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Poster Abstract – F.06

EXPERIMENTAL STRATEGIES FOR THE GENETIC DISSECTION OF QUANTITATIVE TRAITS IN HAZELNUT (*CORYLUS AVELLANA*)

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Molecular markers useful for assisting selection for phenological and yield trait improvement are not available in hazelnut. Before undertaking DNA-based studies aimed at genetic dissection of quantitative traits to find useful molecular genetic markers, it is necessary to define the reference population and to infer as much as possible about the genetic basis of a trait by measuring the heritability of the quantitative phenotype in the reference population and the significance of the detected phenotypic differences. The choice of the reference population dictate the methods used for the genetic dissection of quantitative traits. In hazelnut, two types of reference population might be used: (1) a large collection of accessions from the cultivated gene pool, or (2) a progeny from a cross between parents showing a wide range of phenotypic variation.

The first type of population allow genetic dissection through association studies. However, this method is useful only when two allele types at each molecular genetic locus occur over the population range. Previous studies have shown that more than two SSR molecular marker alleles can be found in a large collection of hazelnut accessions, each with its own genetic background, which lower the efficiency of discovering molecular alleles underlying quantitative phenotypic traits.

The second type of population allow the use of the genetic dissection methods of allele-sharing and genetic analysis in the more homogeneous genetic background provided by the alleles of only two parents. We produced an half-sib progeny from intercropping “Tonda Gentile Romana” (TGR) and “Nocchione” (NOCC) accessions. Due to self-pollen incompatibility of the parental plants, the progeny was considered similar to a full-sib offspring and new homozygote phenotypes for recessive alleles shared between parents are expected among the 133 individuals of the progeny. One such novelty was the “evergrowing” phenotype which fail to cease growth and to enter dormancy under the dormancy-inducing (i.e. short days) conditions suitable for the wild-type phenotype. Extreme ends were also found for the distribution of phenotypic values related, among others, to the date of vegetative budbreak, date of first male bloom, kernel length, kernel width, seed weight, and eriophyid mite symptoms. Such divergences were significant over the two years of observation, and can greatly increase the ability to discover shared molecular alleles within each of the progeny group expressing the extreme phenotypic values. Test for differences in the shared alleles among groups is being carried out using bulk segregant analysis (BSA) at SSR loci. The SSR-allele that BSA indicated as differing between extreme phenotypic groups, will become markers of flanking quantitative trait loci important in determining phenological, yield and biotic stress resistance traits in hazelnut.