

Gene flow by sexual reproduction, what did we learn for Switzerland in the context of risk assessment?

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Gene flow in agriculture

Risk of gene flow by sexual reproduction between selected crops and wild relatives is an important issue in risk assessment for the introduction of genetically modified plants (GMPs). Hybridisation and introgression may lead to transgenic wild relatives. Activity of the transgene in the wild species could confer new ecological properties to the wild species and may lead to disturbances of the ecosystem.

Investigations have been carried out since 1993 for Switzerland on conventional crops. A thorough literature screening has been done, each crop being characterised by a code [1,2,3]. Codes facilitate the evaluation of risk of gene transfer to the Swiss flora. They consist in four risk categories ranging from 0 (no effect) to 5 (high risk): Dd (dispersal of seeds), Dp (dispersal of pollen), Df (distribution frequency), Dg (effect of transgene). The last category is left out here due to lack of field experiments in Switzerland. Risk is a function of the combination of the values of the risk categories.

Empirical and experimental studies have focused on selected species. Except for one case, results were in accordance with expectations from literature. For example, a very low risk was expected for *Hordeum vulgare* and *H. murinum* and no evidence of hybridisation was observed neither in nature or in experiments [4].

Investigations on alfalfa and wheat

Thorough investigations on alfalfa and wheat have pointed out interesting features for risk assessment, that was partially not predicted by the bibliographical study. Alfalfa (*Medicago sativa* L.) is widely cultivated in Switzerland and forms feral populations. It hybridises freely with its wild relative sickle medic (*M. falcata* L.) in most parts of Switzerland, except the Unterengadin. In this particular area, hybrids have been mentioned as a rarity in literature, but none were discovered in the field. In Switzerland high hybrid rate is related to places where alfalfa and sickle medic are both tetraploid (four chromosome sets). Exclusively in the Unterengadin sickle medic is diploid (two chromosome sets) and, according to field research and experimentation, does very rarely hybridize with alfalfa [5]. Morphological and genetical analysis with isozymes and RAPD confirm these results [6]. Our research on alfalfa illustrates that genetic structure may greatly influence the risk of gene flow between crops and their wild relatives. Therefore, risk assessment in one region may not necessarily be extended to other areas. Indeed, investigations illustrate that risk assessment studies must be carried out at a regional scale.

Investigations on wheat (*Triticum aestivum* L.) allowed the development of genetic markers suitable for evaluation of gene flow with wild relatives [7]. For Switzerland, wheat can hybridise freely with jointed goatgrass (*Aegilops cylindrica* Host.), which forms rare spontaneous populations in Wallis. Nevertheless, up to now, wheat fields in Wallis are far from jointed goatgrass populations and risk of gene flow is very low [8]. Our study on wheat illustrates that distribution of the crop and its wild relatives may greatly influence risk of gene flow, and demonstrates the necessity of empirical and experimental studies. Risk assessment is a necessary prerequisite to the cultivation of GMPs in

Switzerland. The assessment of gene flow follows the precautionary principle, since the results are achieved in a first phase without using transgenic crops. Field tests prior to commercialisation and monitoring are further steps if GMPs are to be commercialised.

Consequences for future risk assessment of transgenic crops

Future risk assessment should be directed mainly in two new directions. Based on existing literature, empirical studies and experimental data, specific monitoring and study of consequences of release of the transgene in the wild should be set-up. The BUWAL has implemented a monitoring for biodiversity [9] which will be useful for monitoring of commercialised transgenic crops [10]. This concerns the conservation of the genetic of individual species, as well as that of ecosystems and their biodiversity. Ecological consequences of transgenic crops has been intensively discussed based on extrapolations for example on observations on invasive plants and conceptual and theoretical models. Nevertheless, only for a few cases empirical data exist on the ecological long term consequence of transgene escape in ecosystems and on rare events. For example, long distance migration of pollen has been rarely investigated related to the persistence of pollen fertility. Existing theoretical models need to be enhanced in order to give insights on long term consequences of introduction of transgenes in natural ecosystems.

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