Entry No. 8RGS-0035	
Category	: 8th Rice Genetics Symposium
Select Theme	: High through-put technologies: Genotying, Phenotyping and Omics
Endorsement email	:
High through put technologies Genotying Phenotyping and Omics Keyword 1	: SNPs
High through put technologies Genotying Phenotyping and Omics Keyword 2	: Variants
High through put technologies Genotying Phenotyping and Omics Keyword 3	: Phenotype
Title of Entry	: Characterization and diversity analysis of heirloom rice varieties in five provinces of the Philippines
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Select only one type of presentation	: 3-5 minute flash talk
Abstract	: Heirloom rice varieties are on-farm conserved traditional varieties attached to the lives and cultures of the indigenous communities tending them. Unique grain quality traits and symbolic value related to heritage conservation and environmental preservation have contributed towards a premium valuation for heirloom rice and an increasing consumer demand for these varieties both in domestic and in international markets. However, the production side of the heirloom rice value chain faces several challenges in meeting market demand. Producers may not have adequate in-process quality control measures, leading to variety mixing in packages and ultimately to the unreliable quality of heirloom rice despite being sold at premium prices. In this study, we aim to establish baseline genetic and phenotypic characterization on the diversity of the traditional heirloom rice varieties from four provinces in the Cordillera Administrative Region (CAR) and in the province of Cotabato. The information generated will contribute to product profiles for varietal identification and for quality control. Eventually, such information will contribute to the mitigation of immediate reputational risk associated with variety mixing of heirloom rice. A total of 119 variants were identified based on the characterization of paddy grain and of panicles of 78 traditional rice varieties collected in seven municipalities in CAR and in three municipalities in Cotabato, reflecting the diversity of heirloom rice samples that had been collected. The variants were classified into four different groups based on genotypic diversity on 4,606 SNPs. On the other hand, the variants could be classified into two major groups: heirloom rice varieties from CAR belong to either tropical japonica or (upland) indica

rice subgroups, while traditional varieties from Cotabato belong to tropical japonica based on both genotype and phenotype. Some commonly named varieties being planted by different farmers have different traits, and some varieties coming from different sites have common characteristics. Other findings show several farmers planting mixed varieties. Genetic and phenotypic diversity analyses show the uniqueness and diversity of these heirloom rice varieties among the established rice clusters.

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