

Status of Marker-Assisted Breeding in U.S. Rosaceae Breeding Programs, 2010 and 2014

RosBREED Breeding Program Survey



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Summary

Since 2009 the RosBREED project has aimed to improve the capacity of plant breeders in the United States to use genetic tests in their programs—through a variety of applications collectively known as marker-assisted breeding or MAB—with the goal of helping breeders provide improved cultivars for growers of apple, peach, strawberry, sweet and tart cherries, and other rosaceous crops. The project was initiated because of the perception that the science of Rosaceae genomics and bioinformatics have been developing rapidly but have not been translated to routine practical application in plant breeding programs.

As part of an external evaluation of the extension education work carried on as part of the project, a baseline survey of Rosaceae breeders and their allied scientists in the United States was conducted in spring 2010, and a follow up survey was conducted in winter 2013/2014. This report includes information gathered at these two times from Rosaceae plant breeders and breeding-allied scientists.

The survey included several sets of questions designed to measure how much the Rosaceae breeding community knows about marker-assisted methods in plant breeding, the value they place on these methods, their perception of their own capacity to use these techniques (“self-efficacy”), and the extent to which they are using marker-assisted methods in their work. Response rates for each question are included in the report, along with scale scores for each major topic for both breeders and allied scientists.

The report also contains recommendations from breeders and allied scientists about topics and formats for additional professional development opportunities and educational materials, as well as their recommendations regarding practical problems in plant breeding and plant sciences that could be addressed using marker-assisted techniques.

In 2014, participants were also asked to rate various aspects of the RosBREED extension education activities, their observations about the impact of the project on the Rosaceae breeding community, and their interest in software tools for breeders and genome scan tools that were under development.

Survey Participants

The survey sample for 2010 included 70 percent of the breeders and 62 percent of the breeding-allied scientists known to be working in the U.S. Rosaceae breeding community at that time (35 breeders and 58 allied scientists). In 2014, 62 percent of known U.S. breeders and 41 percent of breeding-allied scientists participated in the follow up survey (40 breeders and 37 allied scientists).

Crop and Cultivar Focus

In both 2010 and 2014, 25 percent or more of breeders who responded to the survey worked with each of the crop groups of raspberry/blackberry, strawberry, or peach/nectarine. Apple was a focus for 17 percent of breeders in 2010 and 25 percent in 2014. Sweet cherry and almond were each a focus for 11 percent of breeders in 2010, rising to 22 and 18 percent in 2014. Pear was a focus for 6 percent of breeders in 2010 and 15 percent in 2014. Tart cherry was a focus for 2-3 percent of breeders.

Among allied scientists, apple was a focus for 58 percent of respondents in 2010 and 57 percent in 2014, while peach/nectarine was a focus for 38 percent in 2010 and 27 percent in 2014. Strawberry and raspberry/blackberry were a focus for 22 to 38 percent of allied scientists in these years, while pear and sweet cherry were a focus for 11 to 32 percent. Tart cherry (5-12 percent) and almond (3-5 percent) were least likely to receive attention from breeding-allied scientists. (Respondents may work with multiple crops so these percentages do not sum to 100 percent).

In both 2010 and 2014 a majority of breeders and allied scientists reported working on scion production and on cultivars for the fresh market. Among allied scientists, half also reported working on rootstock production, while among breeders, work on rootstock cultivars was reported by only 20-25 percent of survey respondents. Cultivars for the processing market were a focus for 23-38 percent of breeders and 32-43 percent of breeding-allied scientists.

General Knowledge of Commercial Horticulture and Rosaceae Breeding

To provide context and better understand the survey sample and the U.S. Rosaceae breeding community, participants were asked to rate their general background and familiarity with horticultural crop production, commercial plant propagation, plant genetics and genomics, and crop breeding methods, as well as their general familiarity with marker applications in plant sciences. For these topics, in both 2010 and 2014 more than 80 percent of breeders reported knowing “a fair amount,” knowing “a lot about this topic,” or being an expert who “can teach or advise others,” with the exception of plant genomics. For plant genomics, 54 percent of breeders in 2010 and 60 percent in 2014 reported similar expertise.

Respondents were also asked about their knowledge of breeding specific crops. About half of the breeders in both 2010 and 2014 reported knowing “a fair amount” or more about apple, peach, and strawberry breeding. Fewer breeders reported this level of knowledge for sweet or tart cherry breeding, though this group grew from 17-29 percent of breeders in 2010 to 32-48 percent in 2014.

Allied scientists reported somewhat lower background knowledge about these topics in both years, with the exception of plant genomics — 61 percent in 2010 and 69 percent in 2014 reported “a fair amount” of knowledge or more about plant genomics. Fewer than a third of allied scientists reported that level of expertise in apple, peach, or strawberry breeding, and 11 percent or fewer reported such expertise in sweet or tart cherry breeding.

General Knowledge of Genetic Testing and Genetic Marker Applications for Breeding

Participants rated their own knowledge of several topics related to technologies for DNA testing and the use of genetic markers in plant science and breeding. These questions were substantially revised for the follow up survey, so 2010 and 2014 scale scores are not directly comparable. At both times, breeders and allied scientists did not differ significantly in their overall self-rated general knowledge of these technologies and methods. In 2014, breeders were more likely than allied scientists to report advanced expertise in specific breeding program topics: marker applications to enhance genetic gain, program efficiency, or program accuracy through parent and seedling selection, and marker applications for identity and relatedness.

Familiarity with Marker-Assisted Plant Breeding

A second set of questions asking about general knowledge of marker-assisted breeding was used in both 2010 and 2014, allowing a comparison of the response across this time period. Again, among all respondents each year, there was no difference between the overall scores of breeders and allied scientists on this measure. Among those who answered the survey in both 2010 and 2014, there was no significant difference between groups, or between their 2010 and 2014 ratings. There was some evidence that breeders and allied scientists had broader views of marker-assisted breeding in 2014, compared to 2010, with fewer respondents viewing markers strictly as research tools and more viewing markers as useful for seedling screening or parent selection in breeding program operations.

Attitude Toward Marker-Assisted Plant Breeding

Participants were asked to indicate their agreement with a set of 17 statements indicating the value they placed on DNA testing and marker applications for their own plant breeding or related scientific research or for horticulture and agricultural crop improvement in general. In both 2010 and 2014 the average responses to these questions among both breeders and allied scientists indicated moderate agreement with positive attitude statements and moderate disagreement with negative attitude statements. However, among those participants who responded to both surveys, breeders reported significantly higher positive attitudes about the potential usefulness and impact of marker-assisted methods in 2014 than in 2010. There was no significant change among allied scientists from 2010 to 2014.

Self-Efficacy for Use of Markers

The survey included questions about participants' self-efficacy for the use of marker-assisted methods in plant breeding or allied sciences. Self-efficacy questions ask people to predict their level of performance of particular tasks or skills. Breeders and allied scientists reported similar levels of ability to apply DNA testing and marker methods in their work. The average responses to these questions among both breeders and allied scientists indicated "slight" agreement with positive efficacy statements and "slight" disagreement with negative efficacy statements. Among breeders and allied scientists who responded to both surveys, there was no significant change from 2010 to 2014.

Program Use of Marker-Assisted Methods

Applied use of genetic markers was measured with a set of questions asking about personal use by the respondent and programmatic use within their organizations. In both 2010 and 2014, there was not a significant difference between breeders and allied scientists in their reported levels of use. However, among those participants who responded to both surveys, breeders reported significantly higher estimated use of marker-assisted methods in their programs in 2014 than in 2010. There was no significant change among allied scientists from 2010 to 2014.

Rosaceae Breeding Community Assessment of the RosBREED Extension Effort

The 2014 survey asked members of the Rosaceae breeding community for their opinions and observations about the extension efforts of the RosBREED project, including information resources provided by RosBREED, the overall impact of RosBREED on the community, and their interest in online tools for breeders and scientists that are currently in development.

Workshops. Three quarters of breeders and 55 percent of allied scientists who responded had attended one or more RosBREED workshops or presentations. Of these, 72 percent of breeders and 81 percent of allied scientists reported the workshops to be "fairly" or "very" helpful, with 54 percent of breeders and 62 percent of allied scientists describing them as "very helpful."

Program Consultations. About half of respondents had received program-specific consultations with RosBREED team members. About 85 percent of these rated the consultations as "fairly" or "very" helpful; 58 percent of breeders and 52 percent of allied scientists rated the consultations as "very helpful."

RosBREED Website and Newsletter. Over 90 percent of breeders reported having experience with the RosBREED newsletter and website. Among this group, over half reported these resources to be "fairly helpful" or "very helpful." Among allied scientists, 41 percent had read the RosBREED newsletter and 72 percent had used the website. Of these, 41 percent found the newsletter to be "fairly" or "very" helpful and two thirds found the website to be "fairly" or "very" helpful.

eXtension. RosBREED is one of several projects that have contributed materials to the Plant Breeding and Genomics section of eXtension.org. At the time of the 2014 survey, articles, videos, live webinars, and recorded webinars published through eXtension.org had been accessed by 54 percent or fewer of the Rosaceae breeders and 21 percent or fewer of the Rosaceae allied scientists who responded to the survey. Among those who reported having tried these resources, 39 to 55 percent of breeders and 40 to 80 percent of allied scientists rated them as being “fairly” or “very” helpful.

Breeder Information Management System (BIMS). Another set of questions measured interest in a suite of tools in development to assist both breeders and allied scientists in their work. Unsurprisingly, since these tools are primarily intended to assist breeding program operations, breeders reported more interest than did allied scientists. Breeders gave their highest ratings to the *Trait Locus Warehouse*, *QTL Validator*, and *Cross Assist* tools, but reported strong interest in all of the software modules and the SNP arrays. Allied scientists gave their highest ratings to *Cross Assist* and the SNP arrays.

Recommendations for Further Learning Opportunities

In both 2010 and 2014, breeders and allied scientists expressed strong interest in further learning opportunities of all types—professional development sessions on genetic marker methods and uses, printed and online information about markers and marker-assisted breeding, and information about how to change breeding programs to make more effective use of markers.

The specific content areas that were recommended as topics of further training sessions or information resources were also similar in 2010 and 2014, and included the following:

- Available genes, markers, and marker-locus-trait associations in particular crops, and the information and analytic/database tools needed to use them
- Case studies, site visits to study successful marker-assisted breeding programs
- Pros, cons, availability of different genotyping platforms
- Theory, fundamentals, overview of marker applications
- Costs, economic feasibility of marker applications
- Training on laboratory technical details and software
- Recommended reading lists, literature reviews

Recommendations for the format of additional learning opportunities included the following:

- Web-based resources, webinars, videos, training modules, courses, recorded seminars
- Workshops, hands-on sessions
- Collaboration, touring or training in other labs/programs, visits by experts to other programs
- Case studies
- Printed materials
- Genome Database for Rosaceae (GDR)
- Visual, graphical presentations of genes and genotypes
- Spreadsheets

Recommendations for Further Research and Development

In 2010, the most frequent recommendations for further marker applications involved disease or insect resistance, fruit quality or flavor, and post-harvest shelf life. In 2014, themes included disease resistance, increasing the genetic diversity in program materials, better understanding gene linkage, developing indicators of tree health or hybrid vigor, and developing better tools to follow genes across ploidy levels.

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Introduction

As part of the external evaluation of the RosBREED Project (see www.rosbreed.org), a baseline survey of Rosaceae breeders and allied scientists in the United States was conducted in spring 2010, with a follow up survey in winter 2013/2014. The *Rosaceae Breeding Program Survey* is a self-report instrument designed to gather information from plant breeders and allied scientists about their awareness and general knowledge of marker-assisted selection and breeding techniques, their attitude toward the value of these methods in Rosaceous crops, their self-efficacy for applying knowledge of genetic markers in their work (i.e. their perception of their own current ability to successfully use these techniques), and the actual use of genetic markers in U.S. Rosaceae breeding programs and breeding-allied scientific work.

This report includes a summary of findings from the 2010 and 2014 surveys. Response frequencies are provided for each item, with the responses of professional plant breeders presented separately from those of allied plant scientists. Survey modules B through F are designed so that responses to specific questions are of interest, but all items in each module can also be combined to produce a scale score useful for monitoring change over time. Information about scale development and scale scores is presented in a separate section of the report. Table 1 presents an overview of the survey modules.

Table 1. Rosaceae Breeding Program Survey modules

Module	Purpose
Intro	Crop and Cultivar Focus. Crop groups included in breeding-related work; focus on scion and/or rootstock, fresh market and/or processing market.
A	Knowledge of Horticultural Production and Rosaceae Breeding. Background and general knowledge of horticultural plant breeding and production; knowledge about breeding apple, peach, strawberry, sweet cherry, and tart cherry.
B	Knowledge of Genetic Marker Applications. Background and general knowledge of technologies and applications related to genetic markers.
C	Familiarity With Marker-Assisted Plant Breeding. Exposure to the general concepts of marker-assisted plant breeding.
D	Attitude Toward the Use of Genetic Markers. Attitude toward the integration of genetic markers into plant breeding programs and related scientific efforts for crop improvement.
E	Self-Efficacy for Use of Markers. Self-efficacy (perception of their own current ability) for using marker-assisted methods in breeding or allied sciences.
F	Actual Use of Marker-Assisted Methods. Actual use of markers in breeding programs or related scientific programs.
G	Interest in Further Learning. Interest in further professional development or information resources related to marker-assisted methods, and recommendations for content and format.
H	Suggested Applications of Genetic Markers in Horticulture. Ideas for practical problems that could be addressed by marker-assisted methods and genomic research.

