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An Approach to the Genetic Improvement of Clonal Cultivars via Backcrossing

For several vegetatively propagated crops (e.g., grape, *Vitis vinifera* L., hop, *Humulus lupulus* L.), consumers are reluctant to accept new cultivars. Hence, the breeder's task often is to improve elite clones for one or a few traits only. In breeding lines or hybrids, improvement for simply inherited traits like disease resistance is achieved via backcrossing with the cultivar or its parents. Because clones are usually highly heterozygous, using them as the recurrent parent in a backcross program does not restore the original genotype because of segregation and inbreeding. Hence, conventional backcrossing cannot be applied directly to clones.

Consider two gametes produced from a diploid clone. Let them be totally complementary with respect to the origin of their chromosomes or chromosomal segments (origin referring to the parents of the clone). Then, for every heterozygous locus of the clone, the first gamete received one allele and the second gamete the other. Consider two doubled haploid lines (DHLs), derived from this very pair of gametes. Crossing them reproduces the genotype of the original clone. Prior to resynthesizing the clone, alleles of monogenic traits could be transferred to these two DHLs via backcrossing. By this approach, superior clonal cultivars could be improved at single loci with two complementary DHLs as recurrent parents in a backcross program.

The main problem in this approach is identifying two complementary DHLs. Consider the four microspores (tetrade) arising from the same microspore mother cell (MMC) and assume crossing over to be absent. The result of the first meiotic division is a pair of fully complementary daughter cells. The second meiotic division causes no further genetic alteration. Hence, each group of four DHLs produced from the same MMC consists of two pairs of completely complementary DHLs.

At present, crossing over cannot be prevented. Assume one crossing over per pair of $x = 19$ chromosomes (grape) and an exchange of segments containing 30% of the chromosomes. Consider one of four DHLs produced from the same MMC. The three other DHLs include one that is complementary to the considered one for only 30% of its genome. This DHL can easily be identified. The expected complementarity of the considered DHL to the two other DHLs is 85%. The probability that one of these two DHLs is complementary regarding all 19 chromosomes is $(0.5)^{19}$. The probability of at least 14 out of 19 chromosomes being complementary is 0.032; in this case, the remaining chromosomes are complementary for 70%. Crossing such a pair of nearly complementary DHLs will restore at least 92% of the original heterozygosity. Identifying pairs of highly complementary DHLs could be based on molecular marker assays.

Simulation studies should be conducted to quantify the effect of ploidy level, chromosome number and size, and chiasmata number and location on the number of DHLs that have to be regenerated and screened in order to restore a given level of heterozygosity in the resynthesized clone.

This proposal concerns two areas of research: (i) regeneration of DHLs from microspores derived from the same MMC and (ii) search for procedures to reduce or prevent crossing-over events in meiosis.

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References and Notes

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