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Evaluating the Effects of Sclerotinia Rot Resistant Genotypes on Different Indian Mustard Traits and Yield Using Generation Analysis

Manjeet Singh [a], Ram Avtar [a], Neeraj Kumar [a], Manjeet Singh Ghanghas [b], Neeru Redhu [c], Atul Loyal [a], Ankit Dhillon [a] and Mandeep Redhu [a,d*]

[a] Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (Haryana)-125004, India.
[b] Department of Plant Pathology, CCS Haryana Agricultural University, Hisar (Haryana)-125004, India.
[c] Department of Molecular Biology, Biotechnology and Bioinformatics, CCS Haryana Agricultural University, Hisar (Haryana)-125004, India.
[d] Department of Plant, Soil, and Agricultural System, Southern Illinois University, Carbondale (IL)-62901, USA.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Sclerotinia stem rot caused by the pathogen *Sclerotinia sclerotiorum* is a serious threat to Indian mustard cultivation and causes up to 90% loss in seed yield. The present investigation was conducted to understand the inheritance pattern of Sclerotinia stem rot resistance through

**Corresponding author: E-mail: mandeep.redhu@siu.edu;*

generation mean analysis, as a first step in addressing the problem. Six generations *i.e..,* P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 of a cross between a sclerotinia stem rot resistant genotype *viz.,* RH 1222-28 and two susceptible genotypes *viz.,* EC 766300 and EC 766123 were evaluated for sclerotinia stem rot resistance, yield and its component traits at timely sown conditions. For resistance assessment, plants were artificially inoculated with 5 days-old pure culture of *S. Sclerotiorum* at the post-flowering stage and stem lesion length was measured (cm) from each inoculated stem at 20 days after inoculation. Sclerotinia stem rot resistance, seed yield, and their component traits were adequately explained by the epistatic interaction model. Furthermore, additive, dominance, and epistatic gene effects were implicated in the expression of resistance, yield, and traits associated with it. In order to generate Indian mustard cultivars with high yielding potential and resistant to sclerotinia stem rot, reciprocal recurrent selection would be the most successful method.

Keywords: Sclerotinia stem rot; generation mean analysis; gene action; duplicate epistasis; yield attributes.

1. INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is one of the most widely cultivated oilseed crops of India. Because of its wide adaptability to grow under diverse agro-climatic conditions, it holds a strong place in Indian agricultural crops. India ranks fourth among top oilseed producers of the world, contributing around 7 % in global production. Along with this, it also scores top in global consumers list of edible oil, with a huge domestic annual need of 21.69 million tonnes. Around 60% of the requirements are met through imports, incurring an annual expenditure of approximately ten billion dollars [1]. However, mean productivity of Indian mustard is quite low (1245 kg/hectare) as compared to global productivity (1994 kg/hectare). One of the major causes for the large disparity between demand and supply is the poor yield productivity of edible oilseed crops. In India, the mean productivity of major oilseeds is more than 50% lower than global mean productivity. Several fungal infections have severely affected the output of Indian mustard in the face of shifting environmental circumstances. A soil-borne fungus, *Sclerotinia sclerotiorum* (Lib.) de Bary causes one of the most devastating diseases called as Sclerotinia stem rot which is found responsible up to 90-100% yield losses in Indian mustard. Due to very complex mode of infection, disease management measures including both cultural as well as chemical approaches seem to be ineffective [2]. Consequently, the only effective way to control this disease is to use host genetic resistance. A high-yielding, *Sclerotinia* stem rot-resistant cultivar of Indian mustard is urgently needed to overcome the edible oil demand-supply imbalance. In order to choose the best breeding strategy, plant breeders need to concentrate on the inheritance pattern of complex traits like yield and disease resistance. Generation mean analysis is a very simple, convenient and crucial technique, widely used to evaluate the inheritance pattern and type of gene activity in agronomic traits. The great advantage of generation mean model is that it clearly distinguishes among additive effects, dominance deviations, and non-allelic interactions (dominance × dominance, additive × dominance, and additive × additive) in determining genotypic values of specific polygenic traits [3]. The current study was designed with the objectives of genetic dissection of complex seed yield and its component traits along with an investigation of genetic resistance for sclerotinia stem rot.

