

Persistence and genetic variation of feral oilseed rape (*Brassica napus*)

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Introduction:

Plants escaping from cultivation – such as oilseed rape - are one source of neophytes. Oilseed rape is capable of establishing feral populations on roadsides and other semi-natural habitats. These populations represent a factor of uncertainty regarding the potential risk of transgene escape from genetically modified oilseed rape.

Questions

- ➡ Does feral oilseed rape form persistent populations?
- ➡ Are feral oilseed rape populations a subset of single varieties or is there evidence for multiple source varieties?
- ➡ What is the extent of intraspecific hybridisation between different varieties of oilseed rape?

Methods & Results

A total of 78 sites occupied by feral oilseed rape populations were monitored from 2004 to 2008 in northwest Germany (area of Osnabrück, Lower Saxony). Seven common *B. napus* cultivars (winter-, summer oilseed rape and swede) and 18 feral populations were analysed by four SSR markers covering six loci in allotetraploid *B. napus* genome.

Eighty percent of the sites were inhabited by feral oilseed rape populations in at least two of the years studied (fig. 1). Seed set was observed in 41,5% of the feral populations.

Cross compatible relatives such as *B. rapa* & *Raphanus raphanistrum* were found in sympatry with feral oilseed rape populations. Evidence for interspecific hybridisation was found at two sites.

The analysed varieties were distinguished based on SSR markers. One to four varieties were detected in feral populations (table 2). Feral populations showed an enhanced variation within populations compared to the reference varieties (AMOVA: 66.3% versus 15.7%, table 1). There was a direct relationship between the number of different varieties detected in feral populations and the number of alleles ($r=0.53$, $p<0.05$; Spearman's rank correlation). Three feral individuals were assigned to F1- hybrids between the varieties.

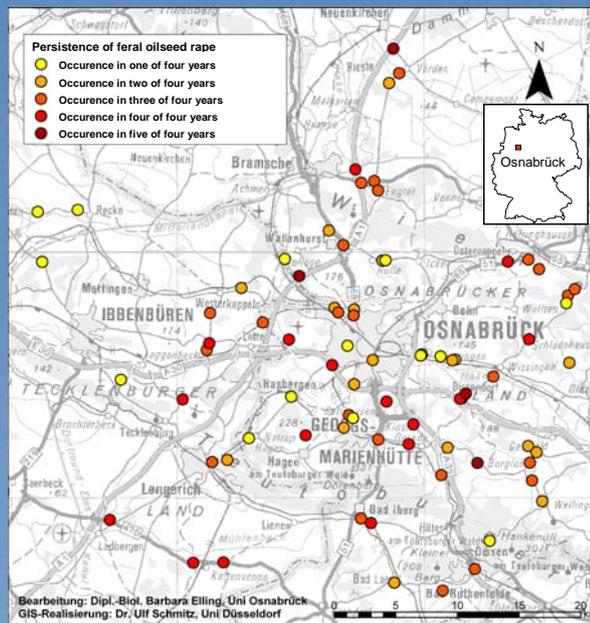


Fig. 1: Persistence of feral *Brassica* populations in the area of Osnabrück 2004 - 2007

Table 1: Analysis of molecular variance (AMOVA) among and within the analysed seven *B. napus* varieties and 18 feral populations

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Seven <i>B. napus</i> varieties				
among varieties	6	204.35	4.89	84.35
within varieties	41	37.17	0.91	15.65
Total	47	241.52	5.79	
Eighteen feral populations				
among populations	17	288.22	1.56	33.70
within populations	143	439.64	3.07	66.30
Total	160	727.86	4.64	

Table 2: Allocation of *B. napus* plants from 18 feral populations to seven *B. napus* varieties and their hybrids (AFLPop, MDL>1).

	Smart	Talent	Express	Mendel	Artus	Heros (SR)	Swede	Hybrid	None	Total
Pop10	4	1	1					1 ExpxSma	3	10
Pop11	3	3	1					1 SmaxHer	3	11
Pop14	2	1							5	8
Pop17	1				1		3		5	10
Pop54	2		3			5		1 MeruxHer	4	15
Pop57							1		7	8
Pop59						11	1		5	17
Pop61					1		2		5	8
Pop69	1						2		6	9
Pop71	4	1	1							6
Pop87					1				8	9
Pop90						2	1		6	9
Pop97	2	1	2				2		2	9
Pop105									4	4
Pop114	5	4							1	10
Pop115	5		1						2	8
Pop202	4								1	5
Pop223	5								5	5
Total	38	11	6	3	3	18	12	3	67	161

Conclusions

Multiple escapes from different source varieties & intraspecific hybridisation between these varieties are the most important sources of genetic diversity in feral oilseed rape populations.