

RosBREED's Pedigree-Based Analysis (PBA) Team – Support in data analysis through software development, trainings and hands-on assistance

By RosBREED's PBA Team (Eric van de Weg, Marco Bink, Gennaro Fazio, Hans Jansen, Jim Luby, Chris Maliepaard, Cameron Peace, Umesh Rosyara, Roeland Voorrips, Dechun Wang)

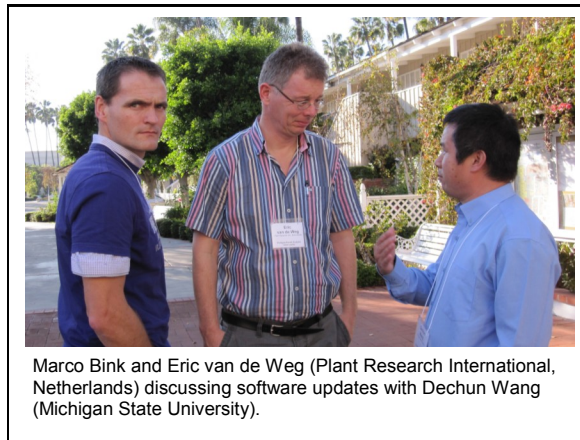
The Pedigree-Based Analysis (PBA) Team is dedicated to developing a Rosaceae-wide statistical platform for identifying and validating diagnostic genetic tests. PBA will be established and demonstrated in RosBREED's Demonstration Breeding Programs.

The PBA Team

In short, the PBA Team develops and documents software and training material, trains breeding personnel in PBA use, and aids in data analyses. The PBA Team Leader is Eric van de Weg, located at Plant Research International (PRI) of Wageningen University and Research Centre in The Netherlands. Eric's fellow Dutch members are Marco Bink, Hans Jansen, Chris Maliepaard, and Roeland Voorrips. Primarily, this group is responsible for development of the statistical methodology and software, as well as manuals, tutorials, and training materials to improve understanding of underlying genetic and statistical concepts and their implementation. Regularly, this group provides in-person whole-group training to the U.S.-based Demonstration Breeders and RosBREED-supported breeding trainees (graduate students). The MSU-based members, Dechun Wang and Umesh Rosyara are located at Michigan State University, East Lansing, MI, USA. Dechun and Umesh are the on-the-ground local PBA experts who will provide immediate support in PBA data analysis to breeders and trainees. The PBA Team is enforced by Jim Luby (Breeding Team Leader), Cameron Peace (MAB Pipeline Team Leader), and Gennaro Fazio (BIMS Team Leader), thus ensuring full coordination with other closely associated RosBREED activities. Please see page six for pictures of these Team members.

PBA - an innovative concept

PBA is a statistical framework designed to identify diagnostic genetic tests to inform breeding decision-making. In the PBA approach, DNA information and performance data are integrated in multiple populations of pedigree-linked plants. This approach is suited to ongoing breeding programs of Rosaceae crops, as it uses typical breeding germplasm and routine data, unlike the conventional method of identifying trait-controlling genomic regions in dedicated, single, experimental populations and then ad hoc validation in a wider array of genetic backgrounds more relevant to breeding interests. Of great value to breeders, the outcome of PBA is the association of particular DNA profiles with superior traits such as excellent flavor and keeping qualities. PBA results predict the genetic potential of any breeding parent examined. This information can be used to design efficient parental combinations and to indicate new seedling populations to genetically screen (and weed out inferior seedlings).



Marco Bink and Eric van de Weg (Plant Research International, Netherlands) discussing software updates with Dechun Wang (Michigan State University).

Adopting the PBA approach has many advantages, including:

1. Immediate relevance to breeders of genetic tests developed as they have been found in breeders' own germplasm and using breeders' own performance data records.
2. Improved chance for detecting important trait-controlling genes, because:
 - Combined families will usually exceed the size of a single experimental family;
 - Continuity over generations within breeding programs accumulates a tremendous amount of data, increasing statistical power and thereby the ability to detect genes with major effects as well as those with moderate effects.
3. Increased opportunities for identification of multiple variants (alleles) of trait-controlling genes due to the use of multiple families (known as allele mining).
4. Obtaining knowledge on the robustness of diagnostic genetic tests in many genetic backgrounds.
5. Reduction in costs of genetic research as breeding populations already exist and are already evaluated as part of the breeding process.
6. Bridging the chasm between pure science and breeding due to the merging of intentions, germplasm, and data from both "sides" into a mutually intelligible language.

