Increasing the Efficiency of Breeding Without Breeding Through Phenotypic Pre-selection in Open Pollinated Progenies

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Abstract: Unlike classical methods used by forest tree breeders that rely on pre-determined mating designs to construct pedigreed materials for testing and selection, the concept of Breeding Without Breeding (BWB: El-Kassaby et al., 2007) was introduced to allow the assemblage of full-sib (FS) and half-sib (HS) families from seed orchards' wind-pollinated offspring without conducting any crosses. The method relies on using highly informative molecular markers (e.g., SSRs) and pedigree reconstruction methods to unravel the genetic relationship among individual's offspring. Fingerprinted large wind-pollinated families are required to allow the assemblage of FS and HS families with reasonable size for field testing. To maximize the method's efficiency while minimizing methodological efforts, we propose the inclusion of phenotypic pre-selection from existing open-pollinated family tests to substantially reduce the number of fingerprinted individuals. The proposed application (merging mass selection with BWB) capitalizes on the efficiency of mass-selection in identifying groups of superior individuals and the use of pedigree reconstruction to delineate the paternal parents of the phenotypically selected individuals, hence complete pedigree tracking. Methods for expanding the BWB utility through either slight modification of the production populations' structure or the introduction of desired genotypes through pollen management techniques are presented. The most breath-taking possibility offered by BWB is offering opportunities to abandon not only clonal archives and crosses but also field testing. If both maternal and paternal pedigrees could be reconstructed in commercial plantations originating from a seed orchard, the same type of mass selection could be performed for the orchard's clones and long term breeding could be practiced in commercial plantations rather than of investing efforts and resources on specialized progeny test trials.

Keywords: Breeding Without Breeding, pre-selection, mass selection, pedigree reconstruction, seed orchards

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CONCEPTUAL APPROACH

The concept of Breeding Without Breeding (BWB: El-Kassaby et al., 2007) is extended to include phenotypic pre-selection from open-pollinated family tests to maximize the method's efficiency while minimizing methodological efforts. The proposed application (merging mass selection with BWB) capitalizes on the efficiency of mass-selection in identifying groups of superior individuals (Lindgren and Wei 1994, 2007) and the use of pedigree reconstruction to delineate the paternal parents of the phenotypically selected individuals, hence complete pedigree tracking.

The BWB scenario presented by El-Kassaby et al. (2007) starts with the selection of the top 15 performing individuals form a 40-parent seed orchard to from a nucleus population. The nucleus population consisted of a half-diallel (105 full-sib families, each with 100 individual) that was created after pedigree reconstruction and the top 40 individuals (forward selection) from the progeny test were selected to establish the new orchard using group-merit selection (Figure 1)

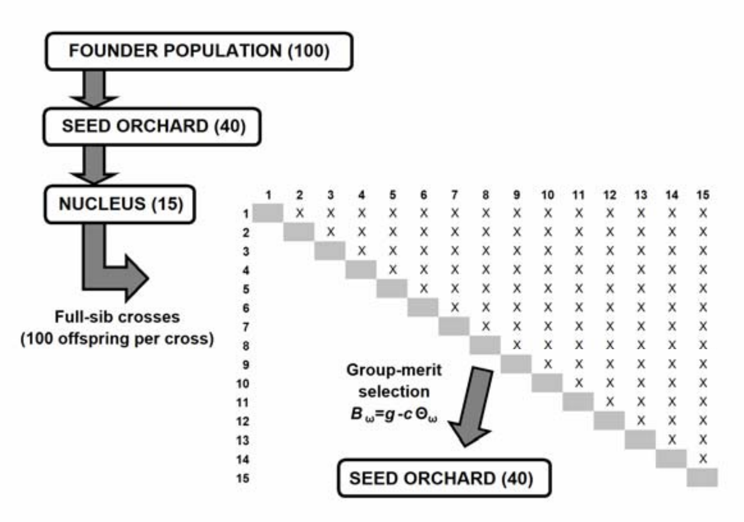

Figure 1. Schematic description of the breeding strategy implemented in El-Kassaby et al. (2007). The founder population is equivalent to a phenotypically selected breeding population in which the top 40 parents form the original seed orchard population and the partial diallel represents the FS and HS produced through pedigree reconstruction and the selected best individuals within these families form the parents for the new production population (seed orchard).

The offspring available for selection from the top 15 families represents the remaining individuals after the elimination of those resulted from contamination (assumed at 40%), sired by the other 25-orchard parents (assumed at 70% of the within orchard pollination) and selfing (assumed at 1%). If selection of the best individuals, for forward selection, is done after pedigree reconstruction (i.e., mating among the top 15 parents), then a large number of individuals are required for fingerprinting to permit capturing and identification the top 15 parents' offspring; however, the application of phenotypic truncation selection, prior to fingerprinting, will drastically reduce the fingerprinting and restricting laboratory efforts only to those selected individuals by orders of magnitude. The genotype-dependent laboratory costs will be almost negligible. The estimated gain – effective number relation for the 40 selected individuals could be adjusted at different levels by the parameters of the group merit selection algorithm to a desired level.

