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Opportunities of genetic association studies in pepper: estimation of the genetic structure and linkage disequilibrium in a germplasm sample

Mélissa Cantet, Stéphanie Mallard, Maryse Nicolai, Anne-Marie Sage-Palloix, Véronique Lefebvre

Institut National de la Recherche Agronomique (INRA), UR 1052 Génétique et Amélioration des Fruits et Légumes (GAFL), Montfavet, France

Genetic association studies permit to dissect complex traits, but the resolution depends on the extent of the linkage disequilibrium (LD). When LD declines rapidly around a target locus, locus scans help to identify candidate genes. To avoid false positive associations, the germplasm genetic structure has to be considered. To evaluate opportunities of genetic association in pepper (*Capsicum* spp.), we investigated the LD extent and the genetic structure in a germplasm sample, at two levels: the whole-genome and a 1-Mb target locus. INRA maintains a pepper collection of 1322 accessions from 5 cultivated and 6 wild species. We randomly sampled 381 accessions from the 5 cultivated species (*C. annuum*, *C. chinense*, *C. frutescens*, *C. baccatum*, *C. pubescens*) and one wild species (*C. eximium*). We genotyped them with 7 SSR markers from 7 chromosomes and 6 SNP markers within the target locus. The genetic diversity of the sample was higher at the genome-wide level ($H_e=0.48$, expected heterozygosity, Nei, 1973) than at the target locus ($H_e=0.39$). However, SNPs are generally less polymorphic than SSRs. The SSR data revealed that the sample was structured into two major groups. Group1 mostly contained *C. annuum* accessions, while group2 consisted in a mixture of the other species. As expected, group2 presented more allelic diversity than group1. Group2 was itself structured into 3 sub-groups, roughly splitting the accessions from *C. pubescens*, *C. baccatum* and *C. frutescens*. At the whole-genome level, the LD was high ($r^2_{\text{mean}}=0.28$) compared to other species (0.06 for potato). This is favourable for genome-wide association studies. A high LD could be due to the sample structure or related to the limited number of markers. At the target locus, the LD extended up to 300 kb ($r^2_{\text{mean}}=0.9$) in group1, and was also high compared to other species (7 kb for maize, 200 kb for lettuce). But it was specifically low ($r^2_{\text{mean}}=0.09$) in group2. A high LD is unfavourable for locus-specific association studies. To highlight genotype-phenotype fine associations on pepper, we will focus on haplotype analysis with more markers and within a larger germplasm sample, in considering especially accessions from group2.

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