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UNRAVELING THE GENETIC DIVERSITY OF A GLOBAL COLLECTION OF HAZELNUT (CORYLUS AVELLANA L.) TO IMPROVE SENSORY AND AGRONOMIC TRAITS

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Hazelnut (*Corylus* spp.) has a prime importance in the confectionery industry for production of high-value products. Its success depends on agronomic characteristics including production traits and on its unique sensory profile. Cultivars show a large variability in their phenotypical traits which is often associated to differences in the cultivars' genetic background as quality traits are highly heritable. Hazelnut recently entered the genomic revolution, having the genome of the reference line Tombul fully sequenced since 2019. Next-generation sequencing (NGS) technologies allow identifying single nucleotide polymorphisms (SNPs) and offer greater specificity than other DNA markers used in the past to investigate hazelnut diversity.

Our project aims at unraveling the genetic diversity of a world collection of hazelnut cultivars and at identifying the genetic basis of agronomic and quality traits in *Corylus avellana* L. We also aim at developing a DNA barcoding tool for varietal identification, based on a minimal number of genetic markers.

We collected and sequenced a set of 233 world hazelunt samples with a double-digestion RAD sequencing approach to describe the relatedness existing across individuals. We also characterized kernel traits for each

individual in the collection using an imaging platform and automated seed anallysis. MinimalMarker was used to determine the smallest necessary number of markers needed to accurately discriminate varieties, and neighbor joining trees and PCAs were produced to get first insights into the influence of sample origin and growth location on genetic diversity and clustering of varieties.

Of the 178K SNPs that have been found among the sequenced samples, a preliminary set of 23 SNP markers allowed to discriminate known varieties and to identify so far unknown varieties clustering together with known ones in a neighbor joining tree. It was shown that sample clustering is altered both by the origin of the varieties as well as the location of the orchard in which they were grown. A genome-wide association study (GWAS) will be used to allow the identification of genomic loci responsible for agronomic traits of commercial interest (e.g. yield, fruit size, defects) and qualitative traits, including the amount of key aroma-active compounds.

GWAS results together with a marker set allowing to easily distinguish varieties will benefit the prediction of the usefulness of hazelnut samples for various purposes. The project will lay the basis for a genomic-driven exploitation of hazelnut germplasm, an enduring platform allowing future projects to push the boundaries of hazelnut breeding and research for industrial exploitation.