

**Introgression of resistance to multiple pathotypes of *Plasmodiophora brassicae* from turnip (*Brassica rapa* ssp. *rapifera*) into spring *B. napus* canola**

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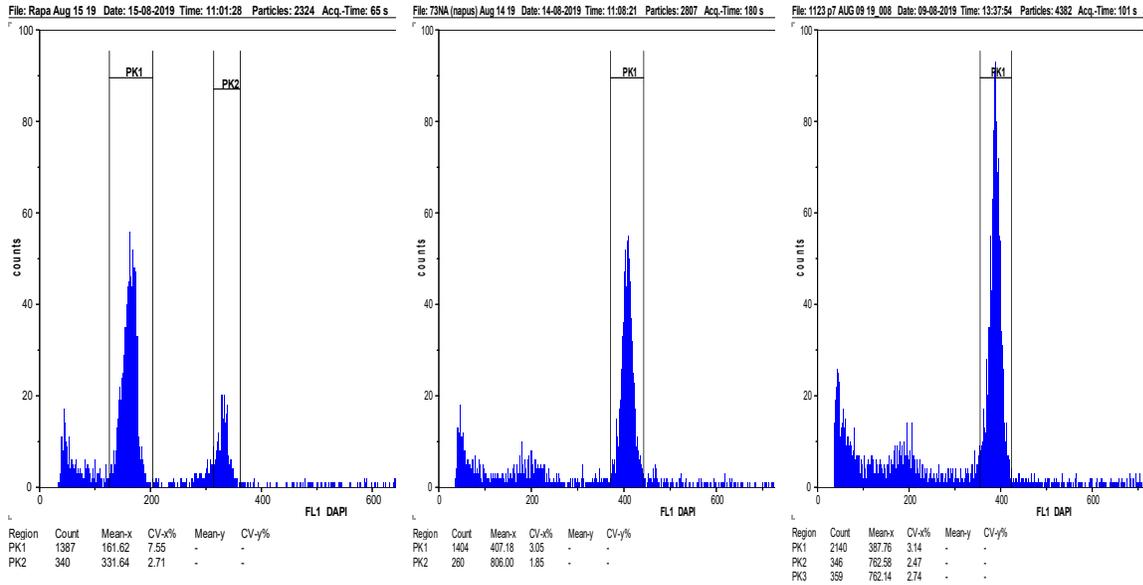
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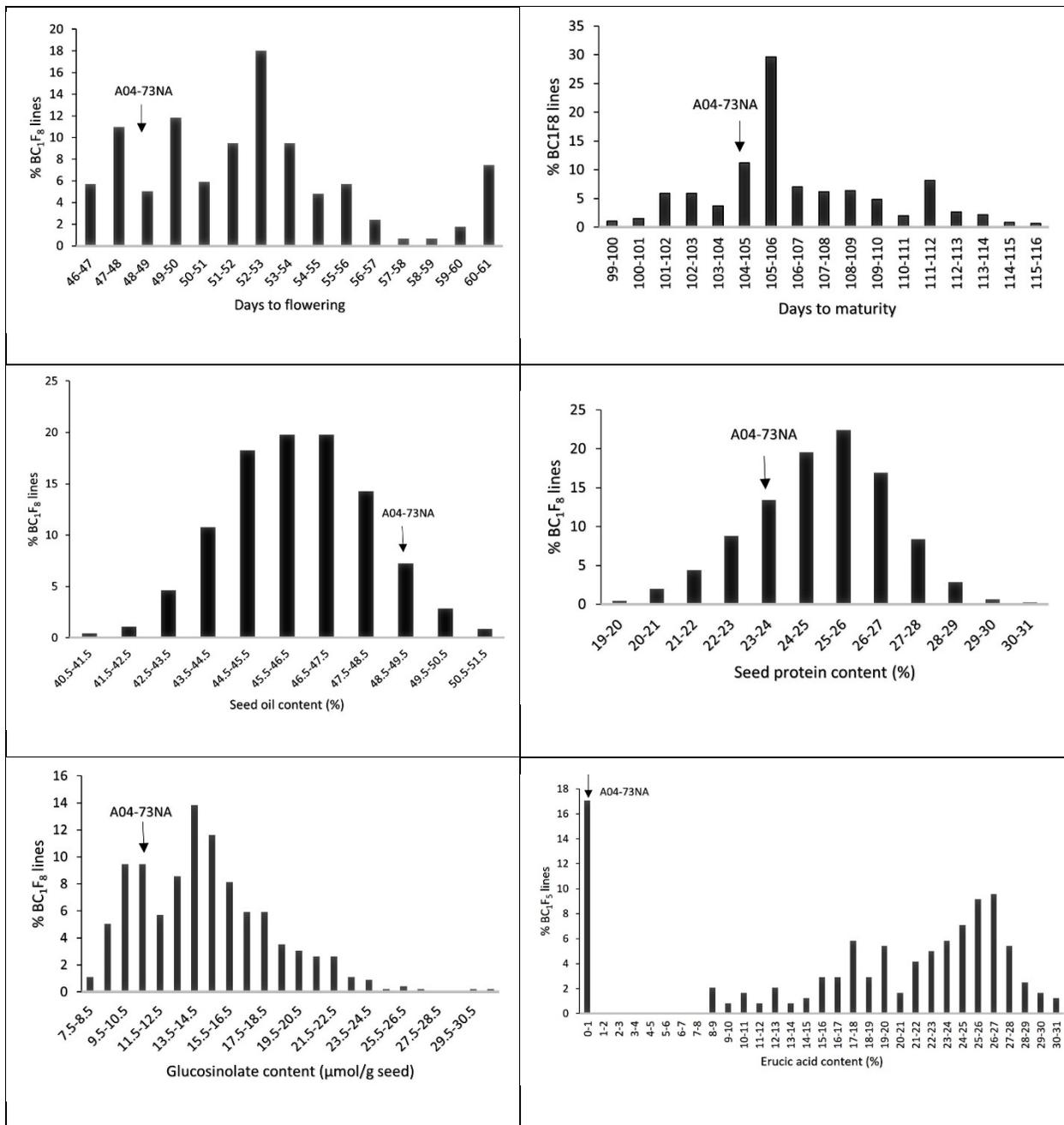
Number of pages = 5

