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HIGH-THROUGHPUT PHENOTYPING AND GENOTYPING TO UNDERPIN POPLAR RESISTANCE TO WOOLLY POPLAR APHID (PHLOEOMYZUS PASSERINII, L.).

BISELLI C.*, VIETTO L.**, PICCO F.**, ROSSO L.**, CATTIVELLI L.***,
NERVO G.**, FRICANO A.***

*) CREA-VE, Council for Agricultural Research and Economics – Viticulture
and Enology, viale Santa Margherita 80, 52100, Arezzo, Italy
**) CREA-FL, Council for Agricultural Research and Economics – Forestry and
Wood, strada Frassineto 35, 15033, Casale Monferrato (AL)
***) CREA-GB, Council for Agricultural Research and Economics – Genomics
and Bioinformatics, via San Protaso 302, 29017, Fiorenzuola d'Arda (PC),
Italy

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Poplar is one of the most economically important forest trees. It is used to produce plywood and paper and represents a source of lignocellulosic for biofuels and for phytoremediation.

Woolly Poplar Aphid (WPA; *Phloeomyzus passerinii*, L.) causes up to 10% reduction of potential production in Europe and USA, where most cultivated clones are susceptible. Only one major and two minor QTLs associated to WPA resistance have been mapped on poplar chromosomes 5, 16, and 19, respectively (Carletti et al., 2016). In the present work, to contrast WPA, the identification of new resistance QTLs/loci and genomic prediction are currently applied to expand the list of genetic sources for resistance and enable efficient breeding, respectively.

QTL identification is pursued using two F1 populations: DxN consisting of 179 individuals derived by the cross between D066 (resistant *P. deltoides*) × N074 (susceptible *P. nigra*), and NxN including 265 individuals obtained from the cross between N355 (resistant *P. nigra*) × N385 (susceptible *P. nigra*). Besides, a Genome Wide Association Scan (GWAS), aimed at detecting markers statistically associated to WPA resistance, is currently ongoing on a collection of 377 poplar genotypes including 289 *P. nigra* and 91 *P. deltoides* clones. Both F1 populations and the diversity panel have been

phenotyped for WPA response and genotyped using a newly developed SNP array that interrogates 13,409 loci.

A pseudo-testcross method is in progress to create high density genetic maps for DxN and NxN. 3,760 polymorphic SNPs were discovered for DxN (1,838 for D066 and 2,053 for N074), whereas 2,856 polymorphic SNPs were found for NxN (2,391 for N355 and 2,397 for N385). 19 linkage groups, corresponding to each of the 19 poplar chromosomes, have been obtained for all the parental clones of the two populations. The construction of the genetic maps is undergoing.

For the GWAS panel, higher resistance for *P. deltoides*, with respect to *P. nigra*, was recorded. Moreover, the *P. nigra* genotypes from Northern Italy were more susceptible to WPA in comparison to the *P. nigra* accessions from Central and Southern Italy. The analysis of population structure clearly separated *P. deltoides* and *P. nigra* sub-groups. A separated distribution of *P. nigra* clones according to their geographical origin was also observed. A preliminary analysis revealed significant marker-trait associations on different chromosomes: 1 SNP on chromosomes 2, 3, 6, 8, 9, and 11, respectively, and 2 SNPs on chromosome 13.

Using both segregating populations and the diversity panel, genome-enabled prediction based on GBLUP and reproducing kernel hilbert space along with Gaussian Kernel is currently ongoing to assess whether the predictive ability of these models might allow the efficient selection of new WPA resistant clones.

The present work will provide valuable tools for breeders to develop new breeding programs aimed at improving poplar resistance to WPA.