2. MATERIALS AND METHODS

2.1 Experimental Plant Materials and Crop Cultivation

The experimental material consists of F1 population developed from a cross between three genetically diverse mustard genotypes RH 1222-28 EC and 766300 and EC 766123 at Oilseeds Research Farm, CCS HAU, Hisar during Rabi 2018–19. RH 1222-28 is a sclerotinia stem rot resistant genotype, whereas EC 766300 and EC 766123 are agronomically superior and disease susceptible genotypes. The F1s were raised at a national off-season nursery, regional research station of IARI at Wellington (Nilgiris), TN, India, during the off season of 2019. Meanwhile, selfing and backcrossing operations with corresponding parents were performed to produce F2, BC1P1 and BC1P2 generations. During Rabi 2019–20, the six

generations including parents, F1s, F2s, and two backcross generations along with three replications were sown in a five-meter length plots having two, two, four, and three rows with a spacing of 0.30 m X 0.10 using a compact family block design (CFBD) at the Research Farm, Oilseeds Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. For artificial stem inoculation and resistance screening purpose, five plants from each parent, ten plants from the F1 generation, 100 plants from the F2 generation and 40 plants from the BC1P1 and BC1P2 generations were tagged from each replication.

2.2 Preparation of Inoculum of Pathogen along with Inoculation and Disease Assessment

Sclerotinia isolates were isolated from diseased stem part of Indian Mustard plants collected from the oilseeds Research Farm's permanent sick plot at Department of Genetics and Plant Breeding, CCS HAU, Hisar. Afterwards, stem parts were sanitized and aseptically put in Petri-plates having potato dextrose agar medium (PDA, Hi Media Laboratories, India). These plates were kept at 22.2 °C in a BOD incubator and sub-cultured on a routine basis to retain the pure culture. Singh et al. [3] employed a five-day-old pure culture for artificial stem inoculation purpose during post flowering period. A linear ruler was utilized to determine the stem lesion length (cm) at 20 days post-inoculation stage from each infected plant, and the mean value was used to assess the efficiency and generation's resistance behavior.

2.3 Biometrical Analysis

Generation mean analysis was performed using TNAUSTAT 2.0 version statistical software using the means of distinct generations over replications (TNAU, Coimbatore, India).

3. RESULTS

3.1 Analysis of Variance and Generation Mean Analysis

In both crossings, analysis of variance indicated significant variations among generations for all studied characteristics except days to flowering and number of secondary branches/plant in Cross-I. (Table 1). Table 2 depicts the average mean values along with standard errors for the investigated attributes. In both crosses, there were significant variations between the parental genotypes for all characteristics except main shoot length. Although the F_1 had a longer stem lesion length than the mid parent, it seemed to be heterozygous in both crossings, performing high for oil content, number of primary and secondary branches/plant, number of seeds/siliqua and thus, superior seed yield/plant. In general, the BC_1P_1 and BC_1P_2 progenies matched their recurrent parents in terms of their features, however the F_2 individuals segregated genetically and significantly differed in terms of seed yield and its component traits and disease resistance. Resistance against sclerotinia stem rot was determined in terms of stem lesion length. The resistant parent, RH 1222-28, had a small and restricted water-soaked lesion (3.24 cm), whereas comparatively longer lesion length (> 10.0 cm) and fluffy mycelial development were recorded for both susceptible parents (EC 766123 and EC 766300). The symptoms of the F1 from the Cross-I were comparable to those of the susceptible parent, whereas the F1 from the cross-II was close to the mid-parent value. Segregating generation's viz., F2's showed susceptible reaction (SLL, 7.5 to 10.0 cm), BC1P1 demonstrated moderately resistant reaction (SLL, 5.0-7.5 cm), and BC1P2 showed extremely susceptible reaction (SLL, >10.0 cm) in both crosses based on mean values of stem lesion length.