Who Took The Survey?

The RosBREED Breeding Program Survey was administered in spring 2010 and again in winter 2013/2014 using an online survey facility. A database of all known active breeders of Rosaceae crops and allied scientists in the U.S. was compiled during winter 2009/10 for use in project communications, including the survey. This database is updated periodically to maintain a comprehensive contact list of Rosaceae breeders and allied scientists, including molecular biologists, plant pathologists, physiologists, entomologists, and other plant and food scientists directly assisting Rosaceae breeding programs.

In 2010, all 50 known Rosaceae crop breeders based in the United States were invited by email to answer the questionnaire. Of these, 35 participated, resulting in a response rate of 70 percent. Among the 96 allied scientists invited to participate, surveys were completed by 58 individuals, for a response rate of 62 percent. (Allied scientists in key RosBREED project roles were excluded from the samples.)

In 2014, many of the same individuals participated, including 27 Rosaceae breeders and 29 allied scientists, along with many new respondents. Again, all known Rosaceae crop breeders based in the United States were invited by email to answer the questionnaire, a total of 65 breeders. Of these, 40 participated, resulting in a response rate of 62 percent. Among the 90 allied scientists invited to participate in 2014, surveys were completed by 37 individuals, for a response rate of 41 percent. (Again, allied scientists in key RosBREED project roles were excluded from the sample.) In both surveys, the sample size for particular questions varied because some participants did not answer all questions.

Crop and Cultivar Focus

Respondents were asked which crop groups they work with and which cultivar types are the focus of their work. Table 2 displays the percentage of each group that reported working with particular crops.

In both 2010 and 2014 the crops receiving the most attention from breeders were peach/nectarine, raspberry/blackberry, strawberry, and apple, with fewer breeders reporting that they worked on almond, pear, sweet cherry or tart cherry. Breeders were also asked about “other Rosaceae” crops and “other plants.” In response to these open-ended questions, several reported working on plums and apricots, rose and other ornamentals, grapes, blueberries, and other crops. The pattern among allied scientists was similar, with the exception that almost 60 percent of allied scientists in both 2010 and 2014 reported working on apple (more than twice the rate of apple crop focus reported by breeders).

The survey included questions about whether participants’ programs focused on scion or rootstock production, and whether focal cultivars were intended for the fresh market or the processing market. Table 3 displays these findings. A majority of breeders and allied scientists reported working on scion production. Among allied scientists, about half also reported working on rootstock production; in contrast, 20 percent of breeders in 2010 and 25 percent in 2014 reported working on rootstock.

In both surveys, 80 percent or more of breeders and 60 percent or more of allied scientists reported working on crops produced for fresh market sales, while fewer than half reported working on crops destined for the processed food market.

Table 2. Rosaceous crops addressed by respondents' breeding programs

Crop group:	Proportion of respondents (percent) working with each crop group:			
	Breeder		Allied Scientists	
	2010	2014	2010	2014
Apple	17 %	25	58	57
Peach, Nectarine	31	35	38	27
Strawberry	29	28	27	38
Tart Cherry	3	2	12	5
Sweet Cherry	11	22	32	11
Raspberry, Blackberry	31	25	22	24
Pear	6	15	18	11
Almond	11	18	5	3
Other Rosaceae	26 ¹	28 ¹	15 ²	22 ²

Note. Respondents could mark more than one crop group, so proportions do not sum to 100 percent.

1. Other crops noted by breeders in 2010 included "various landscape species," "blueberry, *Actinidia arguta*, *Schisandra chinensis*," "rose," "apricot, plum, table grape," "rootstock, apricot," "plum, apricot, interspecifics," "plum," "apricot," "apricots and plums." In 2014, other crops reported by breeders included "plums and apricots," "plum, apricot," "roses," "*Prunus salicina*," "plum," "grapes, blueberries," "*Prunus rootstock*," "Beach plum," "apricot," "blueberry, *Actinidia*," "*Juglans, punics*," "apricot, plum," "grape," "Japanese plums," "blueberry, grape," "apricot," "plum/interspecifics," "rose and other ornamentals."
2. Other crops noted by allied scientists in 2010 included "Rose (landscape)," "apricot, plum," "plum," "European plum/prune," "Apricot, plum," "apricot," "basic physiology," "apricot, almond." In 2014, other crops reported by allied scientists included "prune plum," "Cydonia, *Mespilus*, *Sorbus*, *Amelanchier*," "Saskatooneberries," "plums," "kiwifruit, grape walnut, pistachio, olive, fig, pomegranate, persimmon, mulberry," "ornamentals (woody, bedding and palms)," "ornamental roses," "family-wide phylogenetic studies," "orange," "plums."

Table 3. Cultivar types addressed by respondents' breeding programs

Cultivar type:	Proportion of respondents (percent) working with each cultivar type:			
	Breeder		Allied Scientists	
	2010	2014	2010	2014
Scion	54 %	52	68	62
Rootstock	20	25	53	49
Fresh market	80	85	70	60
Processing market	23	38	43	32

Note. Respondents could mark more than one cultivar type, so proportions do not sum to 100 percent.

Knowledge of Horticulture and Rosaceae Breeding

Participants were asked to report their general background knowledge of several fundamental topics for rosaceous crop breeding, including horticultural crop production, commercial plant propagation, plant genetics and genomics, crop breeding methods, and breeding of five specific crops: apple, peach, strawberry, sweet cherry, and tart cherry. Respondents reported their knowledge level on a scale ranging from “I’ve never heard of this before” to “I’m an expert in this topic and can teach or advise others.” A five-point scale was used in 2010; a six-point scale was used in 2014. Results for breeders are presented in table 4; results for allied scientists are presented in table 5.

Table 4. General knowledge of horticulture and Rosaceae breeding: Breeders

Please circle one number in each row to tell us about your general background related to plant breeding and horticulture		Year	I've never heard of this before	I don't know much about this	I'm familiar with general ideas about this, but not the details	I know a fair amount about this topic	I know a lot about this topic ¹	I'm an expert in this topic and can teach or advise others
A1	Horticultural crop production	2010	-	-	11 %	49	(NA)	40
		2014	-	5	3	18	45	29
A2	Commercial plant propagation	2010	-	-	17	71	(NA)	11
		2014	-	-	8	29	47	16
A3	Plant genetics	2010	-	-	6	43	(NA)	51
		2014	-	-	13	11	21	55
A4	Plant genomics	2010	-	14	31	43	(NA)	11
		2014	-	8	32	26	16	18
A5	Crop breeding: Crossing, selection, and replicated trials	2010	-	-	-	26	(NA)	74
		2014	-	-	3	3	18	76
A6	Apple breeding	2010	-	34	20	31	(NA)	14
		2014	-	19	30	16	14	22
A7	Peach breeding	2010	-	26	31	23	(NA)	20
		2014	-	26	16	18	24	16
A8	Strawberry breeding	2010	-	20	29	23	(NA)	29
		2014	-	21	24	18	13	24
A9	Sweet cherry breeding	2010	-	40	31	20	(NA)	9
		2014	3	29	21	24	13	11
A10	Tart cherry breeding	2010	-	51	31	14	(NA)	3
		2014	3	42	24	24	3	5

Note. N = 35 in 2010 and 40 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response to the item. Row percentages may not add to exactly 100 percent due to rounding.

1. In 2010, the response option “I know a lot about this topic” was not available (NA) in the survey.

With the exception of plant genomics, breeders reported greater background knowledge of these topics than did allied scientists. In both 2010 and 2014, more than 80 percent of breeders reported knowing “a fair amount” or more about horticultural crop production, commercial plant propagation, and plant genetics; 97-100 percent reported the same level of knowledge regarding crop breeding. In contrast, 45 to 77 percent of allied scientists reported comparable levels of background knowledge of these topics. However, about two thirds of allied scientists reported “fair” or stronger knowledge of plant genomics, compared to 54-60 percent of breeders. A third or fewer of the allied scientists reported “fair” or greater knowledge of breeding of specific crops while approximately half of all responding breeders reported “fair” or greater knowledge with regard to apple, peach, and strawberry breeding.

Table 5. General knowledge of horticulture and Rosaceae breeding: Allied scientists

Please circle one number in each row to tell us about your general background related to plant breeding and horticulture		Year	I've never heard of this before	I don't know much about this	I'm familiar with general ideas about this, but not the details	I know a fair amount about this topic	I know a lot about this topic ¹	I'm an expert in this topic and can teach or advise others
A1	Horticultural crop production	2010	-	7 %	25	42	(NA)	26
		2014	-	9	17	29	14	31
A2	Commercial plant propagation	2010	-	14	40	40	(NA)	5
		2014	-	11	34	26	20	9
A3	Plant genetics	2010	-	8	25	42	(NA)	25
		2014	-	3	20	23	31	23
A4	Plant genomics	2010	-	10	28	33	(NA)	28
		2014	-	6	26	21	24	24
A5	Crop breeding: Crossing, selection, and replicated trials	2010	-	12	35	47	(NA)	5
		2014	-	17	26	26	31	-
A6	Apple breeding	2010	-	28	46	25	(NA)	2
		2014	-	31	37	26	6	-
A7	Peach breeding	2010	2	37	39	23	(NA)	-
		2014	-	46	29	14	11	-
A8	Strawberry breeding	2010	4	44	44	9	(NA)	-
		2014	-	47	35	15	3	-
A9	Sweet cherry breeding	2010	2	42	46	10	(NA)	-
		2014	3	51	34	11	-	-
A10	Tart cherry breeding	2010	2	56	39	4	(NA)	-
		2014	3	54	34	9	-	-

Note. N = 57 in 2010 and 37 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response to the item. Row percentages may not add to exactly 100 percent due to rounding.

1. In 2010, the response option “I know a lot about this topic” was not available (NA) in the survey.

Knowledge of Genetic Marker Applications

The 2010 survey included a set of questions that asked participants about their general background or familiarity with technologies and applications related to genetic markers. In order to both shorten and improve the survey, this block of questions was substantially revised for the 2014 survey; four questions were removed, one new question was added, and minor wording changes were made in another. For both surveys, respondents reported their knowledge level on a scale ranging from “*I’ve never heard of this before*” to “*I’m an expert in this topic and can teach or advise others*,” a five-point scale was used in 2010, and an expanded six-point scale was used in 2014. The questions and response frequencies are reported in table 6 for breeders and in table 7 for allied scientists.

In 2010, eight items in this module (currently labeled B1 through B6, B8 and B9) were averaged to form a scale score. Internal reliability for the scale was .95 (coefficient alpha) among breeders and .96 among allied scientists. The mean scale score for breeders was 3.57 (SD=.79) with a range of 2.25 to 4.88. For allied scientists, the mean scale score was 3.32 (SD=.88) with a range of 1.63 to 5.00. The scale score difference between breeders and allied scientists was not statistically significant. However, for most of the topics, more than 50 percent of breeders reported knowing “a fair amount” or being an expert who “can teach or advise others,” while allied scientists were less likely than breeders to report similar levels of background knowledge. This pattern was reversed for the topic of “current genetic marker technologies,” for which 14 percent of breeders and 37 percent of allied scientists reported knowing “a fair amount” or being an expert who “can teach or advise others.”

In 2014, participants were asked a partially different set of questions and offered a larger set of response options, so a new scale score was constructed based on the new set of five questions. Internal reliability for the new scale was .97 (coefficient alpha) among breeders and .92 among allied scientists. The mean scale score for breeders was 4.37 (SD=1.21) with a range of 2.00 to 6.00. For allied scientists, the mean scale score was 4.06 (SD=.99) with a range of 2.20 to 6.00. The scale score difference between breeders and allied scientists was not statistically significant, and the pattern of answers was very similar for breeders and allied scientists. For both groups, 59 percent or more reported knowing “a fair amount” or more about all the topics.

In an analysis of just the top two scale points, breeders were more likely to respond that they “know a lot about this topic” or are experts who “can teach or advise others” for several topics: genetic marker applications to enhance genetic gain through parent and seedling selection (44 percent for breeders vs. 26 percent for allied scientists), genetic marker applications to enhance program efficiency or accuracy through parent and seedling selection (49 percent for breeders vs. 27 percent for allied scientists), and genetic marker applications for identity and relatedness (56 percent for breeders vs. 37 percent for allied scientists).

Table 6. General knowledge of genetic marker applications: Breeders

Please circle one number in each row to tell us about your background or familiarity with genetic markers, applications, and technologies as related to breeding:		Year	I've never heard of this before	I don't know much about this	I'm familiar with general ideas about this, but not the details	I know a fair amount about this topic	I know a lot about this topic ¹	I'm an expert in this topic and can teach or advise others
			1	2	3	4	5	6
B1	DNA-based genetic markers	2010	-	3 %	31	40	(NA)	26
		2014	-	5	21	26	21	28
B2	Genetic marker types (e.g. RFLP, AFLP, SSR, RAPD, SCAR, CAPS, indel, SNP)	2010	-	9	34	37	(NA)	20
		2014	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
B3	Current genetic marker technologies (e.g., ABI, LiCOR, GoldenGate, Solexa)	2010	6	37	43	14	(NA)	-
		2014	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
B4	Genetic marker applications in research (e.g., QTL identification, genetic diversity analysis, association genetics)	2010	-	20	29	40	(NA)	11
		2014	-	5	36	23	13	23
B5	Genetic marker applications in plant breeding (marker-assisted breeding)	2010	-	3	34	31	(NA)	31
		2014	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
B6	Genetic marker applications to enhance genetic gain (parent and seedling selection)	2010	-	14	34	34	(NA)	17
		2014	-	5	28	23	21	23
B7	Genetic marker applications to enhance program efficiency or accuracy (parent and seedling selection)	2010	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
		2014	-	5	26	21	21	28
B8	Selection for a QTL in a breeding program	2010	3	20	26	37	(NA)	14
		2014	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
B9 ²	Genetic marker applications for diagnostics (e.g., cultivar identification, parentage verification/ deduction, DNA fingerprinting of advanced selections)	2010	-	-	31	34	(NA)	34
	Genetic marker applications for identity and relatedness (e.g., cultivar identification, parentage verification/ deduction, DNA fingerprinting of advanced selections, understanding genetic relatedness among breeding material)	2014	-	3	28	13	23	33
B10	Other genetic marker applications in breeding ³	2010	20	20	40	20	(NA)	-
		2014	-	30	5	20	25	20

Note. N = 35 in 2010 and 40 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response to the item. Row percentages may not add to exactly 100 percent due to rounding. Question B7 was new in 2014; questions B2, B3, B5 and B8 were discontinued in 2014 (NA).

