

## Event Feedback From RosBREED Workshop on Pedigree-Based Analysis, June 15-16, 2010

This document contains a summary of evaluation data from the RosBREED workshop at Michigan State University in June 2010. Survey forms were completed by 33 workshop participants. Sample size for particular questions varies slightly.

### Who Attended the Workshop?

Participants were asked to identify the plant groups they work with, and their current professional role in horticulture. Approximately equally numbers of participants reported working with apple, peach, strawberry, and tart or sweet cherry; some also reported working with other Rosaceae, or focusing on genotyping in general. Most participants were research scientists, students or professional plant breeders:

With which plant group(s) are you currently working?	10 Apple      9 Peach      9 Strawberry      6 Tart Cherry      5 Sweet Cherry 4 Other Rosaceae (1 each: Raspberry, Garden Rose, Rose, Genotyping) 4 Other plants: "All", "All teams", 2 not specified								
Please mark one box to indicate your role:	<table style="width: 100%; border: none;"> <tbody> <tr> <td style="width: 50%;"><b>6 (18.2%) Professional plant breeder</b></td> <td style="width: 50%;">1 (3.0%) Post-doc in plant breeding</td> </tr> <tr> <td><b>12 (36.4%) Student</b></td> <td><b>10 (30.3%) Research scientist</b></td> </tr> <tr> <td>0 Pathologist or other related professional</td> <td>1 (3.0%) Technical staff member</td> </tr> <tr> <td colspan="2">3 (9.1%) Other: Industry stakeholder, post-doc in genotyping, extension</td> </tr> </tbody> </table>	<b>6 (18.2%) Professional plant breeder</b>	1 (3.0%) Post-doc in plant breeding	<b>12 (36.4%) Student</b>	<b>10 (30.3%) Research scientist</b>	0 Pathologist or other related professional	1 (3.0%) Technical staff member	3 (9.1%) Other: Industry stakeholder, post-doc in genotyping, extension	
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## How Were the Specific Workshop Topics and Sessions Rated by Participants?

All of the workshop sessions were viewed as relevant by all or nearly all participants. The amount of time spent on each topic was viewed as “just right” by 88 percent or more of the audience during the introduction and the first two sessions on PediMap. As the agenda progressed to the final two sessions on PediMap, then the sessions on FlexQTL, the fraction of participants who viewed the amount of time spent on the topic as “just right” gradually decreased from 76 percent to 48 percent. It appears that the time allocated for these later sessions was not adequate for some participants.

A similar pattern is found in the data on the clarity and effectiveness of the presentations. The introduction and the sessions on PediMap were seen as “very effective” or “OK” by 94 to 100 percent of workshop participants, with more than 50 percent rating these sessions as “very effective.” The sessions on FlexQTL were seen as “very effective” or “OK” by 84 to 91 percent of workshop participants, with fewer than 47 percent of participants rating them as “very effective” (except for the final summary and wrap-up session.)

The last two sessions on PediMap and all of the sessions on FlexQTL may have contained too much material for the time allotted. The FlexQTL practice session in particular was viewed by almost half of the participants as being too short.

Detailed response frequencies for these questions are presented in the table below.

Please rate each topic by circling an answer to each of the 3 questions to the right. Topic:		Is this topic relevant or important to your work?			Amount of time spent on topic was:			Was the presentation clear and effective?		
		No	Sort of	Yes	Not enough	Just right	Too much	Not very effective	OK	Very effective
A1	Overview of pedigree based analysis	-	9.1 %	90.9	3.0 %	93.9	3.0	-	36.4 %	63.6
A2	PediMap: Overview; installation	-	9.1	90.9	3.0	87.9	9.1	-	36.4	63.6
A3	PediMap: Data input files I: header and pedigree data; formatting views	-	12.1	87.9	3.0	87.9	9.1	3.0	39.4	57.6
A4	PediMap: Data input files II: marker data with error checking and data cleaning; practice session	3.1	3.1	93.8	18.2	75.8	6.1	6.1	27.3	66.7
A5	PediMap: Identity by descent (IDB) probabilities – inside the black box	3.1	9.4	87.5	28.1	71.9	-	-	53.1	46.9
A6	FlexQTL: Getting started, input & output	-	9.1	90.9	27.3	63.6	9.1	9.1	51.5	39.4
A7	FlexQTL: Null alleles; checking consistency data	-	22.6	77.4	28.1	62.5	9.4	9.4	56.3	34.4
A8	FlexQTL: Practice session	-	12.1	87.9	48.5	48.5	3.0	15.6	40.6	43.8
A9	FlexQTL: Summary, Wrap-up	-	9.4	90.6	30.0	70.0	-	10.7	28.6	60.7

