

TRANSLATING GENOMIC INFORMATION TO PRUNUS BREEDING PROGRAMS

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The release of the peach reference genome 10 years ago as well as the availability of genome sequences of the most important stone fruit species including sweet cherry, apricot and plum and related germplasm resources provided a tremendous advance in *Prunus* genomics. Germplasm-wide analysis using DNA-based information enabled the genetic dissection and discovery of causal loci for key traits indispensable for varietal improvement, such as those related to disease resistance, fruit quality and environmental adaptation. However, the practical integration of DNA-based genetic information into breeding programs (DNA-informed breeding) lags substantially behind the publications on QTL findings. Indeed, evidence about the actual transfer and adoption of molecular tools is still scarce. The cost-effectiveness of implementing DNA-informed breeding has been claimed in several published reports, mostly relying on the reduction of tree maintenance costs through early seedling selection. To evaluate the feasibility of translating genomics-derived information to *Prunus* breeding, we chose as case studies the most important diseases affecting peach (brown rot and bacterial spot) and apricot (sharka). In this work, we 1. overview recent scientific progress related to the genetic control of disease resistance; 2. highlight the bottlenecks, challenges and perspectives towards an effective implementation of DNA-informed breeding into breeding programs; 3. describe potential strategies for converting the scientific findings into breeder-friendly practical tools; and 4. report practical examples of implementation of DNA-informed breeding acquired in the ROSBREED (USA) and MASPEs (Italy) breeding programs.