Gene-flow in *Beta* (beet) complex and its consequences for growing of HT sugar beet

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The *Beta* complex includes cultivated forms like sugar beet (*Beta vulgaris* ssp. *vulgaris*), wild sea beet (*B.v.* ssp. *maritima*) and weedy and feral forms derived by hybridisation between the two. The complex has become a recognised case study of gene flow, introgression, conservation of wild plant genetic resources and the agronomic control of weedy forms. From the point of view of gene flow and possible introgression of herbicide tolerance (HT) gene, the trait of annuality is very important. Cultivated forms are biennial and can get the annuality trait due to unintended pollination of maternal plants of sugar beet by annual wild or feral forms of beet. European wild and feral beet biotypes differ in the frequency of the ‘bolting’ gene and the vernalisation requirement along a south-north gradient with higher frequency in southern regions. The offspring (weed beets) is annual and can disperse the genes including herbicide tolerance (HT) in both seed and root production areas, create a persistent soil seed bank and make difficulties as a serious weed. The most important management tools are keeping of isolation distances between multiplication fields, control weedy forms of beet, and prevention of escape of HT traits into weedy and feral populations. Controlling seed quality is essential for sustainable introduction of HT varieties. Attention must be paid to seed multiplication at high quality producers, testing of imported seed lots on impurity and careful selection of annual bolters (primary type of weed beets) in sugar beet fields.

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Methods

The work methodology is structured for the purpose of collating, processing and interrogating data and liaison with other activities within SIGMEA. Major tasks involve the compilation and analysis of existing data and the collection of new data to cover gaps in existing knowledge. Broader ecological areas are included be analytical review of existing and forthcoming experimental work. Six different institutions contributed by submission of standardized data sets from recent or actual research projects on sugar beet. We obtained 14 sugar beet datasets with special focus on a) pollination, hybridization (6 studies), b) genetic diversity (3 studies), c) fitness (3 studies), and d) population ecology (2 studies). Gene-flow in sugar beet may take place between/within populations of cultivated beet, sea beet, and weed beet.

Results

Recently, sugar beet is cultivated in 21 EU countries. This crop is biennial which means that in the first year (root production) does normally create neither pollen nor seeds and it is relatively safe from the point of view of coexistence in sugar production regions. Root (sugar) production takes place in all 21 countries whereas the seed production is concentrated only in Mediterranean areas (southern France and northern Italy).

One of the most important environmental questions regarding the introduction of GM varieties is the conservation of wild populations. Data on demography, gene flow, gene introgression and its biological consequences on populations and plant communities were obtained from four representative geographical areas (Denmark, Germany, Italy, and Croatia). Various molecular-genetic methods were used to describe the genetic structure of populations. All methods were able to differentiate among *Beta* forms. Sea beet and sugar beet were found in genetically distinct group. Differences, although less marked, were also found between weed- and sea beet populations. Genetic diversity of sea beet is much higher than in sugar beet as a consequence of adaptation on site-specific ecological factors. Italian sea beet showed higher diversity probably due to its longer history and more diverse environmental conditions than northern European populations. Inland populations of weed beet are genetically more distant from domesticated beet by reason of restricted gene flow. However, the introduction of GM beet should not influence the structure of natural populations and communities because, first, there is limited gene flow in that direction, and second, there would be no selective advantage of traits such as herbicide tolerance and virus resistance.

In agroecosystems, the economic benefit of sugar beet in both root and seed production areas is threatened by the occurrence of weedy forms because many areas are now highly infested by weed beet. Especially the annual weed beet is very competitive and produces high number of seeds. Studies on biology and ecology of weedy forms were undertaken in representative European regions and are completed in 6 datasets. Presented results show that weed beet has high potential for temporal and spatial dispersion of trangenes due to long-lived seed bank and high production and long-distance polen transport. There is no indication that the tested GM beet (neither plant nor seed) survived differently from non-GM control genotypes.

Harvested parts of sugar beet are vegetative; therefore the contamination of product by transgenes originating from bolting sugar beet or weed beets from neighbouring fields is not probable. Bolting and cross-pollination may result in the presence of GM weed beets in non-GM fields (leading to weed control problems in the case of herbicide-tolerant crops) but not the commingling of GM and non-GM sugar beet roots beyond the field. The highest risk of product contamination is expected trough the usage of seeds containing impurities arising from pollination of conventional multiplication sugar beet stands in Southern Europe by transgenic paternal lines and by weed beets bearing transgenic trait. Here, one of the most important management tools is keeping of isolation distances between multiplication fields, control weedy forms of beet, and prevention of escape GM traits into weedy and feral populations. Controlling seed quality is essential to limit the impact of weed beet for co-existence. Attention must be paid to seed imports from high quality producers. In addition, the development of efficient methods for commercial seed testing is necessary, not only for detection of GM traits but also detection of genes causing bolting. Thus, GM presence in non-GM production will be mainly due to the level of GM presence in sown seeds (assuming that no commingling occurs during sowing and harvesting operations). Where the adventitious GM presence in non GM seed production remains below the defined threshold (0.1% or 0.9%), there is no coexistence issue for sugar beet crop production. Thus, according to Messean et al. (2006), the key issue for the coexistence of GM and non-GM sugar beet is therefore the need to ensure seed purity."

Conclusion

Baseline data including distribution, life cycle, gene introgression and genetic diversity are now available for monitoring the use of GM beet in EU agriculture. Based on recent biosafety research, herbicide tolerance and certain virus resistance genes do not pose an environmental risk. New GM traits (e.g. drought tolerance) should be assessed on a case-by-case basis in the future.

Coexistence measures for sugar beet should primarily address seed purity in seed multiplication areas, e.g. by multiplication in isolated areas or using tetraploid pollinators so that triploid offspring have reduced fertility. Control of weed beet is more an economical than an ecological problem. The present EU threshold of 0.2 % (conventional) weed beet admixture should be re-evaluated in the light that this level of tolerated impurity still allows for the introduction of 200 weed beet seeds/per ha. As gene flow from GM sugar beet to weed beet is will occur if both flower simultaneously, management measures should include appropriate isolation distances in seed production areas and strict control of bolters in crop cultivation areas. Between-field isolation distances can be very low between GM and non-GM sugar beet as long as this crop is grown vegetative and harvest admixture is avoided.

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