

Research Article

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Rare inheritance studies on yellow sarson for petalous and apetalous traits

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Abstract

This study investigates the inheritance pattern of petalous and apetalous traits in yellow sarson (*Brassica rapa* var yellow sarson) and its significance for breeding efforts. Utilizing three crucial crosses between petalous (Pant Sweta, Pant Girija, YSH0401) and ‘apetalous’ parents, we observed the absence of apetalous plants in the F₁ generation, indicating dominant inheritance of petalous plants. The F₂ generation consistently displayed a 3:1 ratio of petalous to apetalous plants, confirming the dominance of the petalous trait. Chi-squared tests on each generation supported this conclusion. Backcrosses with petalous parents yielded no fruit, reinforcing the dominance of the petalous trait. Chi-squared tests on these backcrosses further confirmed the dominance inheritance pattern. Conversely, backcrosses with apetalous parents consistently exhibited a 1:1 ratio, highlighting the recessive nature of the apetalous trait. The study underscores the importance of understanding the inheritance pattern of petalous and apetalous traits in *B. rapa* var yellow sarson crop, as it has implications for breeding goals. Knowledge on trait inheritance can guide future breeding strategies, facilitating the transfer of the apetalous trait as needed. This study provides valuable insights for genetic investigations and breeding initiatives in *B. rapa* var yellow sarson.

Introduction

In India yellow sarson (*Brassica rapa* var yellow sarson) is an important oilseed crop in India and is valued for its oil-rich seeds (Sood and Kumari, 2019); with more oil content than other species of the rapeseed mustard group, yellow sarson becomes an important crop. The present status of rapeseed mustard as the third most important source of vegetable oils is attributable to the success of plant breeders in developing low glucosinolates and zero erucic acid varieties. Quality-wise the improved rapeseed oil is now equivalent to peanut and olive oil. From the nutritional, cooking and stability points of view, possibilities exist for further alterations in the fatty acid composition in favour of increased levels of oleic and linoleic acids simultaneously with a reduction in linolenic acid content (Ahuja and Banga, 1993). Yellow sarson exhibits a beautiful flower colour and diverse floral parts, ranging from petalous to apetalous flowers. It is predominantly found in the petalous form, with some mutants displaying the apetalous trait. Yellow sarson presents a captivating subject for research, specifically focused on unravelling the inheritance patterns associated with the petalous and apetalous traits in this plant species (Rahman, 2001). The petalous trait, marked by vibrant yellow petals, is noteworthy due to its pivotal role in attracting pollinators, particularly bees (Jager *et al.*, 2017). This attraction facilitates effective cross-pollination, thereby enhancing seed production and the potential for increased yield. Conversely, the apetalous trait, characterized by the absence of petals, has its own set of merits in specific agricultural contexts (Evans *et al.*, 2003). The apetalous character in rapeseed has been studied for two reasons. First, a physiological potential advantage has been claimed. Petals cause a reduction in reflection of photosynthetically active radiations (PAR) so that apetalous lines transmit 34% of the incident PAR to the photosynthetic tissues versus 17% in the petalous ones. Moreover, on the main stem, leaves of apetalous plants persist longer and pod production and fertility are higher than in the near isogenic conventional lines. Second, lines without petals may reduce sclerotinia (*Sclerotinia sclerotiorum*) disease transmitted to healthy tissue by petals contaminated with this pathogen, the lack of petals simplifies the harvesting process, mitigating concerns related to petal contamination in harvested seeds (Baltzer *et al.*, 2002). Apetalous genotypes within *Brassica* species exhibit diverse genetic origins. The majority of these genotypes were either serendipitously discovered through spontaneous mutations (Singh, 1961a, 1961b; Buzza, 1983; Lu and Fu, 1990) or emerged as by-products of other research endeavours (Malik *et al.*, 1999). The inheritance



