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Exploring genetic structure and diversity of breeding material producing three-way hybrids in sugar beet: impacts on male-female differentiation, and genome-wide patterns.

Since F.V. Owens' discovery of cytoplasmic male sterility (CMS) in 1945, and G.J. Hogaboam first hybrids in 1957, to manage both heterosis and fixation of alleles, a lot of progress have been done, resulting into male and female pool structuration. Sugar beet hybrids are also characterized by numerous successive introductions of specific and important traits such as monogermity from *SLC101* (Savitsky, 1950), or rhizomania tolerance/resistance from Holly sugar germplasm, wild beets *WB42* and *WB41*... These traits' introductions using more or less distant donors disrupted the structuring of male and female pools, with often loss in genetic values. Identifying the key aspects of the resulting evolution of structuration, and the impacts of these successive introductions is a first step in developing more efficient breeding and pre-breeding methods. Genotyping data are now available and can be used to study diversity within the different breeding programs, both globally and across the genome, and its evolution. Linking these findings with phenotypic data will also help understand the impact of breeding methods. This will enable the development of new efficient strategies for a sustainable response to environmental challenges through optimized breeding approaches for both short- and long-term efficiency in diversity management. This study is then focusing on genetic diversity and its genome distribution in a sugar beet breeding context with a wide panel of 30 thousand plants (parental components and resulting hybrids) covered by 10k biallelic SNPs. One may identify genomic regions that exhibit patterns in response to differentiation between populations, past introductions of traits or genetic drift. Results demonstrate how breeding design is structuring pools globally, and how local regions are impacted. This can provide opposite patterns depending on the breeding methods involved. Using F_{st} (Weir & Cockerham, 1984) between male and female accessions, as well as diversity indexes, highlight shifts in allelic frequencies in those two pools linked with breeding.