Note: N = 31 to 33 for these questions except N = 30 for A9b and 28 for A9c.

## How was the Workshop as a Whole Rated by Participants?

Eighty-five percent or more of workshop participants moderately or strongly agreed that the content was consistent with the publicized description and that learning objectives were clearly stated and met.

Eighty-five percent moderately or strongly agreed that “there was a balance between theory and application.”

Ninety-four percent or more moderately or strongly agreed that they gained new knowledge applicable to their work, that they planned to apply what they learned, that the handouts were useful.

Ninety-six percent moderately or strongly agreed that they would recommend the course to others:

	Please <b>circle one number in each row</b> to indicate how much you agree or disagree with the following statements:	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
B1	Content was consistent with the publicized description	-	-	-	15.2%	39.4	45.5
B2	Learning objectives were clearly stated.	-	6.1	6.1	3.0	39.4	45.5
B3	Learning objectives were met.	-	-	3.0	12.1	54.5	30.3
B4	There was a balance between theory and application	-	-	6.1	15.2	27.3	51.5
B5	I gained new knowledge that is applicable to my work.	-	3.0	-	3.0	3.0	90.9
B6	I plan to apply what I learned.	-	3.0	-	-	6.1	90.9
B7	The handouts were useful.	3.0	-	-	3.0	27.3	66.7
B8	I would recommend this course to others	-	-	3.0	3.0	21.2	72.7

Note: N = 33 for these questions.

The technical level of the workshop was deemed to be “just right” by 66 percent of the audience. Almost a quarter of the audience (22 percent) found the workshop to be “a little too advanced” while 12 percent found it to be “a little too basic”:

B9	This presentation level was: (circle one answer only)	Way too basic	A little too basic	Just right	A little too advanced	Way too advanced
		-	12.5 %	65.6 %	21.9%	-

Note: N = 32.

## What Commendations and Recommendations Did Participants Offer About the Workshop?

Participant comments about positive aspects of the workshop focused on several themes: the focus on useful software, the quality of instruction and organization of the event, the opportunity to network and learn together with colleagues, and the usefulness of the concepts and tools presented:

C1	What was good about this event?
	<ul style="list-style-type: none"> <li>▪ <i>Being able to use the software while we were learning it so mistakes can be made and understood.</i></li> <li>▪ <i>Having the opportunity to have hands-on training with these software programs.</i></li> <li>▪ <i>Getting to know peer researchers; exchanging research information; learning advanced software.</i></li> <li>▪ <i>In general, the instructor did a very good job covering a lot of material with a lot of people, and the material was well explained, both theory and applied. A very useful concept and set of tools.</i></li> <li>▪ <i>The instructor was great. Very patient! Set good expectations and was explicit about why/how we do things in the software. Very organized. Having training materials on each computer was an asset. I feel much more comfortable now with the software. Good communication. Good exercises to practice the skills.</i></li> <li>▪ <i>The hands-on training in the software.</i></li> <li>▪ <i>Questions! - the audience input was great. Relaxed, but directed. Well prepared.</i></li> <li>▪ <i>Useful for application; people exchanged ideas.</i></li> <li>▪ <i>Chance to get help with experienced people.</i></li> <li>▪ <i>Learning two very helpful softwares.</i></li> <li>▪ <i>Excellent effort on the part of the organizers and presenters. Great opportunity to meet colleagues. Good overview of issues involved in the application of PediMap and FlexQTL.</i></li> <li>▪ <i>Opportunity to be able to play around with FlexQTL.</i></li> <li>▪ <i>Excellent information -- good practice -- patient teacher.</i></li> <li>▪ <i>Meeting everyone; learning the software and concepts.</i></li> <li>▪ <i>The training was pitched at just the right level. Good balance of theory vs. practice. Great refreshments!</i></li> <li>▪ <i>Bringing all RosBREED team leaders under a single roof was great for me. Learning with everybody together was awesome.</i></li> <li>▪ <i>The instructor was able to give extra instruction and the course was very good.</i></li> <li>▪ <i>Clear, organized presentation; patience in letting everyone catch up.</i></li> <li>▪ <i>The wrap up really brought everything together well! This really sparked an interest in me.</i></li> <li>▪ <i>The jump drive with all the slides and practice examples.</i></li> <li>▪ <i>Detailed instruction and hands-on.</i></li> <li>▪ <i>Event ran smoothly; it was timely, soon after graduate students have started; the instructor infuses his nurturing personality into the event, which is a special contribution to RosBREED; some examples were used that described discoveries made using PBA; we need to know how to run and interpret this critical software, so this was great; Umesh was helpful, too.</i></li> <li>▪ <i>Learning atmosphere despite the noise distraction; positive engaged presentation; great way to meet and interact with project participants.</i></li> <li>▪ <i>The presentation style was very inclusive for asking questions.</i></li> <li>▪ <i>Learning new software for work related to RosBREED as well as for teaching in other training programs; really nice of the instructor to share the slides and handouts, extremely useful.</i></li> <li>▪ <i>Use of a real data set.</i></li> <li>▪ <i>Brought the RosBREED participants to a level that can allow them to apply and use PediMap and start working with FlexQTL and learn about its capabilities.</i></li> <li>▪ <i>Learned PediMap and FlexQTL (partially).</i></li> <li>▪ <i>The instructor was incredibly patient and dedicated to the task; presentation of several useful tools that can be used in both marker-assisted as well as conditional plant breeding; the instructor moved slowly to accommodate those from diverse backgrounds in terms of knowledge and experience.</i></li> <li>▪ <i>Learning the programs, understanding the important points in file preparation and marker scoring for PediMap and FlexQTL.</i></li> <li>▪ <i>PBA and FlexQTL analysis both are very relevant to my breeding program, so it's good to have this event.</i></li> <li>▪ <i>Getting to network and meet great people.</i></li> <li>▪ <i>Great energy, wonderful new people we met; I learned new "tricks" for PediMap and new formatting steps for FlexQTL; the instructors did a good job.</i></li> </ul>

Participant recommendations for improvement included making the workshop longer, with more time for the topics and exercises; using a computer lab with pre-loaded software and well-organized practice files to lessen the amount of time spent on these issues; providing software, files, manuals, and pre-requisite information (i.e. required Excel skills) ahead of time so participants could be better prepared before they arrived; more clarity about the purpose and instructions of each activity; and a more comfortable room. Additional individual recommendations are included in the verbatim comments for question C2:

C2	What changes would have improved this event?
<ul style="list-style-type: none"> <li>▪ <i>It was hard just being told what to do, instead it would be nice if it could be physically demonstrated.</i></li> <li>▪ <i>The room; too much outside noise. Having the files either loaded perfectly before the event or at the event, not both, and located in the same fashion.</i></li> <li>▪ <i>Issuing a temporary license with limited power to audience members before the workshop to practice FlexQTL would be very helpful for learners.</i></li> <li>▪ <i>I think preparing files ready at each stage to make it possible for people to move on without accumulating problems as the course progresses. In general, I thought the pace was a little ambitious given the size of the group. I thought there was far too much time spent on Excel -- I would hope most people are at least kind of comfortable with manipulating data in Excel.</i></li> <li>▪ <i>An additional day? Two instructors, two rooms, to have a smaller class size.</i></li> <li>▪ <i>If the class was presented in a computer lab where each person can work and learn on his or her own.</i></li> <li>▪ <i>Longer, more days, more hands-on.</i></li> <li>▪ <i>If we could receive files about the workshop before attending it that would be better.</i></li> <li>▪ <i>More time!</i></li> <li>▪ <i>More time.</i></li> <li>▪ <i>For initial training of individuals without any prior experience with these programs, I would strongly recommend an approach in which a relatively simple and completely error free data set is analyzed. The various issues involved in finding and correcting data errors can be better understood and appreciated within a context of understanding and experience of successful outcomes. As a beginner, I found it very difficult to see the big picture when we spent so much time on the issues of error correction, although the latter emphasis is obviously appropriate for those with extensive prior experience. I would be happy to explain this comment in more detail.</i></li> <li>▪ <i>More time. Pre-stage more prepared data so people can "catch up" even if the previous steps didn't work.</i></li> <li>▪ <i>Nicer room facilities - "U" shape of tables. More time.</i></li> <li>▪ <i>Maybe we can have more handouts and booklets.</i></li> <li>▪ <i>I think it went well, I wish I had read the manuals beforehand.</i></li> <li>▪ <i>Longer lunch so I could get a run in.</i></li> <li>▪ <i>Print out all of the slides for everyone; improve the organization of saved files.</i></li> <li>▪ <i>Better direction on what files to open. A bit more time could have been spent on FlexQTL.</i></li> <li>▪ <i>Have all practice files available before the meeting (but this is minor since flash drives were available). More detailed manuals.</i></li> <li>▪ <i>Use more crop-specific examples, so that each group of people can relate to it, especially new discoveries made; have a room without construction distractions; more fruit during breaks, esp. Rosaceae fruit; in fact, only Rosaceae fruit and nuts; even longer -- more days -- especially using crop-specific own data (only possible if workshop was longer); move along quicker, except on critical parts -- grad students seemed to be further ahead than the general pace.</i></li> <li>▪ <i>More participant interaction and getting to know each other (would need more structure and planning); start at 9 AM not 8AM; more hot water for tea.</i></li> <li>▪ <i>If we used computers that already had files organized, e.g. a computer classroom.</i></li> <li>▪ <i>Longer training program; two days are certainly not enough; for those like me learning the software for the first time was information overload.</i></li> <li>▪ <i>Increase the time period.</i></li> <li>▪ <i>To include QTL identification in one workshop.</i></li> <li>▪ <i>Possibly being more organized; generally the instructor could mention the rationale for presenting a new method or exercise before presenting it.</i></li> <li>▪ <i>More time.</i></li> <li>▪ <i>A computer lab with enough machines already loaded with the required software might have improved this event.</i></li> <li>▪ <i>Directions needed to be much clearer; not everybody here is a computer scientist or familiar with computer terminology.</i></li> <li>▪ <i>Have the workshop in a location without construction; even though this was called a "workshop" more emphasis should be put on "work" - make sure all attendees have necessary files in the same location with the same name prior to the start, then mention that we are working, not checking email - if you check email you will slow the class down! A few people lost the objective of particular exercises; more reminders of what we've accomplished and what we'll be doing next would have been extremely helpful - or, handout a more detailed agenda; prior to workshop, ask attendees to be familiar with "XYZ" in Excel -- too much time was spent on these basic steps that most people know.</i></li> </ul>	

## What Did Participants Learn and How Will They Use This Knowledge?

When asked what new knowledge or skills they learned at the workshop, most participants commented on learning about the specific software tools that were the focus of the sessions (PediMap and FlexQTL). Several commented about more general learning about identity by descent, pedigree based analysis, and how these tools and approaches fit within a breeding program:

C3	What new knowledge or skills did you learn?
<ul style="list-style-type: none"> <li>▪ <i>How to use FlexQTL and better understanding of everything it can do.</i></li> <li>▪ <i>Pedimap use, FlexQTL intro.</i></li> <li>▪ <i>PediMap and FlexQTL software.</i></li> <li>▪ <i>Obviously, the ability to use FlexQTL and PediMap, as well as an understanding of how these programs might be incorporated in my breeding program.</i></li> <li>▪ <i>Use of Pedimap: loading files, manipulating and saving data, etc. FlexQTL. Learned how to install the software.</i></li> <li>▪ <i>Intro knowledge of PediMap; how FlexQTL data should look.</i></li> <li>▪ <i>All of FlexQTL (I knew very little about FlexQTL), correcting Pedimap data for entry, i.e. correcting spaces, repeats, etc.</i></li> <li>▪ <i>Data analysis, how to work efficiently with mass data.</i></li> <li>▪ <i>Learned a lot about identity by descent.</i></li> <li>▪ <i>Basic concepts of how to implement PediMap and FlexQTL; many useful operational details.</i></li> <li>▪ <i>How to use all the utilities in PediMap.</i></li> <li>▪ <i>PediMap and FlexQTL.</i></li> <li>▪ <i>FlexQTL and PediMap use.</i></li> <li>▪ <i>Much more PediMap manipulation; more confidence and understanding of FlexQTL input.</i></li> <li>▪ <i>PediMap and FlexQTL.</i></li> <li>▪ <i>How to use these two programs when I had never used them before.</i></li> <li>▪ <i>What PediMap and FlexQTL can do.</i></li> <li>▪ <i>Using PediMap and FlexQTL.</i></li> <li>▪ <i>PediMap and FlexQTL - I have never seen either program and feel this was a great intro to each.</i></li> <li>▪ <i>Applying PediMap and FlexQTL and tricks.</i></li> <li>▪ <i>How PediMap uses IBD values - understanding the raw input and output; how to run FlexQTL with confidence - at least for checking marker consistency; how to generate and view IBD information in PediMap.</i></li> <li>▪ <i>PBA overview; practical implementation.</i></li> <li>▪ <i>I had prior knowledge of these programs so I learned new functions.</i></li> <li>▪ <i>PediMap and FlexQTL, what they can do and how useful they are for a breeding program. Cool!</i></li> <li>▪ <i>Practice with the software.</i></li> <li>▪ <i>To use PediMap and FlexQTL to analyze data and present results.</i></li> <li>▪ <i>With a very limited knowledge or markers, I gained a general, but very valuable understanding of FlexQTL software and pedigree graphing tools.</i></li> <li>▪ <i>How to prepare data files for PediMap and FlexQTL; how to adjust the parameters and use output more efficiently.</i></li> <li>▪ <i>Pedigree based analysis and FlexQTL analysis procedures and methods of installation and use.</i></li> <li>▪ <i>How QTL mapping is important to breeding; PediMap was also interesting to see how chromosome blocks are transferred through generations.</i></li> <li>▪ <i>New tricks for PediMap.</i></li> </ul>	

When asked how they will use the knowledge gained, participants specifically mentioned applications within breeding programs, made more general comments about applications to work in plant sciences, or mentioned sharing the information with colleagues. Additional individual recommendations are included in the verbatim comments for question C4:

C4	How will you use the knowledge and skills you learned?
<ul style="list-style-type: none"> <li>▪ Visualization of pedigrees and data evaluation.</li> <li>▪ With current breeding population data.</li> <li>▪ Input our pedigree data and organize them with PediMap.</li> <li>▪ To plan our molecular approaches, and to help inform aspects of my breeding program.</li> <li>▪ Important for data input and analysis.</li> <li>▪ Sort out pedigree information from our germplasm.</li> <li>▪ This will be used to correlate phenotypic and genotypic data within breeding program seedlings/selections/parents, with the overall goal of marker assisted parent selection (MAPS) and marker assisted seedling selection (MASS).</li> <li>▪ It is definitely helpful.</li> <li>▪ Developing PediMap files for breeding programs.</li> <li>▪ Use PediMap on breeding pedigree data.</li> <li>▪ Analysis of our own program data.</li> <li>▪ Use FlexQTL to analyze sweet cherry data.</li> <li>▪ In the RosBREED project and in breeding program.</li> <li>▪ Understand breeder's data.</li> <li>▪ Application to current breeding work, gaining knowledge of genetic resources, plus RosBREED!</li> <li>▪ I will use this knowledge in my area of research.</li> <li>▪ Use with genotyping the different crops.</li> <li>▪ To plan my future crosses and ultimately do marker assisted breeding.</li> <li>▪ Finding phenotypic traits passed through generations that I can use as a hypothesis for a study.</li> <li>▪ Share with people who were unable to make it to this meeting and for entering strawberry data.</li> <li>▪ PediMap right away; FlexQTL at end of year.</li> <li>▪ To advise grad students and breeders on how best to proceed with integrating PBA into their breeding programs; to use with my own data - fun!</li> <li>▪ Provides insight into RosBREED objectives and output; informs decisions about resource needs in RosBREED programs.</li> <li>▪ I will try to do more analyses.</li> <li>▪ For teaching others and sharing with the plant breeding community.</li> <li>▪ To help others.</li> <li>▪ Directly in my research projects.</li> <li>▪ These new skills will be used along with the phenotyping of the plants used in my study.</li> <li>▪ On my germplasm collections and breeding populations to view and analyze in PediMap.</li> <li>▪ The knowledge will be very helpful for me in analyzing my crop reference set and breeding program set of plants in tracing relationships.</li> <li>▪ Not sure yet, I'm new.</li> <li>▪ Will just continue as I have been working because we've been using FlexQTL and PediMap for several years.</li> </ul>	

