

## Interspecific Hybridisation between Wild Relatives and *Brassica napus* to Introduce New Resistance Traits into the Oilseed Rape Gene Pool

J. SIEMENS

Institute of Biology and Applied Genetics, 01062 Berlin, Germany

e-mail: johannes.siemens@mailbox.tu-dresden.de

**Abstract:** The review of the possibilities to use interspecific hybridisation between *Brassica napus* and some wild species in the family of *Brassicaceae* for introduction of resistance to the important fungal pathogens is presented. A large collection of wild relatives as resources of resistance to *Leptosphaeria maculans*, *Alternaria brassicola*, *A. raphani* and *Plasmodiophora brassicae* has been screened. Successful hybridisation with *Brassica napus* has been achieved using *Brassica elongata*, *B. fruticulosa*, *B. souliei*, *Diplotaxis tenuifolia*, *Hirschfeldia incana*, *Coincya monensis* and *Sinapis arvensis*.

**Keywords:** *Brassica napus*; disease resistance; interspecific hybridisation; sources of resistance

Interspecific hybridisation can be easily forced in the family of *Brassicaceae*, whereas under natural conditions the gene flow is very limited (BROWN & BROWN 1996; RIEGER *et al.* 2001). Sexual incompatibility barriers were overcome by pollination of very young buds and subsequent ovule or embryo rescue techniques (TAKESHITA *et al.* 1980; INOMATA 1985). However, wide variability among different combinations was observed in the ability of pollen to germinate on the stigma, the frequency of pistils showing pollen tubes, and the ovule fertilisation efficiency (BROWN & BROWN 1996). Meanwhile the technically demanding in vitro ovule or embryo rescue techniques has been improved and several species can be used to facilitate the generation of hybrids useful for breeding programs aimed at introducing useful genes, e.g., resistance genes into *Brassica* crop plants (INOMATA 1990; METZ *et al.* 1995; BANG *et al.* 1996). Furthermore, somatic hybridisation increased the number of species, which could be used for gene transfer to the gene pool of oilseed rape (for review see: WAARA & GLIMELIUS 1995).

Oilseed rape (*Brassica napus* L.) is an amphidiploid species that originated from a spontaneous hybridisation of *Brassica rapa* L. and *Brassica oleracea* L., and contains the complete diploid chromosome sets of the highly homoeologous A genome of *B. rapa* and the C genome of *B. oleracea*. Introgression of useful traits was successfully achieved by hybridisations with the species of the B-genome *B. juncea*, *B. carinata* and *B. nigra*. These

intrageneric hybridisations with *B. napus* have been used to transfer resistance genes to *Leptosphaeria maculans* into the gene pool of oilseed rape (ROY 1984; SACRISTÁN & GERDEMANN 1986; ZHU *et al.* 1993), which has been widely used by breeders. Furthermore, intergeneric hybridisations have been achieved to transfer different resistance traits, e.g. nematode resistance to *Heterodera schachtii* (LELIVELT *et al.* 1993), fungal resistance to *Alternaria* ssp. and *L. maculans* (PLÜMPER 1995; SNOWDON *et al.* 2000; KLEWER *et al.* 2002; KLEWER & SACRISTÁN 2002), and protist resistance to *Plasmodiophora brassicae* (XING *et al.* 1988).

PLÜMPER (1995) has screened a large collection of wild relatives of *B. napus* for resistance to the important fungal pathogens *L. maculans*, *Alternaria brassicicola*, *A. brassicae*, and *A. raphani*. A similar screening of a large collection of wild relatives of *B. napus* has been extended to the protist *Plasmodiophora brassicae* (SCHOLZE & HAMMER 1998). In Table 1 the species were listed, which show resistance to one of these pathogens and which have been used for hybridisation studies. Successful hybridisations with *B. napus* have been achieved using *B. elongata*, *B. fruticulosa*, *B. souliei*, *Diplotaxis tenuifolia*, *Hirschfeldia incana*, *Coincya monensis*, *Sinapis arvensis* (PLÜMPER 1995). All these hybrids showed resistance to *L. maculans* in a cotyledon test, but resistance to *Alternaria* was lost in the hybrids *B. napus* × *B. souliei* and reduced in *B. napus* × *B. elongata* compared to the wild species. The hybrids *B. napus* × *Hirschfeldia*