patterns of the apetalous trait vary across different sources. Investigations into genotypes with apetalous flowers are most extensively conducted in *Brassica napus*. Depending on the specific origin of the apetalous trait, it is regulated by either two recessive genes (Buzza, 1983), four recessive genes (Lu and Fu, 1990), an epistatic interaction involving recessive alleles at a pair of homologous loci or interactions between alleles at three loci (Kelly *et al.*, 1995). Regarding *B. rapa* var yellow sarson crops, very scant studies are conducted for petalous and apetalous trait inheritance. Previous studies on *B. rapa* reveal the fact that the trait is controlled by one single recessive gene (Singh, 1961a, 1961b; Cours and Williams, 1977). To date, no research has been conducted over due course of time. The benefits of apetalous traits also drive us in the direction of studying the inheritance pattern of the genes involved in petalous and apetalous traits so that we can incorporate the trait in our hybrid varieties. By conducting segregation and chi-squared analyses on an unprecedented F₂ population exhibiting petal loss derived from a novel yellow sarson cross, we aim to pinpoint loci controlling the apetalous trait in this crop. Achieving this objective will fill a critical knowledge gap inhibiting targeted breeding efforts. More broadly, it will provide fundamental insight into the context-specific genetic regulation of floral morphology with transferability across *Brassica* oilseed crops. Our findings will aid preservation of genetic diversity important for global food security in a changing climate.

Materials and methods

Plant materials

Experiments were conducted at the Crop Research Center, GBPUAT, Pantnagar, India using three yellow sarson crosses: (1) Pant Sweta (petalous) × apetalous, (2) Pant Girija (petalous) × apetalous and (3) YSH0401 (petalous) × apetalous. The petalous parents were selected from the university's germplasm collection. F₁, F₂, BC₁P₁ and BC₂P₂ generations were developed for each cross through controlled pollinations from 2019 to 2021.

Phenotypic evaluation

The petalous trait (yellow petals present) and apetalous trait (no petals) were visually scored in a binary qualitative manner in the parents and different generations (F₁, F₂, BC₁P₁ and BC₂P₂). Numbers of plants exhibiting each phenotype were recorded.

Statistical analysis

Segregation ratios were analysed using chi-squared tests to check for goodness-of-fit between observed phenotypic ratios and expected genetic ratios. The chi-squared (χ^2) formula was as below:

$$\chi^2 = \sum ((\text{Observed} - \text{Expected})^2 / \text{Expected})$$

where the summation is overall phenotypic classes.

For monogenic inheritance, the expected phenotypic ratios were based on the segregation of a single gene with two alleles (A and a) exhibiting complete dominance. The expected ratios were, F₂ generation: 3 petalous:1 apetalous BC₁ generation: 1 petalous:1 apetalous

For digenic inheritance, the expected ratios were based on the segregation of two independently assorting genes. Several possible two-gene models with varying degrees of dominance were

tested. The χ^2 statistics was calculated for each generation and genetic model. This was compared to critical values from the χ^2 distribution at a α significance level of 0.05 to evaluate if the deviations between observed and expected ratios were significant. Significant deviations indicate that the observed inheritance does not follow the proposed genetic model.

Results

Inheritance pattern of petalous trait in Pant Sweta × apetalous cross

From Table 1, it is clear that in the F₁ generation, 20 plants were evaluated. All 20 F₁ plants exhibited petalous flowers, yielding a petalous:apetalous ratio of 1:0. In the F₂ population consisting of 230 plants, we observed 163 petalous and 67 apetalous individuals. This equates to a petalous:apetalous ratio of 3:1 which aligns with the expectation under monogenic inheritance with dominance of the petalous trait. The χ^2 value was calculated to be 1.86, indicating no significant deviation between the expected and observed ratios.

The backcross with the petalous parent Pant Sweta (BC₁P₁) included 320 plants, all of which displayed petalous flowers. The 1:0 petalous:apetalous ratio mirrors the anticipated ratio given the dominance of petalous trait. A chi-squared test showed no significant difference between the observed and expected ratios ($\chi^2 = 0.00$). The backcross with the apetalous parent (BC₂P₂) consisted of 310 plants. We recorded 160 petalous and 150 apetalous progeny, precisely matching the expected 1:1 ratio under monogenic inheritance. This was further supported by a χ^2 value of 0.32.

Inheritance pattern of petalous trait in Pant Girija × apetalous cross

Table 2 and Fig. 1 provide a clear picture about plants in F₁, F₂, BC₁P₁ and BC₂P₂. The F₁ generation comprised of 25 plants, all exhibiting petalous flowers. The 1:0 petalous:apetalous ratio agrees with the prediction under monogenic inheritance with dominance of the petalous trait. In the F₂ population of 250 plants, 163 petalous and 87 apetalous individuals were observed more clearly in Fig. 1, reflecting a 3:1 ratio as expected by the monogenic model. The χ^2 value was 1.52 ($P > 0.05$), confirming no significant deviation from the hypothesized 3:1 ratio.