3.2 Estimates of Scaling Tests (Test of the Additive-Dominance Model) and Gene Effects

Tables 3 and 4 show the findings of the scaling test for seed yield and its component traits and sclerotinia stem rot disease resistance in terms of stem lesion length. On the basis of one or multiple combined scales, all the studied variables *viz.* seed yield and yield contributing traits well as disease resistance especially stem lesion length showed the significance, supporting evidence for the epistatic gene interaction except the variable number of secondary branches/plant in Cross-1 which showed no significance on any of the used scales. The joint scaling test was also modified to fit the data to a 3-parameters model and to assess the simple additive–dominance model's suitability. The digenic non-allelic interaction were absent for the number of secondary branches/plant, as the Chi square value ($\chi 2$) was not found significant in cross -I. The estimations of gene effects in individual

crossings showed the high variability of the recorded features (Tables 5 & 6). Both crosses showed highly significant (P 0.01) mean effects (m), which revealed substantial differences owing to mean, locus effects, and interaction among fixed loci. The additive (d), dominance (h), and their corresponding interaction (I, j, l) factors were used to further investigate the impacts and degree of gene effects. In Cross-I, all six genetic parameters i*.e.,* mean, additive, dominance, and epistatic (additive × additive, additive × dominance, and dominance × dominance) interactions were found significant for number of seeds/siliqua, siliqua length and oil content, whereas stem lesion length had non-significant parameters in cross-II. Among both crosses, additive (d), additive × additive (i) and dominant × dominance (l) gene activities significantly impacted traits especially days to flowering and maturity. Both crosses demonstrated strong additive and non-allelic dominance × dominance interaction in case of plant height. In cross-I, additive and additive × dominance interactions were substantial for the number of main branches/plant, whereas all gene effects were inconsequential for the number of secondary branches/plant. However, all gene effects were significantly recorded in cross-II, except for the dominance × dominance gene impact. In Cross-I, the additive gene effect was the only significant epistatic gene impact for main shoot length, whereas only the dominant gene effect was negligible in cross-II. All the interactions studies were found significant in cross-II, however, only one interaction (dominance × dominance) was found significant in Cross-I for the number of siliquae on the main shoot. Both the additive and dominance × dominance gene effects were substantial in the 1000-seed weight crosses. When compared to P_2 (susceptible parents), the negative sign in the additive gene effect (d) indicates that P_1 (resistant parent) contributes positively to lower the stem lesion duration and build up resistance against sclerotinia stem rot, and vice versa. Additionally, the positive sign in the additive gene impact depicted that P_1 parent had a greater role in enhancing 1000-seed weight, plant height, days to blooming and maturity as compared to P_2 parent. Furthermore, the dominance (h) and dominance × dominance (l) effects were significant, with signs of (h) denoting duplicate gene action in the expression of days to flowering and oil content in both crosses, siliqua length, number of seeds/siliqua, days to maturity and seed yield/plant in Cross-I; and plant height and stem lesion length (Sclerotinia stem rot resistance) in cross-II.

3.3 Estimates of Heritability, Genetic Advance and Potence Ratio

Table 7 depicts the estimates of broad (h^2bs) and narrow (h^2ns) sense heritability, genetic advance (GA), and potence ratio (PR). Broad sense heritability ranged from 0.43 (1000 seed weight in cross-II) to 0.94 (oil content in Cross-I). The broad sense heritability of the bulk of yield-related characteristics (> 0.60) was high. In both crossings, days to flowering and number of secondary branches/plant showed considerable wide sense heritability (0.30 to 0.60), as did number of seeds per siliqua, siliqua length and seed yield/plant in Cross-I, and 1000-seed weight and number of main branches/plant in cross-II. On other hand, the narrow sense heritability varied from 0.05 to 0.76. (seed yield/plant in Cross-I and plant height in cross-II). In both crossings, high narrow sense heritability was recorded for all studied traits, *i.e.,* plant height, stem lesion length and days to maturity except 1000-seed weight and number of primary branches/plant in Cross-I, and main shoot length in cross-II. Contrarily, low estimations of narrow sense heritability were recorded for days until flowering, seed yield/plant in Cross-I and number of seeds/siliqua, number of siliqua on main stalk and 1000-seed weight in cross-II. The remaining attributes had modest heritability in narrow senses. Most of the characteristics investigated had modest estimates of genetic advance. However, only two parameters such as plant height and main shoot length showed modest genetic advance in both the crosses. Generally, all the parameters showed a wide variability for potence ratio values, ranging from – 6.09 to 4.14 in both crosses. In both crosses, oil content and number of seeds/siliqua surpassed the unity (PR > 1) potence ratio, whereas, main shoot length and days to maturity scored negative potence ratio. Rest of the parameters had positive potence ratio values atleast in one cross. Plant height, number of siliquae on main branch, and 1000-seed weight in Cross-I, as well as days to flowering and siliqua length in cross-II, all showed negative potence ratio values.