Table 1. Relatives of *Brassica napus*, which are potential sources of resistance to pathogens *Leptosphaeria maculans*, *Alternaria brassicicola*, *A. brassicae*, *A. raphani*, and *Plasmodiophora brassicae*

Relative of <i>B. napus</i>	Resistance to	Reference
<i>B. elongata</i>	<i>L. maculans</i> <i>A. brassicicola</i> , <i>A. brassicae</i> <i>A. raphani</i>	PLÜMPER (1995) KLEWER <i>et al.</i> (2002) KLEWER & SACRISTÁN 2002
<i>B. souliei</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> , <i>A. raphani</i>	PLÜMPER (1995)
<i>B. fruticulosa</i>	<i>L. maculans</i> <i>A. brassicicola</i> , <i>A. brassicae</i> , <i>A. raphani</i> <i>L. maculans</i> <i>A. brassicicola</i> , <i>A. brassicae</i>	PLÜMPER (1995) KLEWER <i>et al.</i> (2002) ZHU & SPANIER (1991) PLÜMPER (1995)
<i>Sinapis alba</i>	<i>A. raphani</i>	KLEWER <i>et al.</i> (2002)
<i>Sinapis arvensis</i>	<i>L. maculans</i> <i>A. brassicicola</i> , <i>A. brassicae</i>	PLÜMPER (1995) SNOWDON <i>et al.</i> (2000)
<i>Raphanus sativus</i>	<i>L. maculans</i> <i>Plasmodiophora brassicae</i>	PLÜMPER (1995) XING <i>et al.</i> (1988)
<i>Eruca vesicaria</i>	<i>L. maculans</i>	PLÜMPER (1995)
<i>Diplotaxis erucoides</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> <i>A. raphani</i>	KLEWER <i>et al.</i> (2002) KLEWER & SACRISTÁN (2002)
<i>Diplotaxis tenuifolia</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> <i>A. raphani</i>	PLÜMPER (1995) KLEWER <i>et al.</i> (2002)
<i>Coincya monensis</i>	<i>L. maculans</i>	PLÜMPER (1995), WINTER <i>et al.</i> (2002)
<i>Capsella bursa-pastoris</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> , <i>A. raphani</i> <i>Plasmodiophora brassicae</i>	PLÜMPER (1995) SIEMENS (unpubl.)
<i>Camelina sativa</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> <i>A. raphani</i>	PLÜMPER (1995)
<i>Hemicrambe fruticulosa</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> <i>A. raphani</i>	PLÜMPER (1995)
<i>Hirschfeldia incana</i>	<i>L. maculans</i>	PLÜMPER (1995), KLEWER <i>et al.</i> (2002)
<i>Hesperis matronalis</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> , <i>A. raphani</i>	PLÜMPER (1995)
<i>Neslia paniculata</i>	<i>A. brassicicola</i> , <i>A. brassicae</i> , <i>A. raphani</i>	PLÜMPER (1995)

*incana*, *B. napus* × *Sinapis arvensis*, and *B. napus* × *Coincya monensis* has been successfully backcrossed to *B. napus* (PLÜMPER 1995). *S. arvensis* appeared as useful and valuable source of blackleg (*L. maculans*) resistance to oilseed rape (*B. napus*), because this species contains resistance to an isolate which has been found to overcome resistance originating from species with the *Brassica* B genome, until now the major source for interspecific transfer of blackleg resistance (SNOWDON *et al.* 2000). Regarding *Alternaria* resistance *B. elongata* appeared as worthless source, because the weak resistance of the hybrid is completely lost after two backcrosses with *B.*

*napus* (KLEWER *et al.* 2002; KLEWER & SACRISTÁN 2002). In contrast, a stable and valuable *Alternaria* resistance has been introduced by a backcross program using the hybrids *B. napus* × *Diplotaxis erucoides* (KLEWER *et al.* 2002; KLEWER & SACRISTÁN 2002).

In summary, all these intra- and intergeneric hybrids point to value of introgression from wild relatives but also to the bottle-neck of the hybridisation approach. Genetic stability of the resistance traits in the genetical background of *B. napus* within the subsequent backcross generations is the crucial characteristic for an introgression of new genes in the gene pool of oilseed rape.

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