Category	: International Rice Research Conference
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Pre-breeding
Keyword 2	: Germplasm Enhancement
Keyword 3	: Breeding Strategy
Title of Entry	: The genetic dissection of Oryza glaberrima from the AfricaRice genebank for amylose content
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Amylose content (AC) is one of the important quality traits that influence texture and taste of cooked rice, but the genetic control of AC in O. glaberrima still remains poorly understood. The AfricaRice and his partners evaluated amylose content (AC) of 1,020 O.glaberrima germplasm conserved at the AfricaRice genebank. That study reported high variation in AC that ranged from 15.1 to 29.6%, with an overall mean of 26.2%, which is higher than the values reported in O. sativa Nearly 25% of the O. glaberrima accessions had AC values greater than the highest value (28%) reported in indica and japonica. We conducted genome-wide association studies (GWAS) to map the genomic regions associated with AC in a panel of 386 O. glaberrima accessions that represented the phenotypic variation for amylose content. The panel was genotyped with 31,739 single nucleotide polymorphism (SNP) markers using DArTseq, of which 4,135 SNPs were polymorphic. Using a threshold of $p < 10-5$ and weighted mixed linear model, we identified 3 genomic regions that individually explained up to 12.1% of the phenotypic variation of AC in O. glaberrima. We tried to validate the significant GWAS hits using a biparental interspecific population derived from a cross between O. glaberrima and O. sativa, but the genomic regions identified in the two populations were different. . One of the points that we observed in the GWAS panel was a very narrow genetic variation among the O. glaberrima accessions. To identify the most genetically

diverse set of O. glaberrima collection for future use in breeding and gene discovery (including AC), we genotyped 2,179 O. glaberrima accessions conserved at the AfricaRice genebank and developed a mini-core set of 350 accessions that captured 97% of the molecular variation observed in the whole set. We are currently evaluating the mini-core set for diverse agronomic and quality traits, including AC. This presentation will provide highlights of the main results on amylose content and population structure that would serve as prerequisites for developing improved rice varieties for the resource poor farmers in Africa.

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