3.4 Estimates of Genetic Variance, Covariance and Number of Genes Involved in Stem Rot Resistance, Seed Yield and Its Component Traits

Table 8 represents the estimates of various genetic parameters, such as additive variance,

Table 1. Analysis of variance (ANOVA) of Compact Family Block Design (CFBD) for Sclerotinia stems rot resistance, seed yield and its component traits

Cross-I (RH 1222-28 × EC 766300)													
S.V.	**df**	**Mean squares**											
		DF	**DM**	**PH**	**NPB**	**NSB**	**MSL**	**NSMS**	**SL**	**NSS**	**TSW**	**SYP**	**OC**	**SLL**
Replication	2	10.00	3.37	13.86	0.08	2.79	12.56	13.98	0.03	0.51	0.02	1.06	0.06	0.11
Generations	5	5.44	35.50**	256.40**	1.47**	1.63	40.14**	23.47*	0.14**	4.33**	1.89**	20.35**	0.34**	2.34**
Error	10	4.59	0.52	12.038	0.06	0.93	3.15	6.48	0.02	0.29	0.02	3.02	0.02	0.06
Cross-II (RH 1222-28 × EC 766123)													
S.V.	**df**	**Mean squares**											
		DF	**DM**	**PH**	**NPB**	**NSB**	**MSL**	**NSMS**	**SL**	**NSS**	**TSW**	**SYP**	**OC**	**SLL**
Replication	2	5.24	0.17	16.68	0.04	1.78	0.80	2.48	0.01	0.92	0.03	3.60	0.01	0.15
Generations	5	36.83**	110.56**	1035.71**	1.58**	9.40*	97.41**	51.29**	0.22**	6.26**	2.70**	17.19**	0.93**	3.12**
Error	10	3.52	1.36	9.28	0.22	2.66	5.50	7.75	0.01	0.41	0.05	2.15	0.01	0.11

**Significant at P ≤ 0.05 and **Significant at P ≤ 0.01. DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)*

Table 2. Mean comparisons (± SE) for Sclerotinia stem rot resistance, seed yield and its component traits among six generations of two crosses