1. In 2010, the response option "I know a lot about this topic" was not available (NA) in the survey; a value of 5 was assigned to "I'm an expert..."
2. Note minor differences in the wording of this question in 2014 vs. 2010.
3. In 2010, five people noted "other" marker applications but only one provided details: "Detection of viruses and other pathogens in stock material." In 2014, 30 breeders noted "other" marker applications and eight provided details: "confirm pollinator success," "effect on breeding," "epigenetics," "gene expression markers," "genetic markers for gene introgression," "index selection," "screening for simple dominant genes," "to identify sources of disease resistance."

Table 7. General knowledge of genetic marker applications: Allied scientists

Please circle one number in each row to tell us about your background or familiarity with genetic markers, applications, and technologies as related to breeding:		Year	I've never heard of this before	I don't know much about this	I'm familiar with general ideas about this, but not the details	I know a fair amount about this topic	I know a lot about this topic ¹	I'm an expert in this topic and can teach or advise others
			1	2	3	4	5	6
B1	DNA-based genetic markers	2010	-	10 %	30	40	(NA)	19
		2014	-	3	20	37	20	20
B2	Genetic marker types (e.g. RFLP, AFLP, SSR, RAPD, SCAR, CAPS, indel, SNP)	2010	2	10	35	33	(NA)	19
		2014	-	(NA)	(NA)	(NA)	(NA)	(NA)
B3	Current genetic marker technologies (e.g., ABI, LiCOR, GoldenGate, Solexa)	2010	5	30	28	30	(NA)	7
		2014	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
B4	Genetic marker applications in research (e.g., QTL identification, genetic diversity analysis, association genetics)	2010	1	23	32	26	(NA)	18
		2014	-	11	23	26	26	14
B5	Genetic marker applications in plant breeding (marker-assisted breeding)	2010	-	14	42	32	(NA)	12
		2014	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
B6	Genetic marker applications to enhance genetic gain (parent and seedling selection)	2010	4	28	37	25	(NA)	7
		2014	-	6	26	43	20	6
B7	Genetic marker applications to enhance program efficiency or accuracy (parent and seedling selection)	2010	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
		2014	-	9	32	32	21	6
B8	Selection for a QTL in a breeding program	2010	2	30	39	23	(NA)	7
		2014	(NA)	(NA)	(NA)	(NA)	(NA)	(NA)
B9 ²	Genetic marker applications for diagnostics (e.g., cultivar identification, parentage verification/ deduction, DNA fingerprinting of advanced selections)	2010	2	21	30	30	(NA)	18
	Genetic marker applications for identity and relatedness (e.g., cultivar identification, parentage verification/ deduction, DNA fingerprinting of advanced selections, understanding genetic relatedness among breeding material)	2014	-	6	31	26	20	17
B10	Other genetic marker applications in breeding ³	2010	15	31	19	19	(NA)	15
		2014	17	17	17	28	6	17

Note. N = 57 in 2010 and 37 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response to the item. Row percentages may not add to exactly 100 percent due to rounding. Question B7 was new in 2014; questions B2, B3, B5 and B8 were discontinued in 2014 (NA).

1. In 2010, the response option "I know a lot about this topic" was not available (NA) in the survey; a value of 5 was assigned to "I'm an expert..."
2. Note minor differences in the wording of this question in 2014 vs. 2010.
3. In 2010, 26 people responded to this item but only 8 provided details: "Determining parentage," "Development of genetic markers," "Candidate gene mapping," "Disease resistance," "Disease resistance links," "Intra-specific phylogenetics, diversity analysis genetic structure, signatures of adaptation," "Domestication, wild species diversity, core collections," and "Functional DNA marker based on the functionally characterized genes in a pathway and the association with a trait." In 2014, 17 people noted "other" marker applications and five provided details: "candidate gene approaches," "disease resistance screening," "gene-specific functional markers," "phylogenetic analysis," "population structure of CWR."

Familiarity With Marker-Assisted Plant Breeding

Module C of the survey included questions about participants' prior exposure to the general concepts of marker-assisted plant breeding. Respondents were asked to report their general familiarity with marker-assisted breeding by rating their agreement with a series of statements using a scale ranging from 1 (*“Strongly disagree”*) to 6 (*“Strongly agree”*). The questions and response frequencies are reported in table 8 for breeders and in table 9 for allied scientists.

Questions C1, C2, C6 and C7 were averaged to form a scale score, after reverse-scoring the scale for question C6. The scale had good internal reliability; in 2010, reliability was .87 (coefficient alpha) among breeders and .82 among allied scientists; in 2014, reliability was .70 (coefficient alpha) among breeders and .67 among allied scientists.

In 2010, the mean scale score for breeders was 5.21 (SD=1.09) with a range of 1.25 to 6.0. The mean scale score for allied scientists was 4.93 (SD=1.00) with a range of 2.50 to 6.00. The difference between the two groups was not statistically significant.

In 2014, the mean scale score for breeders was 5.33 (SD=0.75) with a range of 3.50 to 6.00. The mean scale score for allied scientists was 5.06 (SD=0.91) with a range of 2.50 to 6.00. The difference between the two groups was not statistically significant.

Scale scores were available for 24 breeders and 26 allied scientists who completed the same survey questions in both 2010 and 2014. The mean score among these breeders was 5.27 in 2010 and 5.50 in 2014 (SDs = 1.14 and 0.76). The mean score among allied scientists who completed surveys in both years was 5.00 in 2010 and 4.97 in 2014 (SDs = 0.90 and 0.90). The difference in scores between 2010 and 2014 was not statistically significant for either group. Further details of the statistical comparisons can be found in the section on Scale Development.

In both 2010 and 2014, breeders and allied scientists on average endorsed “moderate agreement” with the items on this scale that ask about their familiarity with marker-assisted plant breeding.

Questions C3, C4, and C5 were included in order to gauge the extent to which participants' conceptualizations of marker-assisted breeding were limited to research uses, marker-assisted seedling screening (MASS), or had broadened to include other applications such as marker-assisted parent selection (MAPS). Although the percentage of responses linking marker applications with seedling screening was slightly higher in 2014 than in 2010, the recognition of parent selection applications was also higher in 2014 than in 2010, and the percentage who mostly linked marker methods to research (i.e., not to practical breeding operations) was lower in 2014 than in 2010.

Table 8. Familiarity with marker assisted plant breeding: Breeders

Please circle one number in each row to indicate how much you disagree or agree with each of the following statements. Please read each statement carefully; some are worded positively, others negatively		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
C1	I've heard or read a lot about marker-assisted selection, marker-assisted breeding, and other genetic marker methods	2010	3 %	3	3	9	24	58
		2014	-	-	-	13	18	68
C2	I'm familiar with the general concepts of marker-assisted selection and marker-assisted breeding methods	2010	-	3	-	21	12	64
		2014	-	-	-	8	29	63
C3	When I think of "marker-assisted breeding", high-throughput culling at the seedlings stage (i.e., marker-assisted seedling selection) is what mostly comes to mind	2010	3	6	9	21	30	30
		2014	5	5	5	18	42	24
C4	When I think of "marker-assisted breeding", breeding applications other than seedling selection are what mostly come to mind	2010	6	24	21	18	24	6
		2014	5	5	34	21	26	8
C5	When I think of "marker-assisted breeding", use in research studies is what mostly comes to mind	2010	15	9	12	39	24	-
		2014	5	13	18	34	21	8
C6	I really haven't had much exposure to genetic marker methods.	2010	54	18	-	12	6	9
		2014	50	11	11	8	16	5
C7	I understand the difference between genotyping and traditional phenotyping for plant selection purposes	2010	3	-	-	6	18	73
		2014	-	-	-	3	29	68

Note. N = 33 in 2010 and 40 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response to the item. Row percentages may not add to exactly 100 percent due to rounding.

Table 9. Familiarity with marker assisted plant breeding: Allied scientists

Please circle one number in each row to indicate how much you disagree or agree with each of the following statements. Please read each statement carefully; some are worded positively, others negatively		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
C1	I've heard or read a lot about marker-assisted selection, marker-assisted breeding, and other genetic marker methods	2010	4 %	2	-	26	33	35
		2014	3	9	-	14	34	40
C2	I'm familiar with the general concepts of marker-assisted selection and marker-assisted breeding methods	2010	2	-	7.0	10	40	40
		2014	-	3	6	9	29	54
C3	When I think of "marker-assisted breeding", high-throughput culling at the seedlings stage (i.e., marker-assisted seedling selection) is what mostly comes to mind	2010	5	14	5	19	42	14
		2014	3	-	14	17	40	26
C4	When I think of "marker-assisted breeding", breeding applications other than seedling selection are what mostly come to mind	2010	10	19	26	25	16	4
		2014	3	17	31	20	29	-
C5	When I think of "marker-assisted breeding", use in research studies is what mostly comes to mind	2010	9	14	23	26	21	7
		2014	6	11	26	34	17	6
C6	I really haven't had much exposure to genetic marker methods.	2010	33	26	12	9	14	5
		2014	40	23	9	11	11	6
C7	I understand the difference between genotyping and traditional phenotyping for plant selection purposes	2010	-	4	5	4	32	56
		2014	3	-	-	3	23	71

Note. N = 57 in 2010 and 37 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response to the item. Row percentages may not add to exactly 100 percent due to rounding.

Attitude Toward Marker-Assisted Breeding

Participants were asked a set of questions about their attitude toward the integration of genetic markers into plant breeding programs and related scientific efforts for crop improvement. Respondents were asked to rate their agreement with a series of attitude statements using a scale ranging from 1 (“*Strongly disagree*”) to 6 (“*Strongly agree*”). The questions and response frequencies are reported in table 10 for breeders and in table 11 for allied scientists.

In 2010, some questions referred explicitly to “my breeding program” or were otherwise worded as if respondents worked directly in or with a plant breeding program. Despite instructions in the survey invitation to allied scientists about this issue, asking them to respond in view of their work with breeding programs, some of the allied scientists did not find these questions applicable to themselves, and either skipped some questions or stopped taking the survey at this point. The sample size for allied scientists in 2010 was thus smaller for survey sections D through G than for earlier sections. In 2014, in addition to the clarifying information in the invitation to allied scientists, the phrase “or breeding-allied scientific work” was added to many of the survey questions to clarify that these questions were also intended to apply to allied scientists. Three new questions were also added in 2014 (currently labeled D2 through D4).

Responses to all questions present in both 2010 and 2014 in this survey module were averaged to form a scale score for each person, after reversing-scoring the scale for questions that were negatively worded.

In 2010, among breeders, internal reliability for the scale was .94 (coefficient alpha) and the mean scale score was 4.52 (SD=1.12) with a range of 1.57 to 5.93. Among allied scientists, internal reliability for the scale was .88 and the mean scale score was 4.87 (SD=0.75) with a range of 3.14 to 6.00. The scale score difference between the two groups was not statistically significant.

In 2014, scale scores were calculated using the same set of 13 items that had been used in 2010. Among breeders, internal reliability for the scale was .87 (coefficient alpha) and the mean scale score was 4.80 (SD=0.73) with a range of 3.36 to 5.86. Among allied scientists, internal reliability for the scale was .78 and the mean scale score was 4.89 (SD=0.55) with a range of 3.43 to 5.93. The scale score difference between the two groups was not statistically significant.

Scale scores were available for 24 breeders and 24 allied scientists who completed the same survey questions in both 2010 and 2014. The mean score among these breeders was 4.63 in 2010 and 4.90 in 2014 (SDs = 0.99 and 0.70). The mean score among allied scientists who completed surveys in both years was 4.94 in both 2010 and 2014 (SDs = 0.81 and 0.59). The difference in scores between 2010 and 2014 was not statistically significant for allied scientists, but the change from 2010 to 2014 was significant for breeders, $t_{(23)} = 2.323$, $p = .029$. Further details of the statistical comparisons can be found in the section on Scale Development.