The backcross with petalous parent Pant Girija (BC₁P₁) contained 340 progeny, all of which displayed petalous flowers. The 1:0 petalous:apetalous ratio aligns precisely with the prediction given petalous trait dominance. A chi-squared test showed no difference between the observed and expected ratios ($\chi^2 = 0.0$).

The backcross with the apetalous parent (BC₂P₂) consisted of 320 plants. We recorded 170 petalous and 150 apetalous individuals, accurately matching the postulated 1:1 ratio under monogenic inheritance. The χ^2 value was 0.38 ($P > 0.05$), substantiating the lack of deviation between the observed and expected.

Inheritance pattern of petalous trait in YSH0401 × apetalous cross

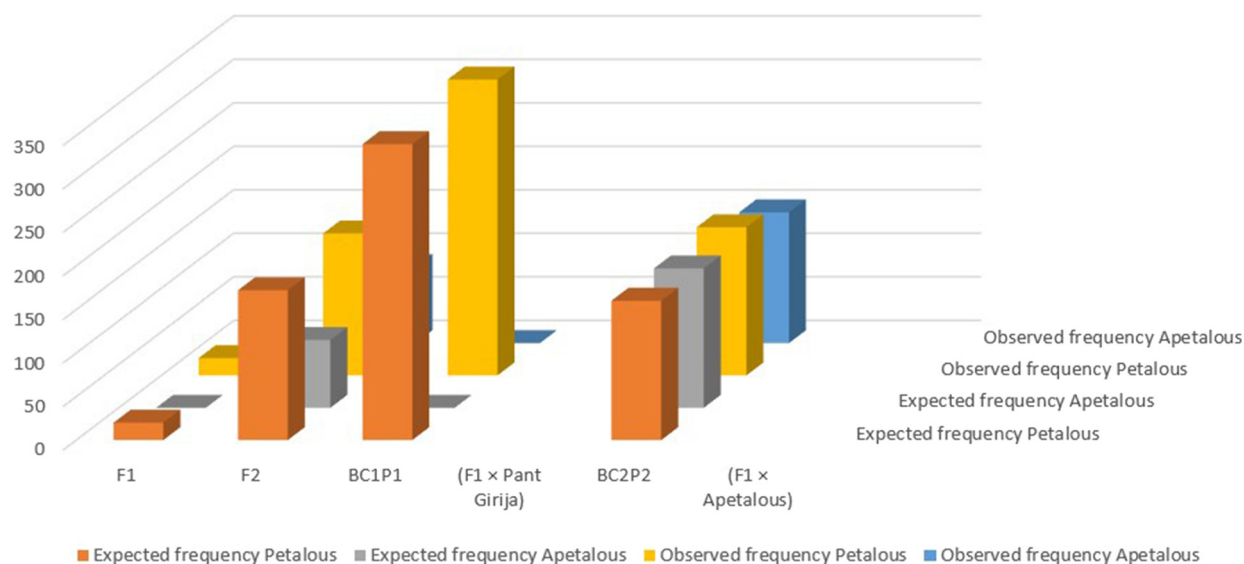
Table 3 and Fig. 2 show us that the F₁ generation consisted of 30 plants, all exhibiting petalous flowers and confirming the expected 1:0 petalous:apetalous ratio under monogenic inheritance with dominance of the petalous trait. In the F₂ population of 260 plants, we recorded 170 petalous and 90 apetalous individuals,

Table 1. Inheritance pattern of petalous condition in different generation of cross Pant Sweta (petalous) × apetalous

Generation	Total number of plants	Expected frequency		Observed frequency		Expected ratio	χ^2 cal.	χ^2 tab. (0.05, 1 df)
		Petalous	Apetalous	Petalous	Apetalous			
F ₁	20	20	0	20	0	1:0		
F ₂	230	172	58	163	67	3:1	1.86	3.84
BC ₁ P ₁ (F ₁ × Pant Sweta)	320	320	00	320	00	1:0	0.00	3.84
BC ₂ P ₂ (F ₂ × apetalous)	310	155	155	160	150	1:1	0.32	3.84

Table 2. Inheritance pattern of petalous condition in different generation of cross Pant Girija (petalous) × apetalous

Generation	Total number of plants	Expected frequency		Observed frequency		Expected ratio	χ^2 cal.	χ^2 tab. (0.05, 1 df)
		Petalous	Apetalous	Petalous	Apetalous			
F ₁	25	25	0	25	0	1:0		
F ₂	250	172	78	163	87	3:1	1.52	3.84
BC ₁ P ₁ (F ₁ × Pant Girija)	340	340	00	340	00	1:0	0.00	3.84
BC ₂ P ₂ (F ₁ × apetalous)	320	160	160	170	150	1:1	0.38	3.84

**Figure 1.** Segregation pattern in Pant girija × apetalous cross.

reflecting a ratio of 3:1 petalous:apetalous as predicted by the inheritance model. The χ^2 statistic was 1.80 ($P > 0.05$), substantiating no significant deviation from the 3:1 expectation.

