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Genetic studies on flower color in crop varieties of yellow sarson

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Abstract
The inheritance study of yellow sarson genotypes revealed that yellow color is dominant and controlled by a single gene (monogenic control). White flowers result from defective chloroplasts, as stated in the scientific literature. The F1, F2, BC1, and BC2 generations demonstrated clear flower color inheritance patterns, with yellow flowers dominating in F1. The observed ratios of yellow and white flowers in F2 and backcross generations adhered to Mendelian inheritance principles. These findings provide valuable insights into flower color genetics and offer practical applications for breeding programs.

Keywords: Inheritance study, flower color, genotypes, yellow sarson

Introduction
Yellow sarson (*Brassica rapa* L. var. yellow sarson) is an important ecotype of rapeseed that has higher oil content due to thin seed coat (Kumar *et al*., 2019; Kumar *et al*., 2020) [11, 12]. The inheritance of yellow flower color and yellow seed coat color in yellow sarson is under monogenic control, with yellow being dominant over white (Singh and Singh, 2017; Singh and Singh, 2018) [9, 10]. Yellow sarson is self-compatible in breeding behavior and is distributed in the eastern part of India (Pradhan *et al*., 2009) [8]. Combining ability, heterosis and maternal effects are some of the genetic parameters that can be used to study the yield and its contributing traits in yellow sarson (Kumar *et al*., 2019; Kumar *et al*., 2020) [11, 12]. Yellow sarson (*Brassica rapa var. yellow sarson*), a mustard family crop plant, has flowers that range in color from yellow to white. Yellow flowers outnumber white blossoms, and this trait's inheritance is governed by a single gene. The white flower phenotype is produced by faulty chloroplasts that fail to generate carotenoids, the pigments that give the flower its yellow hue (Ohmiya, 2011) [3]. Carotenoids are a broad class of isoprenoid chemicals found in plants, algae, fungus, and cyanobacteria (Britton *et al*., 2004) [1]. Xanthophylls are the most prevalent carotenoids found in yellow floral organs, however their number and composition vary. Xanthophylls are the most prevalent carotenoids found in yellow floral organs, and their abundance and composition vary between species and variations (Takaichi, 2011) [5]. 1. Understanding the genetic basis of blossom color variation in yellow sarson can aid in the improvement of its agronomic and decorative value, as well as in the study of the evolution and diversification of this feature in Brassica species. We studied the inheritance of flower color in yellow sarson genotypes using F1, F2, BC1, and BC2 populations produced from crossings between yellow- and white-flowered parents in this study.

Material method-The N. E. Borlaug Crop Research Center, G.B. Pant University of Agriculture and Technology, Pantnagar, which is situated at 29o N latitude and 79.3o E longitude, is where the current study was carried out. The institution is located in the subtropical zone of the Tarai region, situated at the foothills of the Shivalik range of the Himalayas, at an elevation of 243.84 meters above sea level. A sub-humid, sub-tropical climate with hot, dry summers and cool winters prevails in Pantnagar.

The area experiences 1433.3 mm of annual rainfall on average, the majority of which (80–90%) falls during the rainy season. In addition, some precipitation occurs frequently from November to March during the winter. Towards the end of December and sporadically throughout January, frost is common. a towards the end of December and occasionally in January. Maximum temperatures are recorded in May and June, while January witnesses the lowest temperatures. Relative humidity remains relatively high, around 80-90%, from mid-June to February.

The medium to fairly coarse textured calcareous alluvium that formed the soil in this area was carried from the mountains by a number of streams in the Bhabar and Tarai region. These soils have a fine to medium granular structure, are mostly silty and loamy in texture, and have excellent moisture retention and high production.
Pant Sweta x Pant Girija was the particular cross selected to investigate floral color inheritance. This cross produced the F1 generation, which was harvested in the 2019–20 rabi season. The BC1 and BC2 populations were created during the rabi season of 2020–2021 by backcrossing the F1 individuals with both parent genotypes. To produce seeds for the F2 generation, the F1 generation was also self-pollinated. Additionally, throughout the years 2020–21, new F1 individuals were developed.
Six generations were examined: P1, P2, F1, F2, BC1, and BC2. In order to gather information for the inheritance study, four distinct crosses that focused on flower color inheritance in the Pant Sweta x Pant Girija cross were cultivated during the rabi season of 2021–2022.

