Introduction

Marker-assisted selection (MASS) uses DNA marker information to assist conventional seedling selection (CSS), which is based on only phenotypic and pedigree information, in order to enhance its accuracy and efficiency (Collard et al., 2005, Peace and Norelli, 2009).

The routine application of MASS in Rosaceae breeding programs has been limited by a lack of accurate genomic information, access to high-throughput molecular biotechnology and software tools that assist in decision making. Here we report on the development of Seedling Select, a web-based breeding decision-support tool being developed to assist MASS in Rosaceae breeding by helping in answering following questions:

- What is the most cost-efficient selection scheme, in what way and to what degree should MASS be adopted to make the selection scheme more accurate and efficient? – Module 1
- Which seedlings to save/cull? – Module 2

MASS in a general breeding scheme

Fig. 1. CSS and MASS in a generalized breeding scheme

Fig. 2. Seedling evaluation system of WSU Apple Breeding Program (stars indicate logistic windows for implementing MASS)

Blueprint for Seedling Select

Module 1: Selection scheme design

In Module 1, both CSS seedling selection scheme and available DNA tests serve as background information for logistical MASS scheme design. Cost-efficiency values will be calculated for each scheme according to the cost-efficiency comparison model (1.2a). Comparisons of cost-efficiency between different schemes will be conducted for the software to provide recommendations for the most cost-efficient and logistically reasonable seedling selection schemes (Fig. 3).

1.2a Cost-efficiency comparison model:

Cost-efficiency comparisons among different selection schemes are based on the comparison of cost-efficiency (CE) values of each scheme. The calculation of CE requires the knowing of total cost without MASS (CC), total cost with MASS (CM), genetic gain from selection without MASS (GC), and genetic gain from selection without MASS (GM). As an alternative, relative saving by MASS (RS) can also be used as the indicator of cost-efficiency. The less the CE (or the greater the RS), the more cost-efficient the scheme is. In the primary model of Seedling Select, cost-efficiency comparisons are conducted for cost comparisons which assume the genetic gains for schemes with and without MASS are the same.

Cost-efficiency comparison parameters:

\[ CE = \frac{CC - GM}{GC} \]

Output

CE: cost-efficiency
RS: relative saving by MASS
Input

CC: total cost without MASS, CC = C (when PGSI = 0, 1 ∈ C (SM))
CM: total cost with MASS, CM = C (when at least one PGSI = 0, 1 ∈ C (SM))
GC: genetic gain from selection without MASS
GM: genetic gain from selection with MASS
SM: total savings with MASS, SM = CC

1.2b Cost evaluation model:

The calculation of CC, CM in the cost-efficiency comparison model (1.2a) is described in the following equation (1.2b). In this model, total monetary cost of a selection scheme can be calculated by summing up total genotyping cost, phenotyping cost and raising cost for the entire seedling selection process.

\[ C = \sum_{i} (GC_i × PGSI_i + SM_i (RCM_i + PCM_i) × PSM_i) \]

Output

C: total monetary cost of a selection scheme
Input

GCI: genotyping cost for each plant in the ith stage of MASS
PGSI: phenotyping cost per plant in the ith stage of MASS
RCM: raising cost per plant in the ith stage of MASS
PCM: phenotyping cost per plant in the ith stage of MASS
PSM: population size in the ith stage of MASS

Module 2: Selection decision support

To assist in making selection decisions, Module 2 will incorporate functionalities to calculate which seedlings to cull or keep based on DNA marker information and selection thresholds provided by the user. Recommendations as well as DNA marker information will be displayed in a user-friendly way to help users trace DNA marker information as well as review selection recommendations efficiently (Fig. 4).

Software development stages

Stage 1: Establish and test the cost-evaluation model used for Module 1 based on MASS spreadsheet (Edge-Garza et al., 2010); develop software interface and functionality for cost evaluation
Stage 2: Develop selection decision support module
Stage 3: Establish and test efficiency evaluation model for Module 2; develop software interface and functionality for efficiency evaluation

Conclusions

Seedling Select is a web-based breeding decision-support tool being developed to assist MASS in Rosaceae breeding. The aim of this software is to provide recommendations for the most cost-efficient selection scheme (focus of Module 1) and selection decisions made on seedlings (focus of Module 2).

Structures of each module are described in this poster. A primary model of cost evaluation for various selection schemes is constructed 1.2a, 1.2b. In this model, cost-efficiency is estimated by calculating the ratio of total cost without MASS to the total cost with MASS, where genetic gain from selection with and without MASS are assumed to be identical.

In the future, models for estimating genetic gain will be established for single trait selection, which will be further extended to multiple traits. In the meantime, integration of Seedling Select with other MASS decision-support tools will be addressed to collect information for more precise estimations.