The backcross with petalous parent YSH0401 (BC₁P₁) contained 350 progeny, all petalous. The 1:0 petalous:apetalous ratio precisely matches predictions given the dominant petalous phenotype. A chi-squared test validated the lack of difference between observed and expected ($\chi^2 = 0.00$).

For the backcross with the apetalous parent (BC₂P₂), among 330 plants, we observed 170 petalous and 160 apetalous individuals. This 1:1 ratio again aligns accurately with assumptions

under monogenic inheritance. The χ^2 statistic of 0.30 ($P > 0.05$) further confirms that the observed numbers match the expected values.

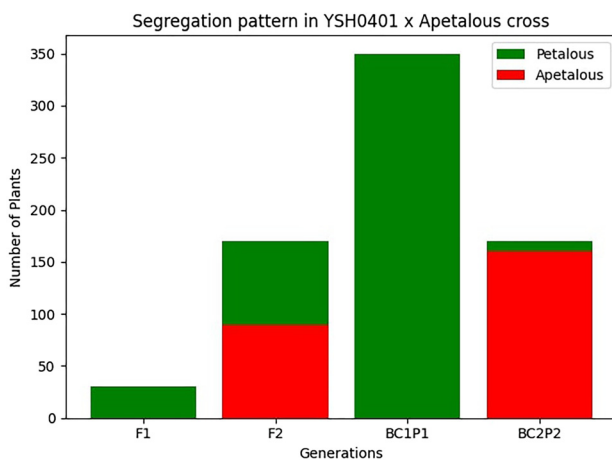
The results endorse the proposed monogenic, dominance inheritance pattern for petalous trait in the YSH0401 × apetalous *Brassica* cross, with complete dominance over the apetalous phenotype.

Crosses and their seed yield

From Table 4, it is clear that all three crosses below had more yield in petalous genotypes than in apetalous genotypes.

Table 3. Inheritance pattern of petalous condition in different generation of cross YSH0401 (petalous) × apetalous

Generation	Total number of plants	Expected frequency		Observed frequency		Expected ratio	χ^2 cal.	χ^2 tab. (0.05, 1 df)
		Petalous	Apetalous	Petalous	Apetalous			
F ₁	30	30	0	30	0	1:0		
F ₂	260	180	80	170	90	3:1	1.80	3.84
BC ₁ P ₁ (F ₁ × YSH0401)	350	350	00	350	00	1:0	0.00	3.84
BC ₂ P ₂ (F ₂ × apetalous)	330	165	165	170	160	1:1	0.30	3.84

**Figure 2.** Petalous and apetalous plant numbers in different generations.

Pant Sweta × apetalous cross:

- Petalous plants achieved the highest seed yields in the F₁ generation at 9.4 g/plant.
- In the segregating F₂ generation, petalous plants averaged 8.1 g/plant, while apetalous averaged 7.1 g/plant. Petalous significantly outpaced apetalous plants by 1.2 times.
- In the backcross BC₂P₂, the seed yield gap between petalous at 7.7 g/plant and apetalous at 6.9 g/plant was at 1.1×.

Pant Girija × apetalous cross:

- Petalous and apetalous plant effects can be compared from the F₂ and backcross generations. In the F₂, petalous plants had a seed yield of 7.2 g/plant versus 6.2 g/plant for apetalous.
- This 1.2× yield advantage for petalous over apetalous also persisted in the BC₂P₂ generation with petalous at 7.5 g/plant and apetalous at 6.1 g/plant, a 1.2× ratio.
- Thus across all generations, petalous plants significantly outyielded apetalous plants by around 20%.

YSH0401 × apetalous cross:

- The highest seed yields were recorded in the F₁ at 9.9 g/plant with all petalous plants.
- In the F₂ generation, yields of 6.7 g/plant for petalous plants and 5.1 g/plant for apetalous plants were observed, a moderately high 1.3× yield gap.

- This gap in the backcross BC₂P₂ generation to 7.8 g/plant for petalous plants and 6.7 g/plant for apetalous plants, was consistent
- Overall, the benefit of petalous plants for seed yield relative to apetalous plants was consistent across generations.

