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## Genetic structure of sweet cherry with 6K SNP array v1

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### **Abstract:**

A set of 45 sweet cherry (*Prunus avium*) varieties which includes ancestors of modern varieties, modern breeding cultivars and local germplasm was genotyped and evaluated with the 6K SNP chip array of Illumina by an Infinium<sup>®</sup> assay. Genotyping filtering revealed that from 5696 SNPs available in the 6K array, 431 (7.5%) were not scored, 3368 (59%) were monomorphic and 1897 (33%) were polymorphic and informative (MAF>0,1). From these up to 1.5% failed Hardy-Weinberg equilibrium ( $p<0.001$ ). The SNP dataset was used to study the genetic structure of the sample. Cluster analysis identified clear substructure within the dataset by differencing 3 major groups. Modern cultivars and breeding founders grouped together in a single cluster suggesting a common Western European Origin (WEO). Local varieties from Spain were separated in two clusters, one from Western Spain (WS) and another from Eastern Spain (ES). Preliminary studies pinpoint to the existence of a unique genomic pool in the Spanish sweet cherry germplasm, evidencing its potential for breeding programs.

**Keywords:** *Prunus avium*