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Assessment of genetic diversity in Peruvian amaranth (*Amaranthus caudatus* and *A. hybridus*) germplasm using single nucleotide polymorphism markers [Abstract]

Amaranth (*Amaranthus caudatus* L.) is an important seed crop in the Andes. It has excellent nutritional value and ample capacity for growth under drought, heat, and soil nutrient deficiency. The objective of this study was to characterize and quantify genetic diversity among a series of 178 mostly Peruvian amaranth individuals genotyped from among 48 accessions using 96 biallelic single nucleotide polymorphism (SNP) markers in KASPar assays on a 96.96 Fluidigm EP1 platform. The 178 seed genotypes included the predominant white-opaque (waxy), white-vitreous (nonwaxy), black, and brown types, all from within the Centro de Investigacion de Cultivos Andinos-Universidad Nacional de San Antonio Abad del Cusco collection. The samples separated into two groups based on the seed color parameter (black, brown, and white-vitreous versus white-opaque) with STRUCTURE analysis but did not form distinct genotypic groups based on geographic origin. When analyzed as seed-color subgroups—black vs. brown vs. white-vitreous vs. white-opaque—83.46% of the genetic variation was explained by genetic differences within subgroup. The highest average observed heterozygosity (H_o) within color-based subgroups was 0.2612 in the vitreous-seeded subgroup, and within-group expected heterozygosity (H_e) was highest in the brown-seeded subgroup (0.398). Cluster analysis and principal component analysis partitioned the amaranth accessions into two clusters with four distinct subclusters. Analyses also revealed evidence for selection of nonwaxy, vitreous-seeded amaranth in the Andes.