PBA software

The use of multiple families for associating DNA profiles with performance raised the need for new statistical methodologies, as well as software for implementing them. The Dutch members initiated the development of such methodology and software nearly a decade ago. Their efforts led to the development of PBA's two main software packages, FlexQTL™ and Pedimap, and PBA-dedicated modules in Genstat have also been developed (see Box 1). Identity-By-Descent (IBD) is a key concept in PBA as it allows integrated analyses of families that are related through common

RosBreed's PBA Team cont.

ancestors. Proof of concept was successfully delivered in a recent large European project focusing on apple fruit quality and involving 27 families and six breeding programs. This software now constitutes the U.S. Rosaceae genomics, genetics, and breeding community's common statistical platform for identifying and validating diagnostic genetic tests. During RosBREED's first year, new software functionalities have been added and user-friendliness has been improved. RosBREED's project director Amy Iezzoni was the first rosaceous crop breeder in the U.S. to adopt PBA and has demonstrated its practical value with sweet cherry at Michigan State University. Independent to Amy, co-PD Cameron Peace (Washington State University) recognized the usefulness of PBA and introduced this approach to Washington apple and sweet cherry breeding.

PBA training activities

In the first year of RosBREED's PBA activities, two training workshops were provided for participants. Last January, during RosBREED I in San Diego, the PBA Team presented genetic and theoretical concepts of PBA and gave the first hands-on training for Pedimap software to excited breeders. This June, a two-day workshop for Pedimap and FlexQTL™ took place at Michigan State University, East Lansing, MI. A total of 30 eager-to-learn participants attended the vibrant workshop, and left with new knowledge and skills that could be applied immediately to their programs. Among the participants were 10 demonstration breeders, 11 project associates and the PBA team members, and two representative from Driscoll's Strawberry Associates (please see www.rosbreed.org/about/project-management/meetings/pba-workshop for handouts from this workshop).

The next training workshop is scheduled for March 2011 to be held at Michigan State University again, with particular focus on QTL mapping. At this workshop, phenotypic data collected of each crop's CR Set in 2010 will be analyzed.



Participants listening to instruction by Eric van de Weg

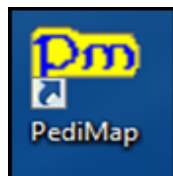


Kate Evans (Washington State University, apple demonstration breeder) and Ben Orcheski (Cornell University, apple project associate)

Box I . Description of the PBA software that RosBREED demonstration breeders and project associates are being trained and will implement in their breeding programs.

**FlexQTL™**

- Performs QTL analyses
- Estimates Identity-By-Descent probabilities of genetic marker alleles
- Error-checks marker inheritance over pedigrees
- Output includes locus-specific and genome-wide breeding values
- Output compatible with Pedimap for pedigree viewing and with MapChart to visualize QTL positions on linkage maps
- Suitable for diploid inbreeding and outbreeding species (extension to polyploids is underway)
- Available under MTA, description: www.biometris.wur.nl/UK/Software/FlexQTL/

**Pedimap**

- Graphical representation of simple to complex pedigree relationships
- Phenotypic and marker information also visualized across pedigrees (e.g. trait values, scored alleles, founder origins of alleles)
- Compatible with FlexQTL™
- Suitable for any ploidy level and mating system
- Available for free: www.plantbreeding.wur.nl/UK/software_pedimap.html

**Genstat modules**

- For in-depth QTL studies (e.g., detection of multiple functional alleles, GxG and GxE interactions)
- Suitable for diploid inbreeding and outbreeding species
- Will become public during the course of RosBREED

Who's Who in the Pedigree-Based Analysis Team?



Team Leader: Eric van de Weg
Plant Research International
Area of interest: Genetics in Fruit Crops towards cultivar development

Plant Research International, Netherlands Team Members:



Marco Bink
Role: Extension of FlexQTL™ software

Hans Jansen

Role: Development of PBA modules within Genstat



Chris Maliepaard
Role: Support in tutorial development

Roeland Voorrips

Role: Extension of Pedimap software



Michigan State University, US Team Members:



Dechun Wang
Role: Support to Umesh Rosyara

Umesh Rosyara

Area of interest: Genomics tools for breeding application
Role: U.S.-wide consultant on PBA software and analyses



PBA supporting Team Leaders:

MAB Pipeline Team leader
Cameron Peace
Washington State University



Breeding Team leader
Jim Luby
University of Minnesota



BIMS Team leader
Gennaro Fazio
USDA - Cornell University