## Recommendations for Additional Training or Information

Recommendations for future training sessions or materials focused on more background information about breeding and marker-assisted breeding to help the graduate students work more effectively with breeders; additional training and practice with PediMap and FlexQTL after participants have some time to work with these on their own; use of JoinMap; technical information about QTL mapping and lab techniques for discovering markers; and applications of these tools to polyploids specifically. Additional individual recommendations are included in the verbatim comments for question C5:

C5	What kind of additional training or information about marker assisted selection or breeding or other uses of genetic markers would be most helpful to you?
<ul style="list-style-type: none"> <li>▪ <i>JoinMap training and further. I will decide once I have used what was presented at this workshop.</i></li> <li>▪ <i>High through-put molecular marker systems and efficient QTL analysis.</i></li> <li>▪ <i>QTL; Applications specifically focused on the issues of polyploids.</i></li> <li>▪ <i>DNA extraction, gels, etc. A good review of the types of markers available, and what RosBREED is using.</i></li> <li>▪ <i>How to perform the QTL mapping; practical application of QTL mapping.</i></li> <li>▪ <i>Making information available to graduate students regarding the genetics/genomics already understood by breeders, such as literature citations, publications, and other resources -- put on RosBREED website or PBGworks.</i></li> <li>▪ <i>Looking forward to progressing to QTL discovery.</i></li> <li>▪ <i>More on using FlexQTL with strawberry.</i></li> <li>▪ <i>It would be very useful to have a refresher course after we have had a chance to work through the applications independently.</i></li> <li>▪ <i>After working with it for a while, more training in PediMap and FlexQTL.</i></li> <li>▪ <i>A booklet that contains definitions of every technical term (jargon) with relevant examples.</i></li> <li>▪ <i>Not sure at this point.</i></li> <li>▪ <i>None. I just need to get inside the programs and start trying to use them.</i></li> <li>▪ <i>How to run and interpret the other major module of FlexQTL (QTL analysis); use FlexQTL and PediMap with SNP-based genome scan data.</i></li> <li>▪ <i>More practice sessions with breeders.</i></li> <li>▪ <i>More advanced training on QTL map preparation.</i></li> <li>▪ <i>Quantitative scoring is becoming essential to learn.</i></li> <li>▪ <i>More rudimentary explanation of the mechanics and procedures used in marker-assisted breeding, although my background on the subject is very limited.</i></li> <li>▪ <i>Genetic mapping, development of markers, principles in selecting parents for breeding, selection and number of progeny needed for planting, advancement of elite progeny, period (years) and selection methods.</i></li> <li>▪ <i>The connection between JoinMap and FlexQTL.</i></li> <li>▪ <i>Summary of how the genotyping is going; more information about SNP technology.</i></li> </ul>	

## Additional Participant Comments:

- *When the instructor wrote steps on the board it was very helpful; if we could not keep up we had a chance to do so by referring to the list on the board.*
- *It was awesome to have the skill, experience, personality, and presence of the presenter in the U.S. before our eager-to-learn and ready-to-be-inspired grad students. We need to have him over more often!!*
- *A little difficult to categorize my "work."*
- *Thank you all for your tireless work to make this event successful!*