Table 10. Attitude toward marker-assisted breeding: Breeders

Please circle one number in each row to indicate how much you disagree or agree with each of the following statements. Please read each statement carefully; some are worded positively, others negatively.		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
			D1	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work become much more efficient	2010	6 %	6	6
		2014	-	3	6	14	36	42
D2	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work become much more accurate	2014	-	-	6	19	33	42
D3	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work become much more creative	2014	3	6	3	36	28	25
D4	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work proceed more quickly	2014	-	3	6	17	42	33
D5	Marker-assisted breeding won't do much to improve plant breeding programs	2010	34	31	19	9	6	-
		2014	53	22	17	-	6	3
D6	Knowledge of the function of genes is crucial to the future success of my breeding program or breeding-allied scientific work	2010	16	6	6	22	34	16
		2014	6	14	8	33	25	14
D7	I'm very excited about the potential for genetic markers to help plant breeding/research programs like mine	2010	6	9	-	19	22	44
		2014	-	-	3	28	19	50
D8	Genetic marker assistance approaches will dramatically improve horticulture and agriculture in general	2010	-	9	3	34	34	19
		2014	-	6	6	19	42	28
D9	I look forward to implementing genetic markers more in my work	2010	12	-	6	16	16	50
		2014	-	-	6	31	8	56
D10	Marker-assisted breeding is the most promising current avenue for crop improvement	2010	19	12	19	12	22	16
		2014	6	14	17	11	31	22
D11	More knowledge about the genetic control of important traits is a top priority for the development of marker-assisted breeding	2010	7	7	10	13	40	23
		2014	-	3	8	28	36	25
D12	More knowledge about the distribution of important traits in breeding germplasm is a top priority for the development of marker-assisted breeding	2010	-	12	3	25	34	25
		2014	-	6	6	22	39	28
D13	More knowledge about linkage of markers for one trait with other traits (i.e., linkage drag or correlated response to selection) is a top priority for the development of marker-assisted breeding	2010	-	6	-	36	36	23
		2014	-	-	6	14	39	42
D14	Development of practical implementation protocols for marker-assisted breeding is a top priority for the development of marker-assisted breeding	2010	-	7	-	13	33	47
		2014	-	-	3	19	22	56
D15	My organization will benefit from investment in research and development in the field of marker-assisted breeding	2010	10	-	3	17	30	40
		2014	-	-	11	28	14	47
D16	It's very important that we make sure our breeding program or breeding-allied scientific work is structured to efficiently use marker-assisted methods.	2010	16	-	6	26	13	39
		2014	3	8	8	17	33	31
D17	Use of genetic markers routinely in my breeding program or breeding-allied scientific work would probably require too much restructuring of current operations to have a significant impact on breeding efficiency	2010	19	28	19	22	6	6
		2014	33	17	19	11	17	3

Note. Sample size ranged from 30 to 32 in 2010; N=36 in 2014 for these questions. Questions D2-D4 were added in 2014. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to exactly 100 percent due to rounding.

Table 11. Attitude toward marker-assisted breeding: Allied scientists

Please circle one number in each row to indicate how much you disagree or agree with each of the following statements. Please read each statement carefully; some are worded positively, others negatively.		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
			D1	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work become much more efficient	2010	3 %	-	6
		2014	3	-	3	24	18	52
D2	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work become much more accurate	2014	3	-	9	21	27	39
D3	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work become much more creative	2014	3	-	12	21	27	36
D4	Genetic markers have great potential for helping my breeding program or breeding-allied scientific work proceed more quickly	2014	3	3	3	18	21	52
D5	Marker-assisted breeding won't do much to improve plant breeding programs	2010	43	28	20	4	6	-
		2014	55	27	12	6	-	-
D6	Knowledge of the function of genes is crucial to the future success of my breeding program or breeding-allied scientific work	2010	3	11	14	14	14	43
		2014	3	6	3	18	24	45
D7	I'm very excited about the potential for genetic markers to help plant breeding/research programs like mine	2010	2	-	5	15	29	49
		2014	3	-	3	18	30	45
D8	Genetic marker assistance approaches will dramatically improve horticulture and agriculture in general	2010	-	2	10	26	24	39
		2014	-	-	12	24	24	39
D9	I look forward to implementing genetic markers more in my work	2010	-	-	5	28	25	42
		2014	6	15	6	27	24	21
D10	Marker-assisted breeding is the most promising current avenue for crop improvement	2010	4	6	20	34	28	8
		2014	3	6	12	42	24	12
D11	More knowledge about the genetic control of important traits is a top priority for the development of marker-assisted breeding	2010	-	-	4	24	33	39
		2014	-	-	6	12	39	42
D12	More knowledge about the distribution of important traits in breeding germplasm is a top priority for the development of marker-assisted breeding	2010	-	-	12	23	31	33
		2014	-	-	-	18	52	30
D13	More knowledge about linkage of markers for one trait with other traits (i.e., linkage drag or correlated response to selection) is a top priority for the development of marker-assisted breeding	2010	-	-	4	37	31	29
		2014	-	-	-	9	61	30
D14	Development of practical implementation protocols for marker-assisted breeding is a top priority for the development of marker-assisted breeding	2010	-	-	6	31	29	35
		2014	-	-	-	12	61	27
D15	My organization will benefit from investment in research and development in the field of marker-assisted breeding	2010	-	-	15	21	26	38
		2014	-	6	6	24	21	42
D16	It's very important that we make sure our breeding program or breeding-allied scientific work is structured to efficiently use marker-assisted methods.	2010	-	-	14	23	26	37
		2014	-	3	6	27	27	36
D17	Use of genetic markers routinely in my breeding program or breeding-allied scientific work would probably require too much restructuring of current operations to have a significant impact on breeding efficiency	2010	26	26	29	13	6	-
		2014	24	30	21	15	6	3

Note. In 2010, sample size was 31 for question D14, 33 for D1, 35 for D3, 40 for D6, 43 for D13, 47 to 51 for all other questions. In 2014 N=33. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to 100 percent due to rounding.

Self-Efficacy for Use of Markers

Module E of the survey included questions about participants' self-efficacy for the use of marker-assisted methods in plant breeding or allied sciences. Self-efficacy is similar to the concept of "confidence," and self-efficacy scales emphasize questions that ask people to predict their actual performance of particular tasks or skills. Respondents were asked to report their self-efficacy for the use of marker-assisted methods by rating their agreement with a series of statements using a scale ranging from 1 (*"Strongly disagree"*) to 6 (*"Strongly agree"*). The questions and response frequencies are reported in table 12 for breeders and in table 13 for allied scientists.

All questions in this survey module were averaged to form a scale score, after reversing the scale for question E5. In 2010, among breeders, internal reliability for the scale was .91 (coefficient alpha) and the mean scale score was 3.87 (SD=1.34) with a range of 1.00 to 6.00. Among allied scientists, internal reliability for the scale was .93 and the mean scale score was 3.91 (SD=1.51) with a range of 1.00 to 6.00. The scale score difference between the two groups was not statistically significant.

In 2014, among breeders, internal reliability for the scale was .95 (coefficient alpha) and the mean scale score was 3.94 (SD=1.60) with a range of 1.17 to 6.00. Among allied scientists, internal reliability for the scale was .92 and the mean scale score was 3.87 (SD=1.36) with a range of 1.17 to 6.00. The scale score difference between the two groups was not statistically significant.

Scale scores were available for 24 breeders and 19 allied scientists who completed the same survey questions in both 2010 and 2014. The mean score among these breeders was 3.96 in 2010 and 4.26 in 2014 (SDs = 1.42 and 1.53). The mean score among allied scientists who completed surveys in both years was 3.68 in 2010 and 4.07 in 2014 (SDs = 1.35 and 1.22). The difference in scores between 2010 and 2014 was not statistically significant for either group. Further details of the statistical comparisons can be found in the section on Scale Development.

Breeders and allied scientists on average endorsed "slight agreement" with the items on this scale, which focus on their self-efficacy for use of (self-perceived ability to perform) marker-assisted methods in plant breeding and plant sciences.

Table 12. Self-efficacy for use of genetic markers in breeding: Breeders

Please read each statement carefully; some are worded positively, others negatively. Please circle one number in each row:		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
E1	It's clear to me what specific steps to take in order to apply knowledge of genetic markers in my organization.	2010	7 %	7	20	20	27	20
		2014	11	3	19	17	25	25
E2	I understand how to change my breeding program in order to more effectively incorporate marker-assisted methods.	2010	7	7	17	27	20	23
		2014	3	8	19	22	19	28
E3	I have the training and skills required to include marker-assisted selection or breeding methods in my work.	2010	10	10	13	23	20	23
		2014	11	14	17	11	22	25
E4	I'm very confident about my own ability to use genomic information when making plant selection or breeding decisions.	2010	10	20	13	17	23	17
		2014	14	17	11	11	17	31
E5	At this point I'm not sure about my ability to apply genetic marker applications correctly in my work situation.	2010	27	20	10	27	10	7
		2014	33	11	6	19	19	11
E6	I am able to teach others how to apply genetic marker-assisted methods in horticultural breeding and production operations.	2010	23	27	7	13	23	7
		2014	28	19	6	6	11	31

Note. N = 30 in 2010 and 40 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to 100 percent due to rounding.

Table 13. Self-efficacy for use of genetic markers in breeding: Allied scientists

Please read each statement carefully; some are worded positively, others negatively. Please circle one number in each row:		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
E1	It's clear to me what specific steps to take in order to apply knowledge of genetic markers in my organization.	2010	3 %	13	10	18	33	23
		2014	3	3	20	27	23	23
E2	I understand how to change my breeding program in order to more effectively incorporate marker-assisted methods.	2010	-	17	21	38	12	12
		2014	3	3	17	23	33	20
E3	I have the training and skills required to include marker-assisted selection or breeding methods in my work.	2010	15	21	6	21	12	24
		2014	13	10	13	17	27	20
E4	I'm very confident about my own ability to use genomic information when making plant selection or breeding decisions.	2010	12	23	6	15	23	21
		2014	10	34	3	10	21	21
E5	At this point I'm not sure about my ability to apply genetic marker applications correctly in my work situation.	2010	27	20	20	7	12	15
		2014	31	28	7	10	17	7
E6	I am able to teach others how to apply genetic marker-assisted methods in horticultural breeding and production operations.	2010	33	10	8	20	13	15
		2014	41	14	3	17	17	7

Note. In 2010, N = 39 for E1, 24 for E2, 33 for E3, 34 for E4, 41 for E5, 39 for E6. In 2014 N=30 or 29. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to exactly 100 percent due to rounding.

Program Use of Marker-Assisted Methods

Participants were asked a set of questions about their actual use of marker-assisted methods in breeding programs or related scientific work. Respondents were asked to rate their agreement with a series of statements using a scale ranging from 1 (*“Strongly disagree”*) to 6 (*“Strongly agree”*). The questions and response frequencies are reported in table 12 for breeders and in table 13 for allied scientists. Questions F1 to F9 were averaged to form a scale score, after reversing the scale for questions F2 and F4.

Three minor wording changes to these questions were made in 2014. The phrase “this year” in several of the 2010 questions was changed to “in 2014.” Question F9 was rephrased to clarify that “genetic marker diagnostics” in the 2010 version was intended to mean “use of genetic markers for verifying or understanding germplasm identity or relatedness.” The phrase “or breeding-allied scientific work” was added to several survey questions to clarify that these questions were intended to apply to allied scientific work as well as breeding program operations.

In 2010, for breeders, internal reliability for the scale was .91 (coefficient alpha) and the mean scale score was 3.19 (SD=1.60) with a range of 1.00 to 5.89. This represents “slight disagreement” with the survey statements about use of marker-assisted methods in breeding programs. Among allied scientists, internal reliability for the scale was .87 and the mean scale score was 3.82 (SD=1.46) with a range of 1.14 to 6.00. This represents “slight agreement” with the survey statements about use of marker-assisted methods. The scale score difference between the two groups was not statistically significant.

In 2014, for breeders, internal reliability for the scale was .93 (coefficient alpha) and the mean scale score was 3.62 (SD=1.56) with a range of 1.11 to 6.00. This represents “slight agreement” with the survey statements about use of marker-assisted methods in breeding programs. Among allied scientists, internal reliability for the scale was .91 and the mean scale score was 3.58 (SD=1.46) with a range of 1.33 to 5.56. This represents “slight agreement” with the survey statements about use of marker-assisted methods. The scale score difference between the two groups was not statistically significant.

Scale scores were available for 24 breeders and 20 allied scientists who completed the same survey questions in both 2010 and 2014. The mean score among these breeders was 3.49 in 2010 and 4.13 in 2014 (SDs = 1.61 and 1.57). The mean score among allied scientists who completed surveys in both years was 3.75 in 2010 and 3.79 in 2014 (SDs = 1.48 and 1.36). The difference in scores between 2010 and 2014 was not statistically significant for allied scientists, but the change from 2010 to 2014 was significant for breeders, $t_{(23)} = 2.909$, $p = .008$. Further details of the statistical comparisons can be found in the section on Scale Development.

Table 14. Use of marker-assisted methods: Breeders

Please circle one number in each row:		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
F1	Genetic marker information will be included this year in how my organization addresses plant breeding and selection.	2010	37 %	3	7	17	13	23
		2014	19	14	8	14	14	31
F2	I don't believe it will be possible this year to use genetic marker tools or information in my work situation.	2010	33	10	20	-	13	23
		2014	44	8	11	8	14	14
F3	We are changing how our breeding program or allied scientific work is structured in order to more efficiently use marker-assisted selection.	2010	32	19	3	19	16	10
		2014	17	17	6	28	25	8
F4	I haven't tried to use marker-assisted selection, breeding, or other genetic marker tools or information in my own work.	2010	36	19	6	3	10	26
		2014	39	8	17	6	14	17
F5	I personally use genetic marker information resources routinely in my work.	2010	39	13	10	13	10	16
		2014	31	19	3	14	11	22
F6	My organization uses genetic marker information regularly in our work.	2010	23	10	7	20	13	27
		2014	26	20	-	9	20	26
F7	Marker-assisted parent selection will be included this year in my breeding program or breeding-allied scientific work.	2010	55	6	-	6	10	23
		2014	22	25	3	8	11	31
F8	Marker-assisted seedling selection will be included this year in my breeding program or breeding-allied scientific work.	2010	52	16	-	10	6	16
		2014	39	19	8	3	14	17
F9	Genetic marker diagnostics will be included this year in my breeding program	2010	45	10	3	6	13	23
	Use of genetic markers for verifying or understanding germplasm identity or relatedness will be included in my breeding program or breeding-allied scientific work in 2014	2014	22	8	3	22	14	31
F10 ¹	Other marker-assisted breeding applications will be included this year in my breeding program or breeding-allied scientific work. (Please specify)	2010	71	14	-	-	-	14
		2014	38	17	13	4	8	21

Note. N = 30 or 31 in 2010 and 36 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to exactly 100 percent due to rounding. In 2014 the phrase "this year" was replaced with "in 2014."

