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

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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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