

ABSTRACT

Africa contains a huge diversity of both cultivated and wild rice species. The region has eight species representing six of the ten known genome types. Genetic resources of these species are conserved in various global germplasm repositories but they remain under collected and hence underrepresented in germplasm collections. Moreover, they are under characterized and therefore grossly underutilized. The lack of in situ conservation programs further exposes them to possible genetic erosion or extinction. In order to obtain maximum benefits from these resources, it is imperative that they are collected, efficiently conserved and optimally utilized. High throughput molecular approaches such as genome sequencing could be employed to more precisely study their genetic diversity and value and thereby enhance their use in rice improvement. *Oryza sativa* was the first crop plant to have its reference genome sequence released marking a major milestone that opened numerous opportunities for functional characterization of the entire rice genome. Studies have however demonstrated that one reference genome sequence is not enough to fully explore the genetic variation in the *Oryza* genus, hence the need to have reference sequences for other species in the genus. An overview of the state of conservation and utilization of African *Oryza* is hereby presented. Progress in the release of reference genome sequences for these species is also highlighted.