Number of Supplemental Figures = 2

Number of Supplemental Tables = 2



**Figure S1.** DNA histogram showing relative nuclear DNA content in the *Brassica rapa* and *B. napus* parents and in a representative  $BC_1F_6$  plant. The X-axis shows relative quantity of DNA in a cell and the Y-axis shows the number of cells counted.



**Figure S2.** Distribution of the BC<sub>1</sub>F<sub>8</sub> lines of (*Brassica napus* × *B. rapa*) × *B. napus* interspecific cross, grown in nursery plots in 2020, for days to flowering ( $n = 452$  lines), days to maturity ( $n = 452$ ), and seed oil ( $n = 450$ ), protein ( $n = 450$ ), and glucosinolate ( $n = 450$ ) contents. Erucic acid content in seed oil of the BC<sub>1</sub>F<sub>5</sub> plants ( $n = 240$ ) grown in greenhouse also presented. The value for the *B. napus* parent A04-73NA are indicated by vertical arrow.

**Table S1.** Performance of the BC<sub>1</sub>F<sub>8</sub> lines ( $n = 450-452$ ; see Figure S2) derived from (*B. napus* × *B. rapa*) × *B. napus* interspecific cross and their spring *B. napus* parent A04-73NA tested in nursery plots in 2020, and the BC<sub>1</sub>F<sub>9</sub> lines ( $n = 112$ ) and an open-pollinated cultivar UA CountyGold tested in replicated field trials in 2021 for different agronomic and seed quality traits.

