and other properties, such as bulk modulus, which are important. The highest intrinsic negative thermal expansion reported in the NZP family is about -1×10^{-6} per °C. The thermal expansion for ZrW_2O_8, on the other hand, is -8.7×10^{-6} per °C.

Roy and Agrawal also suggested that the thermal expansion mechanism in ZrW_2O_8 is the same as in the NZP family. Actually, the thermal expansion of cordierite ($Mg_2Al_2Si_5O_{18}$), β-eucryptite ($LiAlSiO_4$), and NZP is dominated by the thermal expansion of Mg–O, Li–O or Na–O bonds[5]. Such materials never show a strong negative thermal expansion of the unit-cell volume.

The mechanism for thermal expansion in ZrW_2O_8 is very different from that of the NZP family[2]. In the ZrW_2O_8 family, transverse thermal motion of oxygen atoms causes negative thermal expansion, the same mechanism that causes negative thermal expansion in various forms of silica over limited temperature ranges that do not include room temperature. The surprising property of the ZrW_2O_8 family is that negative thermal expansion occurs over such a wide temperature range.

Roy and Agrawal also comment on the use of anisotropic materials in applications. It is true that those at Corning have made good use of anisotropic materials, such as cordierite ($Mg_2Al_4Si_5O_{18}$), for low thermal expansion applications, but it has been generally appreciated that isotropic materials would be favoured for most applications[9]. The anticipated link between anisotropy and microcracking has been verified experimentally in the NZP family[10], and those working on the family considered it a major achievement when they found very low anisotropy in the $(Ca,Sr)Zr_4P_6O_{24}$ system.

The thermal expansion properties in the ZrW_2O_8 family are unlike those of any other known materials. Their intrinsic negative linear thermal expansion over a broad temperature range (including room temperature) is much higher than reported for any other material. This, and the strictly isotropic behaviour, open up many potential applications that could not be contemplated with other materials, such as those of the NZP family.

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Gene flow from transgenic crops

Gene flow from crops to related wild species must be considered when assessing the potential environmental impact of cultivating genetically modified plants[1]. Evidence of pollen dispersal within species has been found for several crops but little information is available on spontaneous gene flow from crops to related species with simultaneous flowering periods[2,3]. To study the genetic mechanisms involved, we have developed an intergeneric model of gene flow from transgenic oilseed rape (*Brassica napus* L.; genotype, AACC; diploid chromosome number, $2n=38$) containing one copy of the *bar* gene, which confers resistance to the herbicide Basta (glufosinate ammonium), to wild radish (*Raphanus raphanistrum* L.; genotype, RrRr; $2n=18$), a widely distributed weed.

We obtained oilseed rape × wild radish F_1 interspecific hybrids[4] and studied the four successive generations under field conditions. The hybrids were surrounded by wild radish plants.

All oilseed rape varieties used as mother plants produced seeds. In the first generation, female fertility of the F_1 interspecific hybrids was poor, with only 28.6% producing seeds. The number of seeds was ten times higher at the second generation, and the increased female fertility was confirmed with the third-generation plants. The seed set (ranging from 0 to 5,673 seeds per plant) was, in some plants, close to the observed fertility of wild radish plants (500 to 10,000 seeds per plant; Table 1). In all generations, the percentage of seed germination never limited the production of successive progeny, which ranged from 74.2 to 88.9%.

In agreement with previous data[4], 99.5% of first-generation interspecific hybrids had the expected genomic structure, ACRr, $2n=28$, that is, half of the genome of each parent. Of the second-generation hybrids, 48% corresponded to the structure, ACRrRr, $2n=37$. All others had either more chromosomes (33.4% of the total, mainly showing an amphidiploid structure, AACCRrRr, $2n=56$) or less chromosomes (18.6% of the total, mainly showing the same chromosome number as the mother plant, ACRr, $2n=28$). Female fertility was highly dependent on the chromosome number of the mother plant. Mother plants with $2n=56$, $2n=37$ and $2n=28$ produced from 0.9, 8.4 and 59.7 seeds per plant, respectively. At the third generation, chromosome number generally decreased, with 83.6% of the plants having less than 28 chromosomes. The plants with the lowest chromosome numbers were the most fertile. We confirmed this tendency towards chromosome decrease in the fourth-generation plants, with 89.5% of the plants having less than 27 chromosomes. We observed a chromosome number close to that of wild radish ($2n=18$) in 25.4% of the plants (Table 1).

Basta resistance in the F_1 interspecific hybrids displayed mendelian segregation, that is, a 1:1 ratio of resistant and susceptible plants, as the oilseed rape mother plants were heterozygous for the *bar* transgene. However, because of unreduced gametes, the *bar* gene transmission was high in first-generation interspecific hybrids. The *bar* gene transmission was dependent on the chromosome number of the mother plant and decreased in successive generations (Table 1).

It seems that intergeneric gene flow might mainly occur by transgene introgression within the genome of the weeds, but slowly and at a low probability under natural optimal conditions because four generations were needed to provide herbicide-resistant plants with a chromosome number and morphology close to that of the weed. It is likely that under normal agricultural conditions this event is rare when the wild radish is the female parent[5].

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Table 1 Gene flow analysis from transgenic oilseed rape to wild radish

	Female fertility				Chromosome number				Basta resistance	
	No. plants	Seeds per 100 flowers	Seeds per plant	Plants with ≥1 seed	No. plants	Range 2*n*	Mode 2*n*	Plants in mode (%)	No. plants	Resistant of plants (%)
Male-sterile oilseed rape	589	43.2	29.2	100	589	(38)	[38]	100	589	100
Generation 1	1,301	0.2	1.1	28.6	2,057	(28–56)	[28]	99.5	2,619	51.8
2	251	1.5	11.9	42.2	686	(25–84)	[37]	48.0	674	81.9
3	443	7.9	229.3	82.5	1,083	(18–60)	[24–27]	45.3	1,028	57.2
4					787	(18–59)	[21–23]	45.3	3,349	23.5

Chromosome number was established either by mitotic chromosome counting or by flow cytometry[4,6]. The presence of the transgene was checked by spraying herbicide solution on 3-4-leaf-stage seedlings[4].