1. In 2010, 14 people responded to this question, but only 2 noted specific applications: "Proof-of-concept for MAB for rose black spot" and "Confidential." In 2014, 24 people responded and five noted specific applications: "assessing genetic consequences of inbreeding," "epigenetics, gene introgression," "index selection," "pathogen characterization," "trueness to type testing of propagated material for release."

Table 15. Use of marker-assisted methods: Allied scientists

Please circle one number in each row:		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
F1	Genetic marker information will be included this year in how my organization addresses plant breeding and selection.	2010	12 %	12	12	15	21	27
		2014	14	18	-	7	36	25
F2	I don't believe it will be possible this year to use genetic marker tools or information in my work situation.	2010	28	16	25	9	9	12
		2014	43	18	4	21	14	-
F3	We are changing how our breeding program or allied scientific work is structured in order to more efficiently use marker-assisted selection.	2010	12	20	16	24	16	12
		2014	18	25	14	14	21	7
F4	I haven't tried to use marker-assisted selection, breeding, or other genetic marker tools or information in my own work.	2010	33	14	6	14	8	25
		2014	32	11	7	4	21	25
F5	I personally use genetic marker information resources routinely in my work.	2010	44	7	7	7	5	29
		2014	39	4	-	21	18	18
F6	My organization uses genetic marker information regularly in our work.	2010	7	7	5	14	36	31
		2014	14	4	11	21	11	39
F7	Marker-assisted parent selection will be included this year in my breeding program or breeding-allied scientific work.	2010	33	14	10	19	5	19
		2014	46	11	-	25	14	4
F8	Marker-assisted seedling selection will be included this year in my breeding program or breeding-allied scientific work.	2010	29	14	10	19	14	14
		2014	39	14	4	21	14	7
F9	Genetic marker diagnostics will be included this year in my breeding program	2010	25	8	8	25	8	25
	Use of genetic markers for verifying or understanding germplasm identity or relatedness will be included in my breeding program or breeding-allied scientific work in 2014	2014	21	7	4	32	-	36
F10 ¹	Other marker-assisted breeding applications will be included this year in my breeding program or breeding-allied scientific work. (Please specify)	2010	31	23	-	8	15	23
		2014	19	14	14	19	14	19

Note. In 2010 N = 42 for F6, 41 for F5, 36 for F4, 33 for F1, 32 for F2, 25 for F3, 24 for F9, 21 for F7 and F8. In 2014 N=28. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to exactly 100 percent due to rounding. In 2014 the phrase "this year" was replaced with "in 2014."

1. In 2010, 13 people responded to this question but only 5 noted specific applications: "Candidate gene mapping," "Confirmation of parentage," "We are at the stage of identifying markers for peach brown rot resistance. We should know this year if we are successful," "chloroplast DNA diversity assessment," "fingerprinting and phylogeny apps + BSA," and "I don't have a breeding program, but routinely use markers for diversity research applications." In 2014, 21 people responded, and seven noted specific applications: "gene expression markers," "gene-based diversity assessments," "genetic diversity assessment," "locus resequencing," "rapid cycle breeding," "screening for virus resistance using markers," "sequence at candidate loci."

Scale Development

The survey questions were initially pilot tested and refined during spring 2010 before the first survey administration to the Rosaceae breeding community that year. Item analysis was conducted prior to scale construction to insure adequate variation, relatively normal distribution, and moderate correlation with other items.

Prior to the 2014 survey, module B was substantially revised before administration, three new questions were added to module D, and a other few minor wording clarifications were made throughout, as noted in the sections for each survey module.

In both 2010 and 2014, the questions within survey modules B through F were averaged to create scale scores. Some negatively-worded questions were reverse-scored before being included in the scales. Only items C1, C2, C6 and C7 were included in that scale; final questions in some modules asking for “other” responses were not included in the scales. The major revisions in module B make it impossible to directly compare 2010 and 2014 scale scores for those questions. For Scale D, only the 13 questions that were present in both 2010 and 2014 were used for scale score comparisons of those years.

The scales are designed to be sensitive to change over time. They are relatively normally distributed, and have good internal reliability. Each scale ranges from 1 to 6, with higher numbers indicating more of the attribute. Table 16 displays the number of items and internal constancy reliability for each scale. Table 17 displays mean scale score differences between breeders and allied scientists; none of the differences were statistically significant at $p < .05$. Table 18 displays mean scale score change from 2010 to 2014 among those individuals who responded to both surveys; in 2014, breeders reported significantly more positive attitudes toward marker-assisted breeding and significantly more actual use of marker-assisted methods than in 2010.

Table 16. Survey scales, number of items, and reliability

Scale	Topic	Year	Number of items	Reliability (Cronbach's alpha) Breeders, Allied Scientists
B	Knowledge of Genetic Marker Applications. Background and general knowledge of technologies and applications related to genetic markers.	2010	8	.95, .96
		2014	5	.97, .92
C	Familiarity With Marker-Assisted Plant Breeding. Exposure to the general concepts of marker-assisted plant breeding.	2010	7	.87, .82
		2014		.70, .67
D	Attitude Toward the Use of Genetic Markers. Attitude toward the integration of genetic markers into plant breeding programs and related scientific efforts for crop improvement.	2010	13	.94, .88
		2014	13 used for comparison with 2010 (16 available)	.87, .78
E	Self-Efficacy for Use of Markers. Self-efficacy (confidence in personal ability) for using marker-assisted methods in breeding or allied sciences.	2010	6	.91, .93
		2014		.95, .92
F	Actual Use of Marker-Assisted Methods. Actual use of markers in breeding programs or related scientific programs.	2010	9	.91, .87
		2014		.93, .91

Table 17. Mean scale score differences between breeders and allied scientists

Scale	Topic	Year	Breeders		Allied Scientists		Difference	t	p
			Mean	SD	Mean	SD			
B	Knowledge of Genetic Marker Applications	2010	3.57	0.79	3.32	0.88	0.25	1.376	.172
		2014	4.39	1.21	4.06	0.99	0.31	1.214	.229
C	Familiarity With Marker-Assisted Plant Breeding	2010	5.21	1.09	4.93	1.00	0.29	1.269	.208
		2014	5.33	0.75	5.06	0.91	0.27	1.398	.166
D	Attitude Toward the Use of Genetic Markers	2010	4.52	1.12	4.87	.75	-0.35	-1.701	.093
		2014	4.81	0.73	4.89	0.55	-0.08	-0.523	.603
E	Self-Efficacy for Use of Markers	2010	3.87	1.34	3.91	1.51	-0.05	-0.132	.895
		2014	3.94	1.60	3.87	1.36	0.07	0.192	.848
F	Actual Use of Marker-Assisted Methods	2010	3.19	1.60	3.82	1.46	-0.63	-1.761	.082
		2014	3.62	1.56	3.58	1.41	0.04	0.108	.914

Table 18. Change in mean scale scores, 2010 to 2014

Scale	Topic	Group (N)	2010		2014		Difference	t	p
			Mean	SD	Mean	SD			
C	Familiarity With Marker-Assisted Plant Breeding	Breeders (24)	5.27	1.14	5.50	0.76	.23	1.357	.188
		Allied Scientists (26)	5.00	0.90	4.97	0.90	-.03	-0.171	.866
D	Attitude Toward the Use of Genetic Markers	Breeders (24)	4.63	0.99	4.90	0.70	.27	2.323	.029
		Allied Scientists (24)	4.94	0.81	4.94	0.59	.00	0.026	.979
E	Self-Efficacy for Use of Markers	Breeders (24)	3.96	1.42	4.26	1.53	.30	1.447	.161
		Allied Scientists (19)	3.68	1.35	4.07	1.22	.39	1.359	.191
F	Actual Use of Marker-Assisted Methods	Breeders (24)	3.49	1.61	4.13	1.57	.64	2.909	.008
		Allied Scientists (20)	3.75	1.48	3.79	1.36	.04	0.137	.893

Note. Only those who answered survey questions in both 2010 and 2014 are included in these comparisons. Rows in bold font are those in which the change from 2010 to 2014 was statistically significant at $p < .05$.

Interest in and Recommendations for Further Learning About Marker-Assisted Breeding

Survey participants were asked about their interest in further professional development or information resources related to marker-assisted methods, and their recommendations for the content and format of additional training or information. Again, respondents were asked to rate their agreement with a series of statements using a scale ranging from 1 (“*Strongly disagree*”) to 6 (“*Strongly agree*”).

For the section on interest in further learning, the questions and response frequencies are reported in table 19 for breeders and in table 20 for allied scientists. Recommendations from breeders are reported in table 21, and recommendations from allied scientists are displayed in table 22.

In both 2010 and 2014 breeders and allied scientists expressed strong interest in further learning opportunities of all types—professional development sessions on genetic marker methods and uses, printed and online information about markers and marker-assisted breeding, and information about how to change breeding programs to make more effective use of markers.

Themes in the specific content areas that were recommended as topics of further training sessions or information resources are listed below; the number of individuals who made the recommendation is noted in parentheses for each year (2010, 2014). In addition to these themes, some unique recommendations are also included in the tables.

- Available genes, markers, and marker-locus-trait associations in particular crops, and the information and analytic/database tools needed to use them for decision making (9, 10)
- Case studies, site visits to study successful marker-assisted breeding programs (6, 5)
- Pros, cons, availability of different genotyping platforms and services (6, 5)
- Theory, fundamentals, overview of marker applications (5, 5)
- Costs, economic feasibility of marker applications (4, 2)
- Training on laboratory technical details (3, 5)
- Recommended reading lists, literature reviews, textbook (2, 1)
- Software training (2, 5)

Recommendations for the format of additional learning opportunities included the following:

- Web-based resources, webinars, videos, training modules, courses, recorded seminars (23, 21)
- Workshops, hands-on sessions (11, 13)
- Collaboration, touring or training in other labs/programs, visits by experts to other labs to provide presentations and consultation (4, 6)
- Case studies (3, 2)
- Printed materials (3, 5)
- Genome Database for Rosaceae (GDR), but it must be kept up to date (3)
- Visual, graphical presentations of genes and genotypes (2, 1)
- Spreadsheets (2)

Table 19. Interest in further learning: Breeders

Please circle one number in each row:		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
G1	I would like to participate in more training or professional development sessions related to genetic marker uses	2010	10%	3	-	26	23	39
		2014	3	6	6	31	26	29
G2	I would like to participate in more training or professional development sessions related to genetic marker methods	2010	10	3	3	29	23	32
		2014	3	6	9	23	26	34
G3	My organization would benefit if more of our people attended training sessions on marker-assisted breeding	2010	10	3	6	19	23	39
		2014	3	3	8	19	39	28
G4	I am interested in using more printed material, internet resources, and other information sources about genetic markers that I can access on my own schedule	2010	10	3	10	23	16	39
		2014	9	-	17	17	26	31
G5	My organization would benefit if more of our people had access to printed material, internet resources, and other information sources about marker-assisted breeding	2010	10	3	3	23	19	42
		2014	6	3	14	17	31	31
G6	I would like more information on how to change my breeding program or breeding-allied scientific work to more effectively incorporate genetic markers	2010	16	-	-	26	29	29
		2014	3	3	23	29	26	17

Note. N = 31 in 2010 and 35 or 36 in 2014 for these questions. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to exactly 100 percent due to rounding.

Table 20. Interest in further learning: Allied scientists

Please circle one number in each row:		Year	Strongly Disagree	Moderately Disagree	Slightly Disagree	Slightly Agree	Moderately Agree	Strongly Agree
			1	2	3	4	5	6
G1	I would like to participate in more training or professional development sessions related to genetic marker uses	2010	5%	18	8	18	28	25
		2014	17	17	3	23	23	17
G2	I would like to participate in more training or professional development sessions related to genetic marker methods	2010	8	12	8	15	38	20
		2014	17	17	7	20	23	17
G3	My organization would benefit if more of our people attended training sessions on marker-assisted breeding	2010	3	3	3	43	43	6
		2014	10	7	3	30	30	20
G4	I am interested in using more printed material, internet resources, and other information sources about genetic markers that I can access on my own schedule	2010	2	5	5	30	18	40
		2014	13	7	10	20	33	17
G5	My organization would benefit if more of our people had access to printed material, internet resources, and other information sources about marker-assisted breeding	2010	8	5	-	32	32	22
		2014	7	13	7	30	20	23
G6	I would like more information on how to change my breeding program or breeding-allied scientific work to more effectively incorporate genetic markers	2010	-	13	9	26	30	22
		2014	17	13	7	27	20	17

Note. In 2010, N = 40 except for question G3 (N=35), and G6 (N=23). In 2014, N = 30. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not add to exactly 100 percent due to rounding.

