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## **BREEDING PATTERNS AND CULTIVATED BEETS ORIGINS BY GENETIC DIVERSITY AND LINKAGE DISEQUILIBRIUM ANALYSES**

### **ABSTRACT**

Genetic relationships and linkage disequilibrium (LD) were evaluated in a set of 2035 worldwide beet accessions and in another of 1338 elite sugar beet lines, using 320 and 769 single nucleotide polymorphisms (SNPs), respectively. The structures of the populations were analyzed using four different approaches. Within the worldwide population, three of the methods gave a very coherent picture of the population structure. Fodder beet and sugar beet accessions were grouped together, separated from garden beets and sea beets, reflecting well the origins of beet domestication. The structure of the elite panel, however, was less stable between clustering methods, which was probably because of the high level of genetic mixing in breeding programs. For the linkage disequilibrium analysis, the usual measure ( $r^2$ ) was used, and compared with others that correct for population structure and relatedness ( $r_S^2$ ,  $r_V^2$ ,  $r_{VS}^2$ ). The LD as measured by  $r^2$  persisted beyond 10 cM within the elite panel and fell below 0.1 after less than 2 cM in the worldwide population, for almost all chromosomes. With correction for relatedness, LD decreased under 0.1 by 1 cM for almost all chromosomes in both populations, except for chromosomes 3 and 9 within the elite panel. In these regions, the larger extent of LD could be explained by strong selection pressure.

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