Traits	Generations					
	P_1	P_2	F_1	F_2	BC_1P_1	BC_1P_2
Cross-I (RH 1222-28 ×EC 766300)						
DF	46.93 ± 1.09	43.87 ± 0.72	45.77 ± 0.60	44.69 ± 0.29	47.48 ± 0.50	45.63 ± 0.38
DM	155.27 ± 0.65	146.80 ± 0.72	149.37 ± 0.56	150.50 ± 0.37	155.76 ± 0.48	150.50 ± 0.46
PH	219.47 ± 2.02	197.27 ± 1.87	206.30 ± 1.21	218.12 ± 1.13	221.20 ± 1.41	211.41 ± 1.43
NPB	6.93 ± 0.21	5.80 ± 0.20	6.53 ± 0.25	5.98 ± 0.11	5.14 ± 0.13	6.89 ± 0.16
NSB	16.53 ±0.93	14.87 ±0.88	16.00 ± 0.61	15.69 ± 0.31	16.53 ± 0.48	15.79 ± 0.40
MSL	79.87 ±1.76	78.27 ± 1.65	74.20 ± 1.59	69.58 ± 0.85	74.20 ± 1.11	73.62 ± 1.24
NSMS	55.87 ± 1.82	49.13 ± 1.79	51.13 ± 0.93	54.84 ± 0.60	55.89 ± 0.91	54.68 ± 0.85
SL	3.91 ± 0.10	3.75 ± 0.09	3.92 ± 0.07	3.97 ± 0.03	3.43 ± 0.05	4.02 ± 0.04
NSS	13.63 ± 0.38	14.52 ± 0.37	15.46 ± 0.19	14.80 ± 0.12	12.17 ± 0.16	15.07 ± 0.17
TSW	5.98 ± 0.14	4.14 ± 0.05	4.90 ± 0.09	4.57 ± 0.06	5.20 ± 0.08	3.75 ± 0.07
SYP	20.27 ±0.94	13.22 ± 0.70	18.72 ± 0.81	16.97 ± 0.32	19.58 ± 0.51	19.36 ± 0.49
OC	38.64 ± 0.05	38.71 ± 0.06	38.82 ± 0.05	38.60 ± 0.09	38.47 ± 0.13	37.87 ± 0.11
SLL	3.24 ± 0.34	12.19 ± 0.68	10.62 ± 0.43	8.79 ± 0.28	6.46 ± 0.29	12.66 ± 0.43
Cross-II (RH 1222-28 × EC 766123)						
DF	46.93 ± 1.09	37.60 ± 0.70	39.37 ± 0.46	42.72 ± 0.28	45.22 ± 0.47	43.19 ± 0.38
DM	155.27 ± 0.65	141.27 ± 0.61	144.00 ± 0.65	150.06 ± 0.35	156.27 ± 0.41	146.49 ± 0.47
PH	219.47 ± 2.02	171.53 ± 1.34	205.29 ±1.50	209.79 ± 0.89	222.78 ± 1.04	197.24 ± 1.18
NPB	6.93 ± 0.21	5.93 ± 0.27	7.03 ± 0.27	5.46 ± 0.10	6.77 ± 0.15	5.50 ± 0.15
NSB	16.53 ±0.93	18.07 ±0.75	19.80 ± 0.73	15.41 ± 0.29	15.31 ± 0.39	18.38 ± 0.44
MSL	79.87 ±1.76	77.53 ±1.78	83.57 ± 1.68	71.22 ± 0.85	68.87 ± 0.97	80.35 ± 1.21
NSMS	55.87 ± 1.82	44.00 ± 1.15	52.57 ± 0.97	50.61 ± 0.65	48.73 ± 0.87	47.43 ± 1.10
SL	3.91 ± 0.10	4.38 ± 0.10	4.12 ± 0.06	3.86 ± 0.04	3.58 ± 0.07	3.99 ± 0.06
NSS	13.63 ± 0.38	15.43 ± 0.26	15.69 ± 0.22	14.15 ± 0.15	12.16 ± 0.21	15.83 ± 0.18
TSW	5.98 ± 0.14	3.26 ± 0.19	4.65 ± 0.13	4.44 ± 0.05	4.93 ± 0.07	3.74 ± 0.08
SYP	20.27 ±0.94	16.80 ± 0.91	21.68 ± 0.87	19.63 ± 0.41	16.70 ± 0.62	22.36 ± 0.58
OC	38.64 ± 0.05	39.68 ± 0.04	39.79 ± 0.05	39.05 ± 0.06	38.63 ± 0.07	38.58 ± 0.07
SLL	3.24 ± 0.34	10.28 ± 0.61	7.24 ± 0.34	8.29 ± 0.30	6.50 ± 0.29	11.63 ± 0.44

DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)

Table 3. Estimates (±SE) of scaling tests for Sclerotinia stem rot resistance, yield and its component traits in cross-I (RH 1222-28 × EC 766300)