Table 21. Recommendations for future learning opportunities: Breeders

G8	What kind of additional training or information about marker-assisted breeding would be most helpful to you or your organization?
<p>2010:</p> <ul style="list-style-type: none"> ▪ Cheap genotyping in the breeding program - how to gain the most information about genotypes without going bankrupt. ▪ Instruction in PediMap and FlexQTL. ▪ Primarily technical training on implementation plus some fundamentals on the theory. ▪ Practical utilization of MLT associations in a breeding program. ▪ Laboratory technique details; software training (MapQTL, JoinMap, etc.) ▪ It is all about becoming cost effective for very specialized or minor crops. How to pony-tail w/ other efforts. ▪ Cost will be a determining factor - so estimates of funds and equipment needed is important. ▪ Current list of genes or QTLs available for MAB ▪ Need summarized information on the markers available and the analytical tools/data needed to use them. ▪ Observe another breeding program that has incorporated MAB successfully into their program. I need to see the logistics, time, space and economic resources that are necessary. ▪ MLT associations available in my crop. Knowledge of robustness of those associations. Institutions or businesses that will do genotyping. ▪ Training of lab technicians to develop molecular markers. ▪ Hands-on training. Less hype on 'potential' and more real word experiences, particularly the successes, limitations and failures (and reasons for failure) following investing heavily in this approach. ▪ Not sure. First research i.e. RosBREED has to show me that this approach will work and then we will begin to think more in depth about whether we can afford and how to implement. ▪ Pros and cons of different genotyping platforms. ▪ It would be most helpful to know what/which phenotypes have identified and confirmed as a 100% prediction of i.e., non-melting, low ethylene release (SSR), peentao, nectarine, clingstone, brix levels, flavor profiles....etc. ▪ Readily applicable markers or maps. ▪ Specific information on how robust the markers are - what genetic background have they been examined in - how confident that favorable alleles have been characterized. <p>2014:</p> <ul style="list-style-type: none"> ▪ A new younger brain would be most useful. Time for training is also a constraint. ▪ Access to the diploid strawberry genome sequence. ▪ An intern to teach us how to apply the technology to our breeding program. ▪ Basics in identifying and using markers. ▪ Free access to good computational decision making software. ▪ Hard to say what the 'organization' is. Probably best considered to be the Landscape Nursery Industry. They would benefit most from an explanation of what the technologies could do for them. ▪ How to do QTL analysis, how to use genomic information for choosing parents for crossing, how to use the software programs for doing such work, and also, simply greater understanding of available markers (how to use, advantages and limitations of the different kinds, hands-on how to do, etc.). Most of this has been developed after I finished graduate school and I am remote from universities or other resources to learn the ropes. It is difficult for me to do lengthy sabbaticals or other transfers of work because of spousal employment, etc. ▪ How to incorporate a lot of marker data in making breeding selection decisions or parent selection. ▪ I think at this point we're in a pretty good position when it comes to the technology to implement markers. What we need is more information on the genetics of specific traits, ideally along with effective linked markers. ▪ I would like information as to where I could sent plant tissue of my advanced selections for genotyping. ▪ Important to keep up with new technologies, applications, and knowledge. ▪ Information on the most current marker types and comparison of methods for marker development and gene identification. ▪ Marker conversion and DNA test development. ▪ More workshops focused on my particular plant type (peach & nectarine). Also collaboration project opportunities. ▪ Parent selection. ▪ The interest is there but the baseline information I, or my lab, needs in order to actually use the tools is not yet there. ▪ RosBREED has done an excellent job in both its research and education, in my opinion. What would be helpful would be to have additional information about how I could apply marker-assisted breeding work in local labs, or through contract with established labs at Cornell University, or other institutions that host RosBREED public breeders. ▪ Use of markers in heterozygous polyploids. ▪ We old guys need a good textbook to read to bring us up to speed about the whole process. 	

Table 21 (continued). Recommendations for future learning opportunities: Breeders

G9	How could information about genetic marker applications be provided to you in a useful format?
<p>2010:</p> <ul style="list-style-type: none"> ▪ <i>Workshops, case studies and examples, webinars.</i> ▪ <i>Website bullets.</i> ▪ <i>Collaboration or sabbatical.</i> ▪ <i>Web-based mini presentations on a range of topics would be useful allowing flexibility of scheduling.</i> ▪ <i>Internet links, webinars.</i> ▪ <i>Excel worksheet would be just fine.</i> ▪ <i>Hands-on training or demonstrations of techniques; hands-on training in software.</i> ▪ <i>Hands on is always best.</i> ▪ <i>Visualized genes and QTLs on graphical genotypes of major founder cultivars.</i> ▪ <i>A good summary booklet/website as well as workshops at professional or other meetings.</i> ▪ <i>Internet, training sessions, tours.</i> ▪ <i>Electronic.</i> ▪ <i>Web-based info is probably most accessible.</i> ▪ <i>User friendly, clearly defined assumptions on populations, etc., compatible with Excel, Access, etc.</i> ▪ <i>Training my folks in someone else's lab.</i> ▪ <i>Seminars on DVD or live workshops</i> ▪ <i>Online, pdf.</i> ▪ <i>I send you leaf material and you send me a phenotypic profile.</i> <p>2014:</p> <ul style="list-style-type: none"> ▪ <i>Book or internet would be fine.</i> ▪ <i>Hands-on training in lab work, or information about how to have an outside lab help me to apply marker-assisted breeding in my program would be the most useful.</i> ▪ <i>I have a small staff and find it difficult to attend meetings during much of the year. I would be interested in viewing lectures online, webinars, and any other materials that could be provided on the web to keep informed of the current strategies in the application of marker-assisted selection. I am also interested if the genotyping could be outsourced, and at what cost.</i> ▪ <i>I like online publications...I travel a lot, and lots of times the last thing I want is another meeting, though I do enjoy and get a lot out of the ones I go to.</i> ▪ <i>I think a sabbatical in depth focus in someone else's lab would be the most useful way to learn and see first hand how to implement these tools into a traditional program. However, half or full day workshops with very practical examples would be a good first step. Have trainers go to traditional programs and show how to step by step implement the new technology, this would only work if the trainers came pre paid and with \$ to help set up the new protocols.</i> ▪ <i>I would prefer workshops or some other in-person coaching approach with small class size. I know there are some resources online already but I feel like I do not even know enough right now to understand how to use them without help. It's also kind of embarrassing to feel so useless at all this stuff.</i> ▪ <i>Printed handout.</i> ▪ <i>Interpretation of results wrt parent selection.</i> ▪ <i>Online as well as workshop format.</i> ▪ <i>Online information sources. Workshops.</i> ▪ <i>Sabbatical or semester leave.</i> ▪ <i>Simulated mapping using the genome sequence, and make that sequence more complete.</i> ▪ <i>Through the use of a summer intern.</i> ▪ <i>Visiting programs that regularly use the information to see how physically carried out.</i> ▪ <i>Web resources, online courses, workshop at meeting.</i> ▪ <i>Webinar format.</i> ▪ <i>Webinars.</i> ▪ <i>Working with a service provider who could provide me genotyping information in a clear format.</i> ▪ <i>Workshops.</i> ▪ <i>Workshops or webinars.</i> ▪ <i>Webinars.</i> 	

Table 22. Recommendations for future learning opportunities: Allied scientists

G8	What kind of additional training or information about marker-assisted breeding would be most helpful to you or your organization?
<p>2010:</p> <ul style="list-style-type: none"> ▪ <i>I think that we do not need much more training in this area.</i> ▪ <i>Comparison of various methods. What's new on the horizon.</i> ▪ <i>I need the Cliff Notes version of marker assisted breeding for starters...backed up by more detail.</i> ▪ <i>I am most interested in the ability to delimit genomic regions to find candidates and demonstrate function of the candidates.</i> ▪ <i>Information and primary source documentation about successful application of this technology in other crops.</i> ▪ <i>Sabbatic with time devoted to study and training of marker assisted selection; designing a program (knowing the limitations and pitfalls).</i> ▪ <i>Basic training for a "classically trained plant pathologist" with general molecular working knowledge. I am working with horticulturists and geneticists in rootstock development for Prunus spp.</i> ▪ <i>A review of current and future marker applications that go beyond traditional seedling selection schemes.</i> ▪ <i>As a plant pathologist, I work on the periphery of the breeding programs. I think better cross-training between the disciplines would be helpful.</i> ▪ <i>A concise, elementary explanation of what it is would be helpful in describing it to employees.</i> ▪ <i>A list of selected readings on this topic for graduate students and others interested.</i> ▪ <i>Application of next generation sequencing methods in marker-assisted breeding.</i> ▪ <i>I am not a breeder, but we use markers for cultivar trueness-to-type.</i> ▪ <i>Marker development. Genotyping options. Implementation strategies. Determining cost/benefit ratios.</i> ▪ <i>Would like training or information about storing and querying marker data in computer databases.</i> ▪ <i>Current implementation. My interests are to use this kind of information in allele mining efforts. Constructing gene geneologies in germplasm collections may be important supporting information for breeders.</i> ▪ <i>Practical examples of how/where MAB has been utilized and how successful it was.</i> ▪ <i>Status of functional markers for key breeding traits that we could incorporate into our neutral and cp marker diversity research.</i> ▪ <i>How relevant are SNP chips to identify markers for specific traits?</i> <p>2014:</p> <ul style="list-style-type: none"> ▪ <i>An online resource on what markers are available for Rosaceous plants, this may be available already. If it is, I am not aware of it, since I rely on breeding colleagues for this information.</i> ▪ <i>As an 'allied researcher' I would benefit from learning more about the basics and opportunities.</i> ▪ <i>Availability of micro-arrays and their interpretation.</i> ▪ <i>Basics of bioinformatics.</i> ▪ <i>Disease resistance screening.</i> ▪ <i>GBS.</i> ▪ <i>I want to know more about how to use marker information to identify insect and mite resistance in various fruit crops.</i> ▪ <i>In-person workshops are the best methods for conveying information. Examples from people using DNA technology in fruit crop research would be helpful.</i> ▪ <i>List of the different approaches to marker-assisted breeding and identification of genes associated with specific traits.</i> ▪ <i>My department has three breeding programs that currently use marker-assisted breeding techniques and they teach it in their courses.</i> ▪ <i>Practical lab protocols for small labs with little sophisticated equipment, and training with computer programs to handle the data.</i> ▪ <i>Price and minimum requirement for facility in current conventional breeding program to start marker assisted breeding.</i> ▪ <i>Supplement classroom teaching in Horticulture classes.</i> ▪ <i>Using SNP data for assessing broad diversity patterns and historical demography.</i> 	

Table 22 (continued). Recommendations for future learning opportunities: Allied scientists

G9	How could information about genetic marker applications be provided to you in a useful format?
<p>2010:</p> <ul style="list-style-type: none"> ▪ <i>We already use the GDR and this format is fine.</i> ▪ <i>Prefer online accessible materials, especially videos of complex methods. Use a variety of media for materials.</i> ▪ <i>Description of overall concept and applications -- diagrams - examples, case studies.</i> ▪ <i>Web browser based is best. What is very important is the rapid updating of databases. GDR has not been updated terribly often. Confidence that the data is up to date is critical.</i> ▪ <i>Professional workshop; online resources.</i> ▪ <i>Well-done internet training modules with pdf references or links for more detail.</i> ▪ <i>On-site visit by experts with presentations and face-to-face time for more focused discussions on our work.</i> ▪ <i>Practically oriented workshops focused on demonstrating that marker assisted selection has been successful for overall improvement of a field breeding program. For what traits and to reach what goals?</i> ▪ <i>A web based "course" would provide the basic level of understanding needed so that I can better assess utility of methods in my program.</i> ▪ <i>Online newsletter, website.</i> ▪ <i>Website, email updates (electronic).</i> ▪ <i>Web-based literature.</i> ▪ <i>A website with relevant information specifically for different Rosaceae species.</i> ▪ <i>Being located on a campus, we have access to seminars that cover the application of the use of genetic markers to address plant breeding goals.</i> ▪ <i>Internet site.</i> ▪ <i>Workshop; Website.</i> ▪ <i>Already is available.</i> ▪ <i>GDR provides most everything I want.</i> ▪ <i>Rosaceae Newsletter/email.</i> ▪ <i>Publications, website, etc... Info on primers, conditions, allelic variation, desirable variants for breeding programs so our data becomes more useful to breeders.</i> ▪ <i>Hands-on training.</i> ▪ <i>Printed or on-line materials to supplement hands-on training.</i> <p>2014:</p> <ul style="list-style-type: none"> ▪ <i>In-person workshops - maybe in conjunction with a meeting like ASHS. Webinars are a distance second choice.</i> ▪ <i>Articles; websites</i> ▪ <i>Breeders need to develop improved collaboration with entomologists and plant pathologists so we can better evaluate breeding material for resistance to pests. This could occur by providing training workshops at Entomology and Plant Pathology Society National meetings to teach us how to collaborate more efficiently with plant or animal breeders so they will add the selection for markers for pest resistance to their current selection for horticultural characteristics.</i> ▪ <i>Conferences/workshops.</i> ▪ <i>Electronic book.</i> ▪ <i>Gene diversity publications, gene-specific primers.</i> ▪ <i>I do not and will not use genetic markers in my research.</i> ▪ <i>I would prefer an online resource, what markers are available and a who's who in breeders of Rosaceous plants. What traits are breeders currently working on in their programs using MAS?</i> ▪ <i>Interactive online class or training videos.</i> ▪ <i>PowerPoint over the internet or webinars hosted by competent teachers.</i> ▪ <i>Printed or web.</i> ▪ <i>Readily available web training sites with practical examples for the naive researcher.</i> ▪ <i>Using practically successful examples would be more useful and effective.</i> ▪ <i>Web-based training modules.</i> ▪ <i>Webinars.</i> ▪ <i>Workshops.</i> ▪ <i>Workshops, webinars.</i> 	

Recommendations for Additional Research and Development of Marker Applications from Rosaceae Breeders and Allied Scientists

Survey participants were asked to suggest ideas for practical problems in breeding or horticulture that could be addressed by marker-assisted methods and genomic research. Their recommendations are reported in table 23 for breeders and in table 24 for allied scientists.