**a. BC<sub>1</sub>F<sub>8</sub> lines tested in 2020**

Population	Seed yield		Days to flowering		Days to maturity	
	Range	Mean ± SE	Range	Mean ± SE	Range	Mean ± SE
BC <sub>1</sub> F <sub>8</sub>	-	-	46 - 60	51.0 ± 0.2	99 - 115	105.8 ± 0.2
A04-73NA	-	-	46 - 49	48.0 ± 0.2	100 - 111	103.8 ± 0.6
	Oil (%)		Protein (%)		Glucosinolate (μmol/g)	
BC <sub>1</sub> F <sub>8</sub>	40.6 - 51.5	46.2 ± 0.1	19.2 - 30.0	24.9 ± 0.1	7.8 - 31.2	14.4 ± 0.6
A04-73NA	45.3 - 51.2	48.7 ± 0.3	21.2 - 26.6	23.4 ± 0.3	10.2 - 14.2	12.0 ± 0.2

**b. BC<sub>1</sub>F<sub>9</sub> lines tested in 2021**

	Seed yield		Days to flowering		Days to maturity	
	Range	Mean ± SE	Range	Mean ± SE	Range	Mean ± SE
BC <sub>1</sub> F <sub>9</sub>	1008 - 3626	1749 ± 17.8	42 - 55	48.7 ± 0.2	86 - 113	96.8 ± 0.2
UA CountyGold	1033 - 2634	1744 ± 93.9	47 - 53	49.0 ± 0.6	91 - 113	97.0 ± 1.5
	Oil (%)		Protein (%)		Glucosinolate (μmol/g)	
BC <sub>1</sub> F <sub>9</sub>	40.8 - 46.6	42.7 ± 0.1	27.1 - 31.8	30.2 ± 0.1	13.8 - 28.9	18.4 ± 0.6
UA CountyGold	43.1 - 46.8	44.8 ± 0.3	28.1 - 31.5	30.1 ± 0.3	15.2 - 22.3	18.3 ± 0.6
	Saturated fatty acid (%)					
BC <sub>1</sub> F <sub>9</sub>	5.96 - 6.71	6.18 ± 0.03				
UA CountyGold	6.28 - 6.30	6.30 ± 0.01				

**Table S2.** Analysis of variance for agronomic and seed quality traits of the BC<sub>1</sub>F<sub>9</sub> lines derived from (*B. napus* × *B. rapa*) × *B. napus* interspecific cross. Data from three trials conducted in 2021 were used in analysis.

Source	Seed yield				Days to flowering				Days to maturity			
	<i>df</i>	MS	F value	<i>p</i> value	<i>df</i>	MS	F value	<i>P</i> value <sup>††</sup>	<i>df</i>	MS	F value	<i>p</i> value
Genotype <sup>†</sup>	112	408096	4.07	<0.0001***	112	38.36	45.05	<0.0001***	112	19.36	8.3	<0.0001***
Location <sup>‡</sup>	2	71488	0.71	0.98	2	3.72	4.36	0.027*	2	2.46	1.05	0.70
G × L <sup>§</sup>	224	104300	1.04	0.76	224	1.52	1.78	<0.0001***	224	2.22	0.95	0.701
	Oil content				Protein content				Glucosinolate content			
Genotype <sup>†</sup>	44	3.44	4.15	<0.0001***	44	1.24	1.29	0.11	44	50.66	26.79	<0.0001***
Location <sup>‡</sup>	2	2.92	3.54	0.06	2	0.17	0.18	0.33	2	35.11	18.78	<0.0001***
G × L <sup>§</sup>	88	0.75	0.91	0.48	88	0.52	0.54	0.000009***	88	3.46	1.83	0.000007***

<sup>†</sup> The field lines developed from (*B. napus* × *B. rapa*) × *B. napus* interspecific cross.

<sup>‡</sup> Three different locations (Michener, West-240 and St. Albert research farms).

<sup>§</sup> Combination of the genotype and location.

<sup>††</sup> \* and \*\*\* = *p* < 0.05 and 0.001, respectively.