Progressive fine mapping in experimental populations: an improved strategy toward positional cloning.

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Abstract
Genetic mapping is one of the key steps in positional cloning. The traditional mapping strategies typically require to genotype a set of markers that are nearly evenly or randomly distributed across the genome or a region of interest. Such "grid" strategies work with low efficiency. We propose an improved mapping strategy by integrating the principle of one-dimensional optimization and information on physical map into the standard mapping procedure used in experimental populations. Computer simulations based on a set of empirical data suggest that our new procedure can reduce the number of markers required for genotyping to less than one-fourth of that of the standard procedure. An illustrative application also demonstrates a pronounced reduction of the burden in genotyping. The proposed strategy offers a quick and cost-effective access to the target gene for positional cloning without any extra expense except for making use of genomic sequence data. A Microsoft Excel spreadsheet, for performing easy calculations described in this article, is available on request from the authors.

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