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Abstract: MAGIC Populations for QTL mapping

Initial attempts at genetic mapping often depend on either using experimental populations derived from crosses, or, more recently, diverse natural populations (e.g., genome-wide association studies). The latter requires a large and diverse population sample, as well as statistical methods to account for the significant population structure that can exist in these populations. The former avoids these limitations, but has the opposing drawback of only including a small subset of possible alleles at any given locus. The extreme case is represented by the commonly-used bi-parental cross, which entirely eliminates concerns regarding population structure, but simultaneously reduces allelic sampling to the two parental lines, which often represent at most two alleles (in the case of inbred founders), and resolve QTL to only 10-30 cM.

Multi-parental experimental populations (e.g., “MAGIC” – multi-parental advanced generation intercrosses – lines) represent an intermediate option. By including a greater proportion of natural genetic variation, and by creating “mosaic” recombinant inbred lines that allow for the representation of these alleles in more diverse genetic backgrounds, finer precision can be obtained in mapping QTL. Important considerations in this respect therefore include founder selection, which – like founder selection in a bi-parental cross – should be performed to maximally capture variation relevant to the given research or breeding program. Additionally, the length and structure of the intercrossing methodology must be considered, as this will determine the extent of “mosaic-ness” in the resulting progeny: typically, multiple parent lines are first crossed through a “funneling” stage, and then subsequently inter-crossed for 1 or more generations before inbreeding. While this approach allows for the use of both statistical techniques drawn from traditional mapping and association-panel research, modeling approaches must therefore account for potential – and, indeed, almost certain – variable degrees of relatedness between founders.

In practical terms, if a breeding program is already considering creating mapping populations derived from several independent bi-parental crosses, it would be useful to consider include intercrosses between these progeny. The additional labor involved in creating crosses between F_1 and F_2 's to create, for example, the 8-way “funneled” progeny that could be used to generate MAGIC lines can often be performed in parallel with the selfing or sibling crosses that would ordinarily be made. As such, multi-parent mapping populations should not be seen as an insurmountable logistical effort, and given the potential refinements that they can offer over traditional mapping or GWAS approaches, they should be pursued widely in crop genetics research.