Traits	Individual scaling tests				Joint scaling test
	A	B	C	D	χ^2
DF	2.25 ± 1.60	1.63 ± 1.21	-3.57 ± 2.12	-3.73** ± 0.86	19.02**
DM	6.88** ± 1.29	4.83** ± 1.30	1.21 ± 2.09	-5.25** ± 0.99	44.46**
PH	16.63** ± 3.67	19.25** ± 3.63	43.16** ± 5.83	3.64 ± 3.03	69.84**
NPB	-3.18** ± 0.42	1.45** ± 0.45	-1.87* ± 0.74	-0.07 ± 0.31	95.44**
NSB	0.52 ± 1.46	0.72 ± 1.33	-0.64 ± 2.16	-0.94 ± 0.88	1.2
MSL	-5.67 ± 3.24	-5.23 ± 3.38	-28.21** ± 5.24	-8.66** ± 2.38	30.63**
NSMS	4.78 ± 2.73	9.08** ± 2.64	12.08** ± 3.96	-0.89 ± 1.72	14.93**
SL	-0.97** ± 0.16	0.36* ± 0.14	0.39 ± 0.24	0.49** ± 0.09	67.22**
NSS	-4.74** ± 0.54	0.16 ± 0.54	0.12 ± 0.80	2.35** ± 0.34	109.48**
TSW	-0.48* ± 0.24	-1.55** ± 0.18	-1.66** ± 0.34	0.18 ± 0.16	81.51**
SYP	0.18 ± 1.60	6.79** ± 1.45	-3.04 ± 2.37	-5.00** ± 0.95	42.64**
OC	-0.53 ± 0.28	-1.79** ± 0.24	-0.59 ± 0.40	0.87** ± 0.26	60.13**
SLL	-0.93 ± 0.80	2.50 ± 1.18	-1.50 ± 1.60	-1.53* ± 0.76	9.79*

**Significant at P ≤ 0.05, **Significant at P ≤ 0.01; Cross-I (RH 1222-28 × EC 766300); Cross-II (RH 1222-28 × EC 766123); DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)*

Table 4. Estimates (±SE) of scaling tests for Sclerotinia stem rot resistance, yield and its component traits in cross-I (RH 1222-28 × EC 766123)

Traits	Individual scaling tests				Joint scaling test
	A	B	C	D	χ^2
DF	4.13** ± 1.51	9.42** ± 1.14	7.61** ± 1.98	-2.97** ± 0.84	71.87**
DM	13.27** ± 1.23	7.72** ± 1.30	15.72** ± 2.11	-2.63* ± 0.94	128.06**
PH	20.80** ± 3.26	17.65** ± 3.10	37.56** ± 5.25	-0.45 ± 2.38	70.98**
NPB	-0.43 ± 0.43	-1.97** ± 0.48	-5.09** ± 0.75	-1.35** ± 0.28	59.74**
NSB	-5.72** ± 1.41	-1.10 ± 1.37	-12.56** ± 2.23	-2.87** ± 0.83	39.08**
MSL	-25.70** ± 3.10	-0.40 ± 3.44	-39.65** ± 5.39	-6.78** ± 2.30	96.59**
NSMS	-10.98** ± 2.70	-1.70 ± 2.66	-2.55 ± 3.89	5.07** ± 1.91	19.41**
SL	-0.87** ± 0.18	-0.53** ± 0.17	-1.08** ± 0.25	0.16 ± 0.12	32.74**
NSS	-5.00** ± 0.60	0.54 ± 0.49	-3.81** ± 0.80	0.32 ± 0.37	78.18**
TSW	-0.76** ± 0.25	-0.40 ± 0.27	-0.79 ± 0.40	0.19 ± 0.15	9.93*
SYP	-8.55** ± 1.78	6.23** ± 1.70	-1.90 ± 2.71	0.21 ± 1.18	48.11**
OC	-1.27** ± 0.16	-2.31** ± 0.15	-1.74** ± 0.26	0.92** ± 0.15	290.35**
SLL	2.52** ± 0.76	5.74** ± 1.12	5.15** ± 1.54	-1.55* ± 0.80	34.08**

