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Farmers’ and academia’s views”

## Molecular characterisation of rice collection using genomic tools and development of the AfricaRice *Oryza sativa* and *O. glaberrima* core collections

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### Abstract

AfricaRice genebank holds 21,724 registered rice samples, which includes the two cultivated species (*Oryza sativa* and *O. glaberrima*) and five African wild species (*O. longistaminata*, *O. barthii*, *O. punctata*, *O. brachyantha* and *O. eichingeri*). Approximately 88% of the registered rice samples at the AfricaRice genebank originated within Africa, of which the African rice (*O. glaberrima* Steud.) represents approximately 17% of the collection. The African rice accessions have adaptive or protective mechanisms for different abiotic and biotic stresses in the continent, but are generally characterised by a wide range of undesirable agronomic traits. Undertaking characterisation and evaluation of such a large number of accessions presents logistical challenges in addition to being resource intensive. AfricaRice genebank have developed core and mini core germplasm sets which comprise a smaller number of genetically diverse accessions that are primarily aimed at getting manageable number of samples that could be evaluated for multiple target traits of interest in multi-location trials. In AfricaRice, efforts to develop germplasm subsets started with the analysis of genetic variation and population structure of the entire *O. glaberrima* accessions using 9,990 SNPs polymorphic SNPs. Using the maximum length sub-tree (MLST) method we have created a mini-core subset of 350 accessions that captured 98% of the SNP polymorphism with most of the genetic variation observed within the studied accessions, and represented the different maturity groups (early, intermediate, late), 19 countries, and eight rice growing ecologies in Africa. The *O. glaberrima* mini core, are grouped based on their tolerances/resistances to drought, iron toxicity, submergence, stagnant, flooding, rice yellow mottle virus, African gall midge, bacterial blight or their anaerobic germination. The process of developing core collections was extended to the *O. sativa* collection where 5,738 accessions were studied using 25,904 DArTseq based SNPs. Using MLST method, we identified a subset of 600 accessions to act as the AfricaRice *Sativa* rice core subset. These accessions captured more than 95% of the SNP polymorphisms in the entire collection. The assembled sub sets forms an important resource that will play a vital role in supporting pre breeding and rice improvement programme of the research communities in the world.

**Keywords:** African rice, AfricaRice, core collection, DArTseq, genebank, *Oryza glaberrima*, *Oryza sativa*, rice, SNP

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