species, for dedicated purposes, such as, diversity and population structure studies, gene/QTL mapping, seed purity assessment, and association studies, etc.

This project seeks to develop high density genetic data for 379 rice varieties, among the mostly used as parental lines in the development of breeding and mapping populations by breeders and geneticists of the African rice community. Information generated will be important (i) for making critical germplasm conservation management decisions for Africa; and (ii) increasing the potential value and utilization of adapted germplasm in breeding programs. Besides, selected accessions are being screened for multiple traits (grain quality, grain yield, drought, heat, cold and salt tolerance, phosphorus deficiency tolerance, weed suppressing ability, etc.) relevant to rice production systems in Africa and useful genetic associations can be also identified.

Expected Outputs

- ❖ Population pattern of the collection of 379 genotypes established (Fig. 1)
- ❖ A database with genomic and phenotypic data on a collection of 379 genotypes comprising most used varieties/breeding lines by AfricaRice scientists for rice improvement established.
- ❖ A panel of 43,088 SNPs identified for use in rice improvement
- ❖ At least 2,000 markers for gene discovery and breeding identified
- ❖ Species specific SNPs and varietal fingerprints available
- ❖ Alleles related to several traits of agronomic importance identified

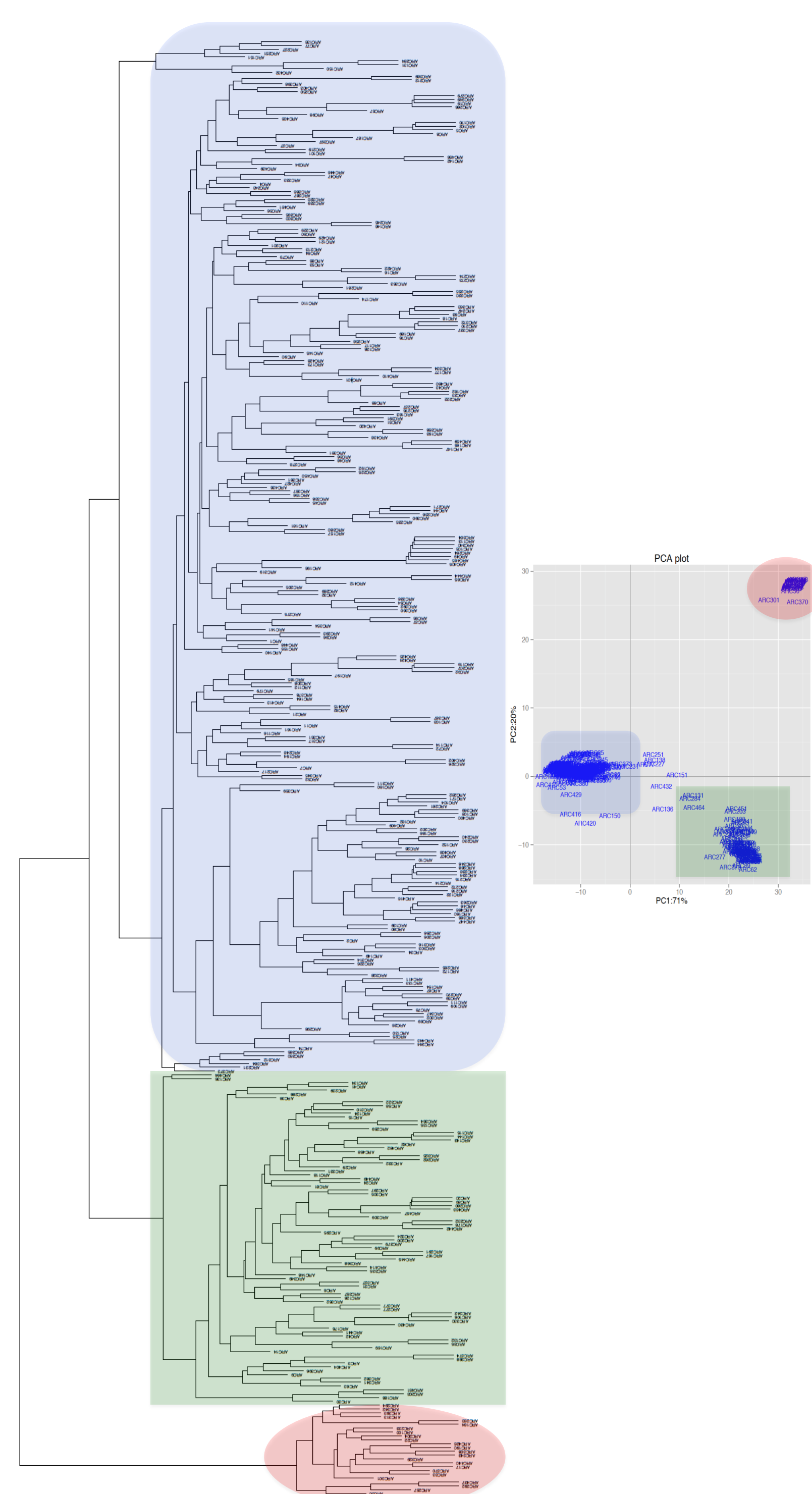


Fig. 1: Population structure from key germplasms widely used for rice improvement at AfricaRice as revealed by a panel of 43K SNPs

Outcomes

- ❖ Key accessions conserved in the AfricaRice genebank with molecular information available, promoted and used in rice breeding programs
- ❖ Best accessions/landraces and markers information associated to these accessions available and used for additional pre-breeding (gene discovery, product profile development) and breeding
- ❖ Marker panels for key traits of interest available and used for genomic assisted breeding

Partnerships



Way forward

- Identification of broader SNP panel or assays for varietal identification and seed purity
- Extensive and accurate phenotyping of the genotyped accessions set for several traits (yield and yield component, disease...) of importance in African agriculture for genome wide association study

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