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## GENOME WIDE ASSOCIATION STUDY OF AGRONOMIC AND SEED TRAITS IN A WORLD COLLECTION OF PROSO MILLET (PANICUM MILIACEUM L.)

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Global food security is threatened by the climate crisis, and crop diversification is recognized as a sustainable adaptation strategy to cope with its impacts. Proso millet (*Panicum milaceum* L) is a neglected and underutilized crop which holds potential for diversification and adaptation to different environmental conditions. Here, we investigated the genomic diversity in a world collection of proso millet consisting of 88 varieties and landraces using single nucleotide polymorphisms (SNPs) developed through ddRAD approach. We characterized the seed diversity in the collection and its field performance to conduct a genome-wide association study (GWAS), the first using SNP markers anchored to the proso millet genome. Genotyping provided approximately 5.14 M reads per sample, from which we derived 2,412 high-quality SNPs distributed across the genome. SNP diversity separated accessions originating in Eastern Asia, Western Europe, and Americas from accessions sampled in Western Asia, Southern Asia, and Africa, shedding light on the origin of the crop. The collection was highly diverse for seed traits: seed color varied from white to dark brown, and seed length spanned from 2.61 to 3.41 mm. Plant height ranged from 30cm to 100 cm and number of leaves varied from 4 to 9, showing a wide variation in the morphology of the crop. The GWAS provided high-confidence quantitative trait nucleotides (QTN) for seed perimeter, seed width, seed length, seed shape and color. The collection identified QTNs associated with plant height and leaf number, indicating the presence of desirable alleles and genotypes with potential for application in proso improvement through marker-assisted selection.