Lindgren and Wei (1993; 2007) compared different selection methods and highlighted the efficiency and ease of mass-selection (phenotypic selection). The bases for their approach was truncation selection on an index where each individual within each HS and/or FS family generates its own index value that is based on a weight of this individual's family value and its phenotypic value. For the particular selection scheme phenotypic selection, the family value has zero weight and all weight is on the individual phenotype. By varying this weight over all possible positive values, a graph could be constructed relating gain and status number (diversity measure) given the number of selected individuals. That graph (example in Figure 2) shows the upper bound for the gain that can be achieved at a specific status number (diversity) and selection intensity. Alternative selection methods such as between-family selection, within-family selection, and combined index selection are also illustrated. Figure 2 demonstrates the efficiency of phenotypic selection in capturing both high gain and high effective number.

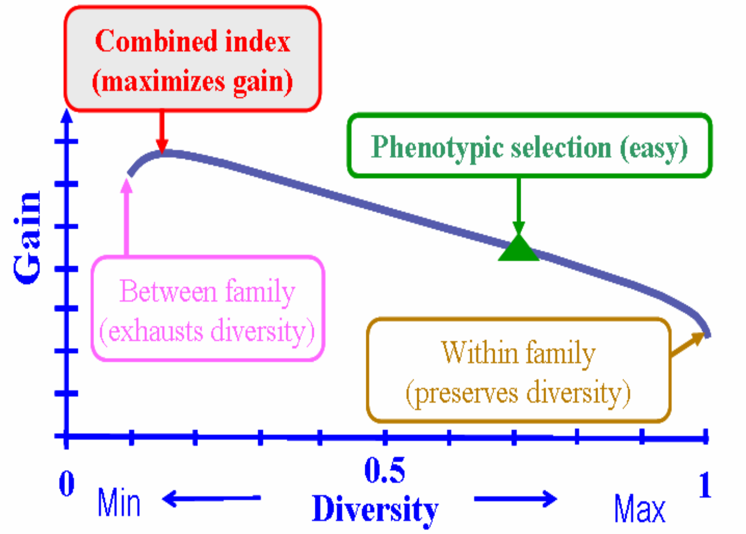

Figure 2. Relation between gain and diversity (relative status number) following selection in a population with a simple family structure. The graph is generated by an optimizing selection procedure where the candidate population was composed of an infinite number of large unrelated full-sib families of equal size. Heritability was set at 0.25 and 10 percent of the individuals were selected (Modified from Lindgren and Wei 1994).

At this stage, no assumption were made regarding knowing the pedigrees or the breeding values of the selected individuals, thus simply why should we consider BWB and invest unwarranted expenses on fingerprinting and pedigree reconstruction where the desired number of top ranking phenotypes to obtain the desired gain and diversity could be selected? The reasons for advocating the use of a scheme involving phenotypic pre-selection followed by pedigree reconstruction and group merit selection is the methods ability in offering better results. These considerations include: 1) phenotypic selection is only approximately optimal in real world applications (Lindgren and Wei 2007), the model by Lindgren and Wei (1994) contained some simplifications, so some of the results are correct only for special cases, 2) phenotypic selection is efficient, but it does not control the point where maximum gain and effective number occur in the way it can be made by pedigreed material, 3) it provides an opportunity to place more emphases on the best segment of the breeding population (Lindgren 2005), 4) the proposed model (Lindgren and Wei 2007) is a one generation model that does not consider the occurrence of inbreeding in future production populations, thus knowing pedigree of the selected material offers advantages for better control of inbreeding and co-ancestry structure in advanced generations, and 5) provides control to the commonly considered unsophisticated and uncontrolled mass-selection making it more acceptable.

The utility of the BWB concept could be expanded to a host of other applications. For instance, since breeding program deals with larger genetic resource base than seed orchards, we propose two options for expanding the seed orchards' genetic base. One that involves the inclusion of few extra ramets representing the additional parents required for completing the breeding population into seed orchards. The impact of these extra ramets on the orchard's pollen pool and genetic gain will be very limited due to their low frequency and their infusion could be viewed as a tool to expand the diversity (Lindgren and El-Kassaby 1989). The other, involves the introduction of the desired clones into the orchard's pool through their pollen by means of supplemental mass pollination (El-Kassaby et al. 1993). Thus the proposed design allows long term breeding without clonal archives or controlled crosses. Additionally, some of the offspring sired by pollen contamination may be worthy of inclusion in the breeding stock, and thus offers a mechanism for enriching the breeding stock with fresh material. The most breath-taking possibility offered by BWB is to abandon not only clonal archives and crosses but also field testing. The pre-selection is efficient and does not require knowledge of pedigree, not even maternal. If both maternal and paternal pedigrees were reconstructed in commercial plantations originating from a seed orchard, the same type of group merit selection could be performed for the orchard's clones as well for practicing long term breeding in commercial plantations instead of investing a lot of effort and resources on specialized progeny test trials.

In conclusion, we recommend the application of mass-selection in identifying superior individuals before applying BWB for controlling the pedigree and group merit selection. This scheme is ideal for untested seed orchards where open-pollinated progeny trials exist. The substantial reduction of the number of pre-select individuals requiring for fingerprinted allows for greater opportunities to broaden the selection for greater flexibility.

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