

# Community Breeders' Page

**The Marker-Assisted Breeding Pipeline: Channeling socio-economic and DNA information into routine breeding operations**  
 By Cameron Peace, MAB Pipeline Team Leader

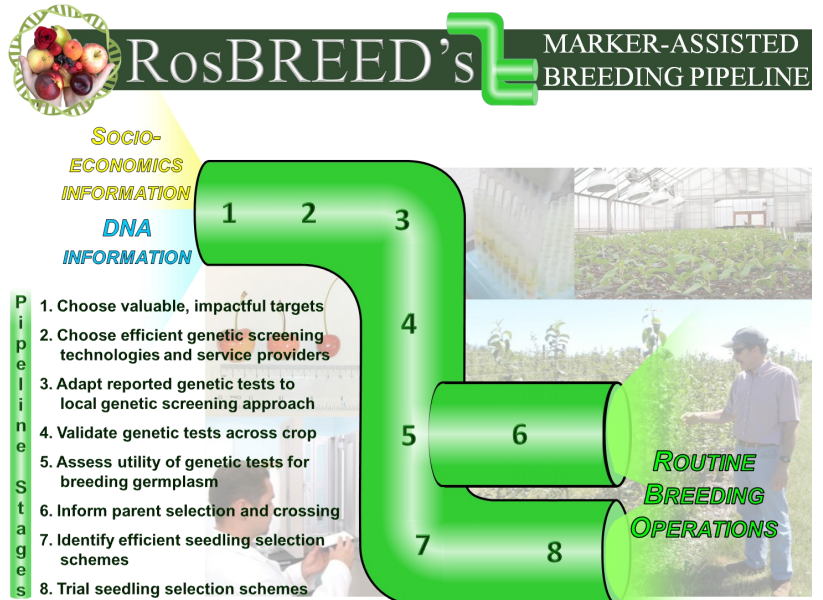
Marker-Assisted Breeding (MAB) is **decision-support** for breeders. Breeding involves many decisions such as choosing parents carrying desirable traits, crossing parents for efficient combinations, selecting the best-performing seedlings and commercially releasing the very best. RosBREED's approach is to integrate two types of information into breeding decisions: socio-economics information (trait values) and DNA information (molecular genetics & genomics describing the underlying genetic control of these traits). This information allows breeders to **objectively define selection targets** and **optimize selection strategies**. The catch, however, is translating the information into the language of breeding and channeling it into routine breeding operations.

Our MAB Pipeline brings focus and creates a sustained infrastructure, or pipeline, for the activities needed to make this happen – activities that have been typically overlooked or only addressed in an ad hoc manner previously. The MAB Pipeline will enable breeders to continuously apply new knowledge without the need for continued resource inputs. In fact, we believe that **successful MAB represents resource savings through improved breeding efficiency** rather than a cost to breeding programs as it is often perceived.

The goal of RosBREED's MAB Pipeline Team is to establish and successfully implement the MAB Pipeline in Rosaceae breeding programs. This involves coordinating with other RosBREED Teams to connect all the dots. The Breeding Team is the most involved, because breeders – both Demonstration and Community Breeders – are the immediate beneficiaries of RosBREED's outputs. While our Demonstration Breeders jump in the deep end, we encourage Community Breeders to at least get their feet wet.

So, what is the MAB Pipeline? It is a series of eight stages (see right and below) to systematically consider, adjust, test, and apply available knowledge regarding Rosaceae crop traits. Many of these activities actually do not require DNA information, but rather compile and mobilize genetic, physiological, and physical data on breeding individuals and practices. DNA information simply enhances this underlying knowledge base, but this enhancement can literally transform current breeding programs.

In upcoming Newsletters, this column will discuss examples of RosBREED's use of the MAB Pipeline in supporting Rosaceae breeding decisions and highlight the role of other RosBREED Teams in this coordinated interplay.



## The MAB Pipeline's Eight Stages:

1. **Prioritization** of reported marker-locus-trait associations is essential to sift through the volumes of available genomics information. Not all genomics discoveries are created equal, and their impact on crop improvement varies by socio-economic (value of a trait to breeding, industry, and consumers) and genetic (the strength of association and effect on performance of the tagged controlling genes) factors. Marker-locus-trait associations are specific genetic markers with a known position (locus) in the genome that tag a specific trait of interest.
2. **Genetic Screening Efficiency** is identified by locating and testing high-throughput genetic screening methodologies (sampling, DNA extraction, genotyping, and timely provision of data to the breeder) that are logistically feasible and suit the idiosyncratic routine operations of individual breeding programs.
3. **Improved Markers** are developed by converting markers from their originally reported format to ensure technical robustness and amenability to use in high-throughput platforms needed for genetic screening of thousands of seedlings, as well as screening potential parents.
4. **Validation** of robust marker-locus-trait associations is performed in the wider germplasm pool of the crop – beyond the experimental material in which associations are usually first discovered, using the new marker type they have been converted to.
5. **Utility** assessment of improved validated markers is conducted to determine their potential application specifically within a breeding program, detecting the maintenance of marker-locus-trait associations in breeding program germplasm and describing functional marker variants (favorable or not) present in and inherited from each potential breeding parent.
6. **MAPS (marker-assisted parent selection) Decisions** are enabled, where the information gained from the previous stage is used to guide crossing decisions with a better understanding of genotype-based breeding value.
7. **MASS (marker-assisted seedling selection) Cost Efficiency and Logistics** calculations and considerations are made to identify optimal seedling selection schemes that integrate available robust, validated, utile genetic tests for some traits into routine breeding operations with phenotypic selection for other traits or for other aspects of the same trait.
8. **MASS Trial Use** is conducted in a high-throughput manner on a subset of breeding program seedlings to gain experience with genotype-based seedling culling, comparing theory with practice to optimize MASS implementation.



## RosBREED definition

**BREEDING PEDIGREE SET (BP Set):** is a Pedigree-linked reference germplasm set of a crop representing alleles across the genomes of important breeding parents. This may include 100-300 extra plants for each breeding program; together with the Crop Reference Sets, this allows full representation of important parents in the program.