RosBREED

Enabling marker-assisted breeding in Rosaceae

www.rosbreed.org

Cross Assist: Online software to identify efficient cross combinations, integrating rosaceous crop genomics, genetics, and breeding

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What is *Cross Assist*?

Cross Assist (www.rosaceae.org/breeders_toolbox/cross_assist) is a decision-support tool for breeders to plan crosses. This software was developed as a component of the RosBREED project's Breeding Information Management System (**Fig. 1**) to support U.S. breeders of crops in the Rosaceae family, and the underlying database is housed on the Genome Database for Rosaceae.

Cross Assist identifies efficient pairwise parental combinations from a breeder's available parent pool. This efficiency is determined by the number of seedlings needed to result in a target number of seedlings predicted to perform within specified trait thresholds. Efficient crosses achieve all trait thresholds with relatively few seedlings.
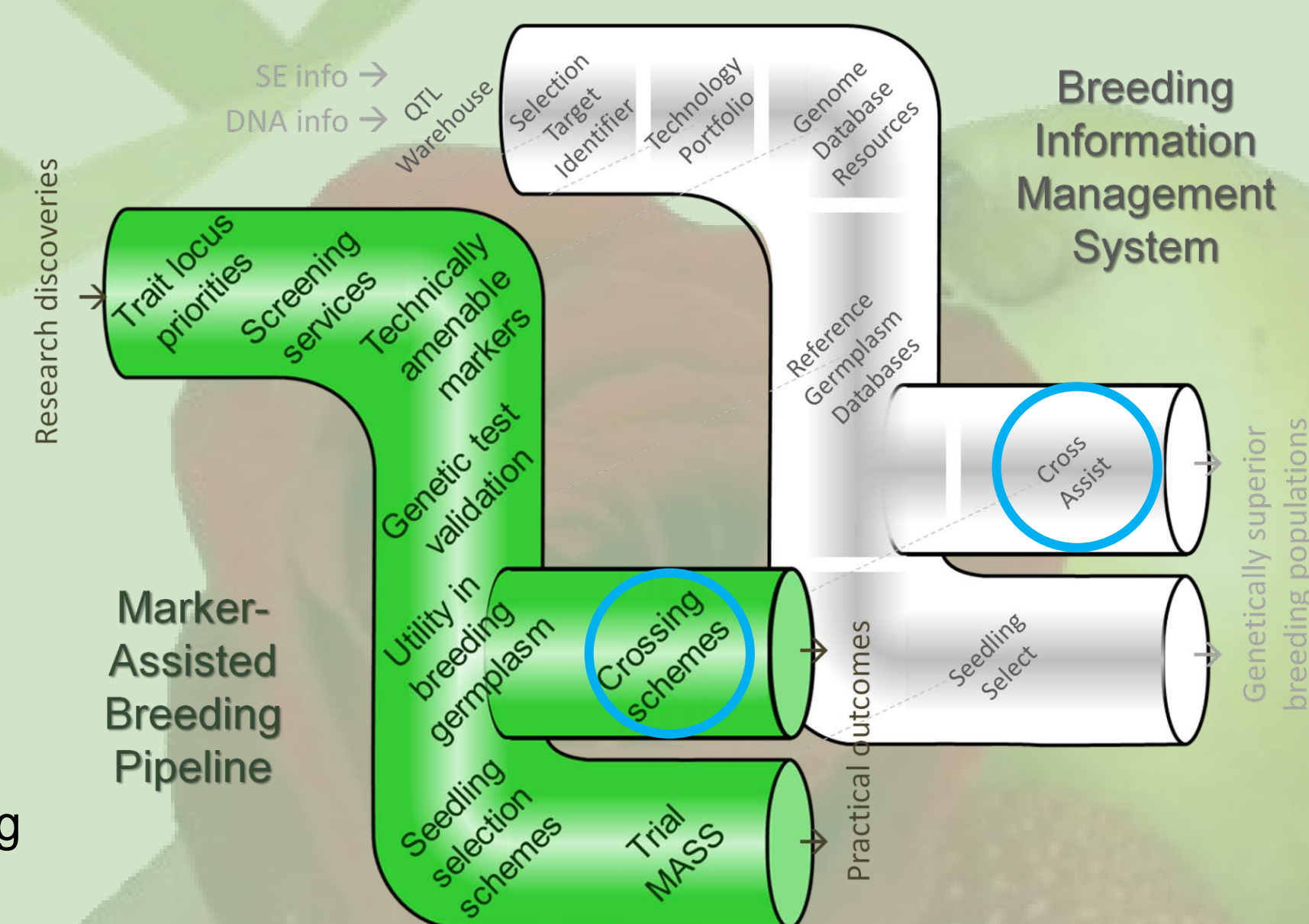

Fig. 1. The role of Cross Assist in the Breeding Information Management System →

How does *Cross Assist* work?

Cross Assist uses available information on the breeding value of each candidate parent to predict how well resulting seedlings would perform. Calculations can be made on three increasing **levels of breeding value information**:

- "*Phenotype*" uses only phenotypic information in the database.
- "*+Pedigree*" adds information provided by pedigree-estimated breeding value.
- "*+Ped+DNA*" further adds information provided by functional genotypes for Mendelian trait loci and QTLs. Where information on pedigree relationships and functional genotypes is not available, calculations revert to use of phenotypes only.

Input:
Crop, breeding group, target number of seedlings, and target trait thresholds.

Output:
A list of crosses, sorted initially by the estimated number of seedlings required. Further functionalities are being added, such as incorporation of linkage information, output addressing the trait loci involved and their available DNA tests, and integration with our sister software, *Seedling Select*.

How do you use *Cross Assist*?

Starting from the front page of *Cross Assist* (www.rosaceae.org/bt_cross_planning_tool/ca_front_page), four steps are taken to get the output with recommended crosses.

Step 1. Choose your crop, breeding group, and calculation method

Fig. 2. Front page of Cross Assist. In this example, we use "*+Ped+DNA*" method on the "APPLE CRS" dataset.

Step 2. Choose target number of seedlings and traits of interest

Fig. 3. The interface for choosing traits and trait levels.

Step 3. Review selection standards and click on "Estimate # Seedlings"

Fig. 4. The interface for reviewing input information.

Step 4. View recommended crosses

Fig. 5. The final output with a list of recommended crosses. By clicking on "fx" in each row, users can learn about calculation equations for that cross.

What's next for *Cross Assist*?

Cross Assist will be enhanced to use DNA information in breeding decisions, for peach, apple, strawberry, and cherry, as well as other crops as in the proposed RosBREED2 project. We will also integrate *Cross Assist* with other modules such as *Seedling Select* to enable breeders to identify cost-efficient and logistically feasible marker-assisted selection schemes that simultaneously consider crosses, resulting families, and specific seedlings toward achieving trait level targets.

The underlying database will be updated with newly collected phenotypic effects of functional alleles and haplotypes for characterized trait loci and haploblocks and functional genotypes of parents. Incorporating effects on trait loci of genetic background and non-genetic effects will also be explored.

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