Seed yields were superior for petalous plants across all crosses and generations, with the relative yield advantage ranging from 1.1× to 1.3× over the corresponding apetalous plants.

Discussion

A comprehensive investigation into the inheritance pattern of the petalous condition in various *Brassica* plants has provided valuable insights into the genetic dynamics of this trait. The consistent observation of complete dominance of the petalous trait in the F₁ generations across different crosses aligns with classical Mendelian genetics, establishing a solid foundation for understanding the genetic control of this important characteristic (Stern, 1970).

The anticipation of a 3:1 ratio in the F₂ generation further confirmed the dominance of the petalous allele, offering practical implications for plant breeders. The ease of obtaining petalous plants due to the dominant nature of the trait simplifies the selection process. However, the persistence of the petalous trait in backcross generations (BC₁P₁ and BC₂P₂) emphasizes the challenges associated with incorporating the apetalous trait into *Brassica* varieties. The need for six to seven generations of backcrossing to achieve a desirable apetalous genotype underscores the stability and dominance of the petalous allele (Chapman *et al.*, 1984).

The chi-squared analysis supports the adherence to an expected 1:1 ratio in the backcross generations, providing statistical validation for the observed dominance pattern (Huang *et al.*, 2006). This concordance between the expected and observed ratios enhances the robustness of the study's findings and contributes to the reliability of the identified genetic patterns.

The implications of these findings extend beyond the immediate understanding of petalous inheritance in *Brassica* plants. Plant breeders can leverage this knowledge to make informed decisions in selecting and developing plant lines with specific trait expressions. The dominance pattern observed in this study guides breeding efforts aimed at improving *Brassica* varieties with the desired petalous characteristics. This, in turn, contributes to a broader goal of advancing crop improvement and enhancing agricultural sustainability.

In advancing the knowledge of this subject, future research could delve deeper into the molecular mechanisms underlying

Table 4. Various generations and crosses and their seed yield

Crosses	Generations																				
	Pant Sweta × apetalous							Pant Girija × apetalous							YSH0401 × apetalous						
	TNP	NPP	NAP	SYPP	SYAP	ASYG	TNP	NPP	NAP	SYPP	SYAP	ASYG	TNP	NPP	NAP	SYPP	SYAP	ASYG			
P ₁	15	15	0	8.2	Nil	8.2	15	15	0	8.3	Nil	8.3	15	15	0	8.5	Nil	8.5			
P ₂	15	0	15	Nil	6.5	6.5	15	0	Nil	6.7	6.7	15	0	15	Nil	6.9	6.9	6.9			
F ₁	20	20	0	9.4	Nil	9.4	25	25	0	9.4	Nil	9.4	30	30	0	9.9	Nil	9.9			
F ₂	230	163	67	8.1	7.1	7.6	250	163	87	7.2	6.2	6.7	260	170	90	6.7	5.1	5.9			
BC ₁ P ₁	320	320	00	8.5	Nil	8.5	340	340	0	7.6	Nil	7.6	350	340	0	8.2	Nil	8.2			
BC ₂ P ₂	310	160	150	7.7	6.9	7.3	320	170	150	7.5	6.1	6.8	330	170	160	7.8	6.7	7.3			

TNP, NPP, NAP, SYPP, SYAP and ASYG refer to total number of plants; number of petalous plants; number of apetalous plants; seed yield per plant of petalous type plants; seed yield per plant of apetalous type plants and average yield of generation.

the dominance of the petalous allele. Investigating specific genes and regulatory elements associated with petal development could provide a more nuanced understanding of the trait inheritance. Additionally, exploring the environmental factors that may influence the expression of the petalous condition could contribute to a more comprehensive understanding of the trait's plasticity.

Furthermore, the study opens avenues for the exploration of marker-assisted selection techniques to expedite the breeding process. Identifying molecular markers linked to the petalous trait can facilitate more efficient and targeted breeding strategies, reducing the time and resources required to develop *Brassica* varieties with specific petalous characteristics.

In conclusion, the present study significantly advances our understanding of the genetic inheritance of the petalous trait in *Brassica* plants. The observed dominance pattern, supported by statistical analyses, provides a practical framework for plant breeders to manipulate and improve petalous characteristics. As we move forward, molecular investigations and the integration of advanced breeding techniques will likely enhance our ability to tailor *Brassica* varieties to meet evolving agricultural needs.

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Competing interests. None.

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