In 2010, the most frequent recommendations for further marker applications involved disease or insect resistance (recommended by 7 individuals), fruit quality or flavor (recommended by 5 individuals), and post-harvest shelf life (recommended by 2 individuals).

In 2014, themes included disease resistance (recommended by 6 individuals), increasing the genetic diversity in program materials, in part by including wild species gene introgression (recommended by 3 individuals), better understanding gene linkage (recommended by 3 individuals), developing indicators of tree health or hybrid vigor (recommended by 2 individuals), and developing better tools to follow genes across ploidy levels (recommended by 2 individuals).

In addition to these, many other specific individuals recommendations are included in the tables.

Table 23. Recommendations for further marker applications: Breeders

H1	Are there questions or problems in breeding or horticulture that you think might be answered, at least in part, through genetic marker research and/or application? If so, please describe:
<p>2010:</p> <ul style="list-style-type: none"> ▪ <i>How many loci and alleles regulate remontancy in strawberry.</i> ▪ <i>So many! Almost any trait probably that can be accurately phenotyped. My particular interests now are in disease and insect resistance, fruit quality, precocity, and for rootstocks, mechanisms of dwarfing, induction of precocity, and production efficiency.</i> ▪ <i>Most of my efforts are directed at disease resistance. Pyramiding major genes, identifying QTLs for partial resistance genes, separating these from major genes.</i> ▪ <i>This type of research is already used for identification of genotypes and to understand the diversity of our germplasm. As we obtain new markers it will help us identify appropriate parents and even eliminate seedlings at a young stage of growth.</i> ▪ <i>Stress tolerance, primocane fruiting.</i> ▪ <i>Identification of unique linkage blocks (from inversions, translocations, etc).</i> ▪ <i>Yes. See RosBREED objectives and description. My biggest hope is to be able to screen for traits that are not seen easily i.e. post harvest fruit quality.</i> ▪ <i>How important is genetic diversity of a breeding program's germplasm relative to phenotypic diversity for important traits?</i> ▪ <i>I use markers in the grape breeding program. Our stone fruit breeding program is only doing evaluation at this time so I have no chance to use markers for seedling selection where I think it has the most immediate promise. We are using markers for disease resistance first and then might use if for seedlessness when a low % would be found in the population. Fruit quality traits for stone fruit would be useful but the confidence level for selecting must be very precise which I think will be a problem for traits that have low heritability.</i> ▪ <i>I'm not sure. I know we've been told for decades that genetic markers can make breeding more efficient. I'd like to find out I can make that happen in my own program, but nothing I've heard or read so far indicates it is possible for at least one of my crops. Mostly it seems to add a lot more work at a high cost compared to just increasing the size of the program.</i> ▪ <i>Linkage.</i> ▪ <i>Internal browning, predictors of post harvest life, brown rot resistance.</i> <p>2014:</p> <ul style="list-style-type: none"> ▪ <i>Functional gene annotation and precise location in the genome. Markers and epigenetic modifications?</i> ▪ <i>Good way to follow traits/genes when working among various ploidy levels.</i> ▪ <i>I am very interested in how marker-assisted breeding could be applied to novel sources of disease resistance in wild Rosaceae germplasm. I feel that marker-assisted selection coupled with current disease-screening techniques could help breeders to quickly and efficiently develop new lines of disease-resistant tree-fruit cultivars, while also reducing costs.</i> ▪ <i>The big one is the core problem of most breeding programs: how to you increase your numbers enough to have a good chance of getting the combination of traits you want, without expanding beyond the ability of your resources to evaluate them effectively.</i> ▪ <i>I think there is great potential, but the use of markers will not be able to shorten/replace some aspects of traditional breeding. You will still need to see and taste the fruit and check the selections for consistency, etc. Plus there are not markers for everything, and most of the important traits are quantitative. Cost is a huge barrier right now. I know the claims that smaller field plantings offset this but I can't pay the upfront costs, and really, nobody is going to plant 100 trees a year. It is more likely that you will plant almost as many plants with a greater chance of getting what you want. So in reality, the costs of marker work are added to the other costs, not replacing them. I work directly with consumers often and there is a huge resistance to the use of GMOs so I do not think that is going to fly for quite a while yet, if ever.</i> ▪ <i>Most certainly so. However, most of the cultivar development, introduction is being done in the private sector. I think they would have a difficult time utilizing such technologies. Maybe the best initial usage would be in intellectual property protection.</i> ▪ <i>One character that I would like to be able to select for using molecular markers is tree health.</i> ▪ <i>Ripening and maturity of fruit.</i> ▪ <i>So many. The number of loci involved in genetic control, loci interactions, linkage drag, choice of parents based upon genomic composition.</i> ▪ <i>Strawberry- Heat resistance combined with remontancy. Anything related to flavor i.e. soluble solids in all crops. Black raspberry- pyramiding aphid resistance. Chilling in all crops- especially interested in low chilling types. Disease resistance- RBDV in red and black raspberry; verticillium in black raspberry, phytophthora root rot in red raspberry and strawberry; blueberry shock resistance in blueberry; resistance to botrytis or spotted wing drosophila would be of interest in all crops.</i> ▪ <i>There are many important traits for which we have no knowledge of their inheritance. Also how does linkage with other traits impact the use of the available "jewels"?</i> ▪ <i>There is still a lot of terminology that is used that can be confusing.</i> ▪ <i>Understanding genetic basis for inbreeding depression and hybrid vigor.</i> ▪ <i>We have observed quite a bit of linkage between traits over the years, and it would be nice to confirm this. We continue to cross early freestone nectarines with late clingstones to get late freestones, and it is not simple to get the desired results. It would benefit us to know exactly why and to confirm our observations.</i> ▪ <i>Yes. I am working on it.</i> 	

Table 24. Recommendations for further marker applications: Allied scientists

H1	<p>Are there questions or problems in breeding or horticulture that you think might be answered, at least in part, through genetic marker research and/or application? If so, please describe:</p>
<p>2010:</p> <ul style="list-style-type: none"> ▪ <i>Breeding for complex traits where phenotypes are difficult to measure in field or lab material.</i> ▪ <i>I suspect yes, but I don't know enough about it really. My impression is that every problem can be solved by marker assisted breeding, but that's probably not realistic, either. Perhaps a candid description of what problems this method is unlikely to solve, in addition to the ones it is?</i> ▪ <i>I particularly find the use of markers valuable as an unbiased line of evidence complimentary to other global approaches to determine candidate genes for regulation of phenotypes. This is particularly important when dealing with perennials where we have consistently found a high percentage of genes with no known function. Our models of genetic regulation from annuals are inadequate for perennial biology. Association studies will maximize and speed this approach.</i> ▪ <i>Resistance to plant parasitic nematodes, Phytophthora spp., graft compatibility with almond cultivars, etc.</i> ▪ <i>I believe the advent of whole genome sequencing will largely replace/transform traditional marker technologies but the use of such information will require a shift from an emphasis on experimental tools to bioinformatic solutions for data processing and interpretation.</i> ▪ <i>Breeding for desirable traits will be one of the major applications.</i> ▪ <i>Screening to pathogen sensitivity.</i> ▪ <i>How successful is phenotypic selection in identifying parents that contain the maximum number of desirable alleles?</i> ▪ <i>Stone fruit flavor and shelf life.</i> ▪ <i>Applications: Fruit quality improvement; rootstock control of scion vigor.</i> ▪ <i>Raspberry bushy dwarf and other disease resistances in Rubus, The characterization of R genes in Rosaceous hosts may benefit a number of crops if functional R genes were identified.</i> ▪ <i>Tree breeding costs.</i> ▪ <i>Yes - assessment of genetic diversity and redundancy in germplasm.</i> ▪ <i>Perhaps the perception that markers themselves will allow identification of combination that will have defined phenotypes....there needs to be some recognition of the huge amount of epistasis or non additive effects.</i> ▪ <i>Yes... so very much! We're focusing on domestication issues in apple, and would love to use more functional traits in our work.</i> ▪ <i>Waiting for full genome sequences to be published.</i> <p>2014:</p> <ul style="list-style-type: none"> ▪ <i>Disease resistance screening.</i> ▪ <i>Domestication history.</i> ▪ <i>Domestication/wild species gene introgression.</i> ▪ <i>For functional genomics, the identification of genes responsible for given phenotypes.</i> ▪ <i>Good markers for disease resistance should be very useful, especially in cases where the infection cycle is very long, making evaluation of plant material extremely time consuming.</i> ▪ <i>Optimizing genetic diversity and reducing redundancy of germplasm collections.</i> ▪ <i>Physiological disorders such as bitter pit.</i> ▪ <i>The recent collection of apple germplasm from apple origin in Kazakhstan seems to be ripe for identifying markers for resistance to diseases and pests from that region for future use in breeding. Recently, primocane fruiting brambles have shown susceptibility to a broad mites whereas these mites do not seem to feed on floricanne fruiting brambles. There is also evidence that 'Wye Berry' (Wyeberries are similar to tayberries but were developed from eastern U.S. blackberries) is much more susceptible to red necked cane borer than are other blackberry or raspberry cultivars. It would be interesting to see if a marker can be identified for these differences in mite and insect susceptibility. There is also a great need to identify if there are any markers for resistance in berry cultivars to the spotted wing drosophila, a new invasive pest of ripening, soft-skinned fruit crops.</i> ▪ <i>There is considerable potential in using this technology to understand horticulturally-important traits.</i> ▪ <i>Understanding the evolution of genes associated with specific horticultural traits would help us understand how these traits function in current germplasm material.</i> ▪ <i>Yes, there are many.</i> ▪ <i>Yes. Patterns of genetic segregation in polyploidy.</i> 	

Rosaceae Breeding Community 2014 Assessment of the RosBREED Project

Questions were added to the 2014 survey to ask members of the Rosaceae breeding community for their opinions and observations about the extension efforts of the RosBREED project. These included questions about the specific information resources provided by RosBREED to assist them in learning about and applying marker-assisted breeding tools and methods, as well as their perceptions of the overall impact of RosBREED on the community and their interest in a set of online tools for breeders and scientists that is currently in development. Their responses are summarized in tables 25 to 32.

Workshops. Three quarters of breeders and 55 percent of allied scientists who responded to the survey had attended one or more face-to-face workshops or presentations provided by RosBREED. Of these, 72 percent of breeders and 81 percent of allied scientists reported the workshops to be “fairly” or “very” helpful, with 54 percent of breeders and 62 percent of allied scientists describing the presentations as “very helpful.”

Program Consultations. About half of breeders and allied scientists had received one-on-one or program-specific consultations with RosBREED team members. Among this group, about 85 percent rated the consultations as “fairly” or “very” helpful, with 58 percent of breeders and 52 percent of allied scientists rating the consultations as “very helpful.”

RosBREED Website and Newsletter. Over 90 percent of breeders reported having experience with the RosBREED newsletter and website. Among this group, over half reported these resources to be “fairly helpful” or “very helpful.” Among allied scientists, 41 percent had read the RosBREED newsletter and 72 percent had used the website. Of these, 41 percent found the newsletter to be “fairly helpful” or “very helpful” and two thirds found the website to be “fairly” or “very” helpful.

eXtension. Four questions asked about participant experiences with educational materials published by the Plant Breeding and Genomics Community of Practice through the eXtension.org website. RosBREED is one of several projects that have contributed materials to this site. At the time of the 2014 survey, articles, videos, live webinars, and recorded webinars published through eXtension.org had been accessed by 54 percent or fewer of the Rosaceae breeders and 21 percent or fewer of the Rosaceae allied scientists who responded to the survey. Among those who reported having tried these resources, 39 to 55 percent of breeders and 40 to 80 percent of allied scientists rated them as being “fairly” or “very” helpful. Articles were rated most highly by breeders, followed by webinars, with videos rated as least helpful. Allied scientists gave their highest ratings to webinars, followed by articles, with videos rated as least helpful.

Breeder Information Management System (BIMS). A final set of questions asked participants about their interest in a suite of software tools in development to assist both breeders and allied scientists in their work (also included was one question about genome scan SNP arrays). Unsurprisingly, since these tools are primarily intended to assist breeding program operations, breeders reported more interest than did allied scientists. Breeders gave their highest ratings to the *Trait Locus Warehouse*, *QTL Validator*, and *Cross Assist* tools, but reported strong interest in all of the software modules and the SNP arrays. The lowest rating from breeders was for the *Selection Target Identifier*. Allied scientists gave their highest ratings to *Cross Assist* and the SNP arrays, and their lowest ratings to *Selection Target Identifier* and *Technology Portfolio*.

