

1.5 IBRAHEEM ADETUNJI¹, GLENDA WILLEMS¹, HENDRIK TSCHOEP¹, ALEXANDRA BURKHOLZ¹, STEVE BARNES¹, MARTIN BOER², MARCOS MALOSETTI², STEFAAN HOREMANS¹, FRED VAN EEUWIJK²

¹SESVanderHave N.V./S.A., Soldatenplein 15, B – 3300 Tienen

²Biometris – Applied Statistics, Wageningen University, PO BOX 100,
NL – 6700 AC Wageningen

GENETIC DIVERSITY AND LINKAGE DISEQUILIBRIUM ANALYSIS IN ELITE SUGAR BEET BREEDING LINES AND WILD BEET ACCESSIONS

**Diversité génétique et analyse du déséquilibre de liaison dans des lignées
sélectionnées de betteraves d'élite et des populations de betteraves sauvages /
Genetische Diversität und Analyse des Kopplungs-Ungleichgewichts
in Elite-Zuckerrübenzuchtlinien und Wildrübenpopulationen**

ABSTRACT

Over 400 genetic markers have been used to analyse the genetic diversity and linkage disequilibrium present in elite sugar beet lines and wild beet accessions. 454 single nucleotide polymorphisms (SNPs) were applied to 233 elite lines, and 418 SNPs to a collection of 91 wild beets. The elite lines were separated into seed parent and pollen parent pools, with the wild beets forming a separate cluster in a Principal Coordinate Analysis. The extent of linkage disequilibrium (LD) was investigated, and persisted beyond 50cM on six of the nine chromosomes in the elite groups, if genetic relatedness was not taken into account. With correction for genetic relatedness, LD decayed after 6cM on all chromosomes. In the wild accessions, LD decayed after 2 to 3 cM and was hardly affected by a correction for relatedness. In the elite material, persistence of LD was observed in some cases between distant SNPs on the same chromosome, and also between SNPs on different chromosomes, pointing to the effect of population structure. This strong LD between markers that are not genetically linked, alongside the persistence of LD in the pollen and seed parent heterotic pools, indicates the consistent selective pressure that has been applied during the breeding process. Regions on chromosomes 3 and 4 that are known to contain genes for disease resistance and for monogermity also showed clear genetic differentiation between the pollen and seed parent pools. Other regions, including some on chromosomes 8 and 9, for which no a priori information is available to indicate their consistent contribution to the phenotype, also contributed to the clustering pattern observed in the elite breeding lines.