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Inheritance pattern of flower colour in different generation of cross Pant Girija (yellow colour flower) x Pant Sweta (white colour flower)

Generation	Total no. of plants	Expected frequency		Observed frequency		Expected ratio	X^2 cal	X^2 tab (0.05, 1 df)
		Yellow	White	Yellow	White			
F_1	30	30	0	30	0	1:0		
F_2	260	195	65	190	60	3:1	0.5	3.84
BC_1P_1 (F_1 x Pant Girija)	360	360	0	360	0	1:0	0.00	3.84
BC_2P_2 (F_1 x Pant sweta)	340	170	170	175	165	1:1	0.28	3.84

Result

Inheritance Pattern

The first filial generation (F1) showed a complete dominance of yellow flower color, with all 30 plants exhibiting yellow flowers (expected ratio 1:0).
The second filial generation (F2) displayed an expected ratio of 3:1 for yellow to white flower color. However, the observed ratio was slightly different with 190 yellow and 65 white flowers, indicating some deviation from the expected ratio.

Chi-square Analysis

The chi-square test was performed to determine whether the observed flower color ratios in F2 and other generations deviated significantly from the expected ratios based on the assumed inheritance patterns.
In the F2 generation, the chi-square value was calculated to be 0.5. Since the chi-square value is less than the critical value of 3.84 (at 0.05 significance level and 1 degree of freedom), we fail to reject the null hypothesis. This means that the observed ratio in F2 is not significantly different from the expected 3:1 ratio, and the flower color inheritance follows Mendelian genetics.
In BC1P1 and BC2P2 generations, the chi-square values were 0.00 and 0.28, respectively, indicating that the observed ratios were not significantly different from the expected ratios, supporting Mendelian inheritance patterns.

Discussion

The inheritance pattern of flower color in plants is determined by the type and distribution of pigments in the petal cells, as well as the genes that control the production and regulation of these pigments. Anthocyanins and carotenoids are two major types of pigments that give flowers different colors, such as red, purple, yellow, and orange. These pigments are synthesized by enzymes that are encoded by genes in the anthocyanin and carotenoid biosynthetic pathways. The expression of these genes is influenced by transcription factors, which are also encoded by genes that act as switches to turn on or off the pigment-producing machinery. Different combinations of these genes result in different flower colors and patterns (Grotewold, 2006; Tanaka *et al*., 2008; Zhang *et al*., 2019) [2, 6, 7]. The chi-square test is a statistical method to evaluate whether the observed results of a genetic experiment deviate significantly from the expected results based on a certain hypothesis or ratio. For example, if we expect a 3:1 ratio of yellow to white flowers in the F2 generation of a monohybrid cross, we can use the chi-square test to compare the actual number of yellow and white flowers we observe with the expected number based on the 3:1 ratio. The chi-square test calculates a value that reflects how much the observed results differ from the expected results. This value is then compared with a critical value from a table that depends on the level of significance (usually 0.05 or 0.01) and the degrees of freedom (the number of categories minus one). If the chi-square value is less than or equal to the critical value, we fail to reject the null hypothesis, which means that the observed results are not significantly different from the expected results, and the hypothesis or ratio is supported by the data. If the chi-square value is greater than the critical value, we reject the null hypothesis, which means that the observed results are significantly different from the expected results, and the hypothesis or ratio is not supported by the data (Reece *et al*., 2011) [4].
In our case, we have performed a chi-square test for the F2 generation of flower color and found a value of 0.5 with one degree of freedom. According to the table, the critical value for 0.05 significance level and one degree of freedom is 3.84. Since your chi-square value is less than 3.84, you fail to reject the null hypothesis, which means that your observed ratio of 65 white and 190 yellow flowers is not significantly different from the expected 3:1 ratio, and our flower color inheritance follows Mendelian genetics.

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