Table 25. Feedback on RosBREED extension resources: Breeders, all responses

The following questions ask about training and information resources provided to the plant breeding and plant sciences community by RosBREED or by the Plant Breeding and Genomics group at eXtension.org. Please select one answer in each row to describe your experience (if any) with each training or information resource:		Not Helpful At All	A Little Helpful	Fairly Helpful	Very Helpful	I Haven't Tried this
I1	Face-to-face group workshops or presentations provided by RosBREED at national conferences or regional meetings	5 %	16	14	41	24
I2	One-on-one or private program-specific consultations with RosBREED team members to assist you in understanding marker-assisted breeding opportunities, using markers, preparing or analyzing marker data, etc.	-	8	14	30	49
I3	RosBREED newsletter	11	30	38	14	8
I4	RosBREED website	14	30	35	14	8
I5	Articles about plant breeding and genomics posted on eXtension.org	5	19	19	11	46
I6	Videos about plant breeding and genomics posted on YouTube or eXtension.org	11	19	11	8	51
I7	Live webinars sponsored by the Plant Breeding and Genomics group through eXtension.org	11	11	11	11	57
I8	Recorded webinars about plant breeding and genomics posted on eXtension.org	11	11	11	11	57

Note. N = 36. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

Table 26. Feedback on RosBREED extension resources: Breeders who have experienced each resource

The following questions ask about training and information resources provided to the plant breeding and plant sciences community by RosBREED or by the Plant Breeding and Genomics group at eXtension.org. Please select one answer in each row to describe your experience (if any) with each training or information resource:		N	Not Helpful At All	A Little Helpful	Fairly Helpful	Very Helpful
I1	Face-to-face group workshops or presentations provided by RosBREED at national conferences or regional meetings	28	7 %	21	18	54
I2	One-on-one or private program-specific consultations with RosBREED team members to assist you in understanding marker-assisted breeding opportunities, using markers, preparing or analyzing marker data, etc.	19	-	16	26	58
I3	RosBREED newsletter	34	12	32	41	15
I4	RosBREED website	34	15	32	38	15
I5	Articles about plant breeding and genomics posted on eXtension.org	20	10	35	35	20
I6	Videos about plant breeding and genomics posted on YouTube or eXtension.org	18	22	39	22	17
I7	Live webinars sponsored by the Plant Breeding and Genomics group through eXtension.org	16	25	25	25	25
I8	Recorded webinars about plant breeding and genomics posted on eXtension.org	16	25	25	25	25

Note. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

Table 27. Feedback on RosBREED extension resources: Allied scientists, all responses

The following questions ask about training and information resources provided to the plant breeding and plant sciences community by RosBREED or by the Plant Breeding and Genomics group at eXtension.org. Please select one answer in each row to describe your experience (if any) with each training or information resource:		Not Helpful At All	A Little Helpful	Fairly Helpful	Very Helpful	I Haven't Tried this
I1	Face-to-face group workshops or presentations provided by RosBREED at national conferences or regional meetings	3 %	7	10	34	45
I2	One-on-one or private program-specific consultations with RosBREED team members to assist you in understanding marker-assisted breeding opportunities, using markers, preparing or analyzing marker data, etc.	-	7	17	24	52
I3	RosBREED newsletter	3	21	14	3	59
I4	RosBREED website	3	21	31	17	28
I5	Articles about plant breeding and genomics posted on eXtension.org	3	3	7	7	79
I6	Videos about plant breeding and genomics posted on YouTube or eXtension.org	3	7	-	7	83
I7	Live webinars sponsored by the Plant Breeding and Genomics group through eXtension.org	3	-	7	7	83
I8	Recorded webinars about plant breeding and genomics posted on eXtension.org	3	3	3	10	79

Note. N = 29. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

Table 28. Feedback on RosBREED extension resources: Allied scientists who have experienced each resource

The following questions ask about training and information resources provided to the plant breeding and plant sciences community by RosBREED or by the Plant Breeding and Genomics group at eXtension.org. Please select one answer in each row to describe your experience (if any) with each training or information resource:		N	Not Helpful At All	A Little Helpful	Fairly Helpful	Very Helpful
I1	Face-to-face group workshops or presentations provided by RosBREED at national conferences or regional meetings	16	6 %	12	19	62
I2	One-on-one or private program-specific consultations with RosBREED team members to assist you in understanding marker-assisted breeding opportunities, using markers, preparing or analyzing marker data, etc.	14	-	14	36	50
I3	RosBREED newsletter	12	8	50	33	8
I4	RosBREED website	21	5	29	43	24
I5	Articles about plant breeding and genomics posted on eXtension.org	6	17	17	33	33
I6	Videos about plant breeding and genomics posted on YouTube or eXtension.org	5	20	40	-	40
I7	Live webinars sponsored by the Plant Breeding and Genomics group through eXtension.org	5	20	-	40	40
I8	Recorded webinars about plant breeding and genomics posted on eXtension.org	6	17	17	17	50

Note. Each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

Table 29. Perceived impact of RosBREED extension efforts: Breeders

Please circle one number in each row:		Not Applicable	Not At All	A Little	A Fair Amount	A Lot
J1	To what extent have the RosBREED workshops, presentations, webinars, articles, videos, newsletters, and consultations improved your overall knowledge about using marker information in your work?	8 %	8	39	19	25
J2	To what extent have the RosBREED activities listed above influenced your attitude toward using markers?	6	19	22	33	19
J3	Have the RosBREED efforts helped you improve your specific skills for applying markers in breeding or research?	6	31	33	19	11
J4	Have the RosBREED efforts helped you improve your confidence for applying markers in breeding or research?	6	20	51	11	11
J5	To what extent has RosBREED changed the way you think about the use of genomic data in the context of a breeding program?	6	17	47	17	14
J6	Please share your comments or recommendations about the questions above:					
<ul style="list-style-type: none"> ▪ During the course of RosBREED I have not had any genomics type projects ongoing, so this has not been the focus of my attention. If we can get funding, it might be the SNPs developed by RosBREED would become useful for rose work. ▪ I am old, but I do look forward to my son-in-law getting involved and educated in this area. ▪ I have a lot of prior knowledge of the use of markers so what I am looking for is marker-trait associations for traits of importance in the breeding program. One of the roadblocks is the lack of a cost-effective service provider that I can trust will not make mistakes or send me data that is poorly presented. ▪ I have been able to directly incorporate RosBREED genotypic and phenotypic info in parent and seedling selection and identity confirmation. ▪ I have not been able to attend the meetings in which workshops were given due to curtailment of travel and conference attendance in my organization, and sometimes due to conference timing [usually during my busiest seasons]. As for SNPs I do not even know how to use them. Once you get so far behind, it is really overwhelming to try to catch up. I was unaware that one-on-one training was even an option. And my organization's restrictive rules on internet use preclude many options like YouTube and webinars that are available in normal university workplaces. I feel like I'm in a race where others have cars and I only have a bicycle!! ▪ I have not used the SNPs because my breeding program is in pear, which has not been a part of RosBREED. RosBREED has not given me the skills or confidence for applying markers only because I need more specific information and hands-on training. I am beginning to apply genotyping for specific genes identified by other programs, and am planning grant proposals to develop marker assisted breeding. ▪ I just have not had much time to explore what RosBREED has to offer. My answers do not in any way reflect my opinion about RosBREED. I wish that I had the time and resources to attend the workshops and presentations. After finishing this survey, I intend to explore what presentations, webinars, articles, and videos are on the site. ▪ I started using markers before RosBREED, however, RosBREED broadened my scope and I believe RosBREED's greatest success is likely to be in DNA test development and also in SNP marker conversion to more PCR based marker systems. ▪ Most of the presentations were rather general and not at the 'cutting edge'. ▪ Much of my knowledge and experience in use of molecular markers has been independent of RosBREED. However, RosBREED has offered extremely valuable reinforcement and amplification of this knowledge and experience. Without RosBREED we would not have a SNP array for strawberry, and this array promises to be a transformative tool in relation to MAB in strawberry. ▪ My major breeding effort is not on a crop included in RosBREED, but I have a minor effort on strawberries. ▪ Prior to RosBREED I knew the importance of marker assisted breeding and planned on working towards its application in my breeding program. RosBREED activities and products helped me get there faster, more confident in my knowledge and skills. ▪ RosBREED has been program-changing to my breeding effort, and the doors are opening widely now to marker-assisted breeding methods. ▪ RosBREED has helped me to understand the value of genomics in fruit breeding, and I now feel that I have a strong understanding of how genomics can be applied to breeding work, but I still lack the skills and facilities needed to apply marker-assisted selection to my breeding projects. I marked the last two questions in this section "not applicable," because while I would like to use SNPs for breeding or research, currently I do not have the tools or funding to do so. ▪ Rubus was left out of the RosBREED funding, but has managed to make progress. The current and future Rubus work needs to be incorporated into the RosBREED website etc. ▪ The RosBREED workshop I attended was also helpful in stimulating linkages / potential collaborations. ▪ To my knowledge, SNP data for strawberry has not been made available, though I haven't checked recently. I would make use of it if it was. 						

Note. For questions J1 to J5, N =36; each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

Table 30. Perceived impact of RosBREED extension efforts: Allied scientists

Please circle one number in each row:		Not Applicable	Not At All	A Little	A Fair Amount	A Lot
J1	To what extent have the RosBREED workshops, presentations, webinars, articles, videos, newsletters, and consultations improved your overall knowledge about using marker information in your work?	29 %	7	29	21	14
J2	To what extent have the RosBREED activities listed above influenced your attitude toward using markers?	25	7	36	25	7
J3	Have the RosBREED efforts helped you improve your specific skills for applying markers in breeding or research?	36	29	21	4	11
J4	Have the RosBREED efforts helped you improve your confidence for applying markers in breeding or research?	36	18	29	7	11
J5	To what extent has RosBREED changed the way you think about the use of genomic data in the context of a breeding program?	25	14	21	32	7
J6	Please share your comments or recommendations about the questions above:					
<ul style="list-style-type: none"> ▪ All of your questions are about marker-assisted breeding and plant breeding. Although I collaborate with a RosBREED-affiliated breeder, my own research mostly uses genomic information available through the GDR website (mostly the physical map and alignments, not markers). I have used SSRs to verify germplasm parentage, but I learned these skills through primary literature, not via RosBREED tools. ▪ Are RosBREED researchers actively recruiting entomologists and plant pathologists to collaborate on improving pest resistance in breeding material by using markers and marker-assisted selection procedures? ▪ As an "allied" researcher I'm not directly responsible for much of the above. ▪ I am out of the loop here. ▪ I'm not directly involved with a breeding program and I'm usually so busy that I barely get time to search out things that appear to be peripheral to my research. Only through attending meetings have I been exposed to RosBREED, but then never seem to get the time to look into what they have done and are doing. I'm not sure how important it is to reach people like me, but I'd like to be kept more "informed" as things happen (new webinar, newsletter, etc.). ▪ It has opened up more opportunities for gene-diversity research. ▪ Not sure they apply to my foci area. ▪ RosBREED has been very valuable in developing a community of expertise that is able to provide information and resources to those of us who are not molecular geneticists. ▪ RosBREED is a very successful program. ▪ The breeders in my department have not paid much attention to RosBREED because they do not work with Rosaceous species and they have been using these techniques for more than a decade. 						

Note. For questions J1 to J5, N =28; each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

Table 31. Interest in Breeder Information Management System (BIMS) tools: Breeders

The following questions ask about technical resources that have been developed or are in development for the plant breeding and plant sciences community. Please select one answer in each row to indicate your interest (if any) in each technical resource that is being developed by RosBREED:		I'm not interested in this	Slightly Interested	Somewhat Interested	Very Interested
K1	Trait Locus Warehouse software for managing and analyzing information about marker-locus-trait associations	-	19 %	42	39
K2	Selection Target Identifier software for understanding socio-economic value of available marker-locus-trait associations	17	44	25	14
K3	Technology Portfolio software for browsing information about commercial genetic testing service providers	8	39	22	31
K4	Marker Converter software to develop new genetic tests from marker information	11	31	23	34
K5	QTL Validator software tools for identifying sources and confirming the effects of valuable alleles in specific breeding germplasm	8	22	33	36
K6	Cross Assist software for combining available phenotypic, pedigree, and DNA knowledge to inform crossing decisions	9	24	26	41
K7	Seedling Select software for modeling the costs, logistics, and benefits of traditional breeding operations and potential uses of genetic tests for seedling selection	11	34	23	31
K8	Genome scan SNP arrays such as the 9K, 8K and 6K peach, apple and cherry SNP marker Infinium® II Illumina arrays (Illumina Inc.) or the 90K SNP marker (IStrow90™) Axiom® genotyping array	33	14	31	22

Note. N =36; each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

Table 32. Interest in Breeder Information Management System (BIMS) tools: Allied scientists

The following questions ask about technical resources that have been developed or are in development for the plant breeding and plant sciences community. Please select one answer in each row to indicate your interest (if any) in each technical resource that is being developed by RosBREED:		I'm not interested in this	Slightly Interested	Somewhat Interested	Very Interested
K1	Trait Locus Warehouse software for managing and analyzing information about marker-locus-trait associations	36 %	39	11	14
K2	Selection Target Identifier software for understanding socio-economic value of available marker-locus-trait associations	61	21	11	7
K3	Technology Portfolio software for browsing information about commercial genetic testing service providers	43	43	11	4
K4	Marker Converter software to develop new genetic tests from marker information	46	29	21	4
K5	QTL Validator software tools for identifying sources and confirming the effects of valuable alleles in specific breeding germplasm	46	29	18	7
K6	Cross Assist software for combining available phenotypic, pedigree, and DNA knowledge to inform crossing decisions	46	21	29	4
K7	Seedling Select software for modeling the costs, logistics, and benefits of traditional breeding operations and potential uses of genetic tests for seedling selection	64	11	18	7
K8	Genome scan SNP arrays such as the 9K, 8K and 6K peach, apple and cherry SNP marker Infinium® II Illumina arrays (Illumina Inc.) or the 90K SNP marker (IStrow90™) Axiom® genotyping array	54	14	21	11

Note. N =28; each row contains the proportions of the group (percent) that gave each response. Row percentages may not equal 100 percent due to rounding.

