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GBS characterization of watermelon germplasm and breeding against fungal pathogens

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Watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) is the most important cucurbit in terms of world production. Genomic tools and genetic resources for an efficient genetic breeding are of great importance in this crop, especially to develop cultivars resistant to pathogens and adapted to different growing conditions. Fungal diseases, such as powdery mildew, *Fusarium* wilt, *Monosporascus* root rot, and charcoal root, caused by *Macrophomina phaseolina,* cause important losses in this crop. The screening of large germplasm collections, searching for wild types or landraces bearing resistant alleles is the first step in genetic breeding programs. In the framework of the project CONMESAN (AGL2017–85563-C2–1, 2), the molecular characterization of 54 Spanish *C. lanatus* accessions from two Genebanks (BGHZ and COMAV) has been performed, using the genotyping-by-sequencing (GBS) strategy, also including some international references and genotypes belonging to the related species *C. amarus* and *C. colocynthis.* More than 12,000 SNPs were identified after trimming, cleaning raw reads, and mapping them to Charleston Grey genome assembly v.2. Principal Coordinate and Cluster Analyses performed, including GBS data of 57 USDA-NPGS accessions from Spain, showed that our germplasm presents new alleles regarding the Spanish USDA collection, being an interesting source for breeding. Spanish accessions were compared with 243 USDA accessions selected based on the GBS-based clustering to represent the variability of these three *Citrullus* species, and including most of the accessions previously reported with resistances to highlight the potential value of the collection presented. The analyzed Spanish collection is being phenotyped for resistance to fungi.

Key words: diversity, GBS, *Citrullus*, biotic stress

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