**Significant at P ≤ 0.05, **Significant at P ≤ 0.01; Cross-I (RH 1222-28 × EC 766300); Cross-II (RH 1222-28 × EC 766123); DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)*

Table 5. Estimates of gene effects (± SE) for Sclerotinia stem rot resistance, yield and its component traits in cross-II (RH 1222-28 × EC 766300)

Trait	Genetic parameter						Type of epistasis
	m	d	h	i	j	l	
DF	44.69** ± 0.29	1.84** ± 0.63	7.82** ± 1.93	7.46** ± 1.71	0.31 ± 0.91	-11.34** ± 3.29	Duplicate
DM	150.50** ± 0.37	5.26** ± 0.67	8.84** ± 2.12	10.50** ± 1.99	1.03 ± 0.83	-22.22** ± 3.40	Duplicate
PH	218.12** ± 1.13	9.79** ± 2.01	-9.34 ± 6.33	-7.28 ± 6.05	-1.31 ± 2.43	-28.61** ± 9.92	-
NPB	5.98** ± 0.11	-1.75** ± 0.21	0.30 ± 0.68	0.13 ± 0.61	-2.32** ± 0.25	1.60 ± 1.11	-
NSB	15.69** ± 0.31	0.73 ± 0.62	2.17 ± 1.97	1.87 ± 1.76	-0.10 ± 0.89	-3.11 ± 3.29	Absent
MSL	69.58** ± 0.85	0.58 ± 1.66	12.45* ± 5.16	17.31** ± 4.76	-0.22 ± 2.05	-6.41 ± 8.47	-
NSMS	54.84** ± 0.60	1.22 ± 1.24	0.42 ± 3.79	1.79 ± 3.45	-2.15 ± 1.78	-15.65* ± 6.36	-
SL	3.97** ± 0.03	-0.59** ± 0.07	-0.90** ± 0.21	-0.99** ± 0.19	-0.67** ± 0.10	1.59** ± 0.36	Duplicate
NSS	14.80** ± 0.12	-2.90** ± 0.24	-3.31** ± 0.75	-4.70** ± 0.67	-2.45** ± 0.36	9.28** ± 1.25	Duplicate
TSW	4.57** ± 0.06	1.45** ± 0.11	-0.53 ± 0.35	-0.37 ± 0.33	0.54** ± 0.13	2.39** ± 0.55	-
SYP	16.97** ± 0.32	0.22 ± 0.71	11.98** ± 2.15	10.01** ± 1.90	-3.30** ± 0.92	-16.98** ± 3.69	Duplicate
OC	38.60** ± 0.09	0.60** ± 0.17	-1.58** ± 0.52	-1.73** ± 0.51	0.63** ± 0.18	4.05** ± 0.80	Duplicate
SLL	8.79** ± 0.28	-6.19** ± 0.52	5.97** ± 1.63	3.06* ± 1.52	1.72* ± 0.64	-4.63 ± 2.62	-

**Significant at P ≤ 0.05, **Significant at P ≤ 0.01; DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)*

Table 6. Estimates of gene effects (±SE) for Sclerotinia stem rot resistance, yield and its component traits in cross-II (RH 1222-28 × EC 766123)

Trait	Genetic parameter						Type of epistasis
	m	d	h	i	j	l	
DF	42.72** ± 0.29	2.03** ± 0.60	3.04 ± 1.86	5.94** ± 1.68	-2.64** ± 0.89	-19.49** ± 3.12	Duplicate
DM	150.06** ± 0.35	9.78** ± 0.63	1.00 ± 2.04	5.26* ± 1.88	2.78** ± 0.77	-26.25** ± 3.28	-
PH	209.79** ± 0.89	25.54** ± 1.57	10.69* ± 5.13	0.89 ± 4.75	1.58 ±1.99	-39.34** ± 8.19	Duplicate
NPB	5.46** ± 0.10	1.27** ± 0.20	3.29** ± 0.64	2.69** ± 0.56	0.77** ± 0.26	-0.29 ± 1.09	-
NSB	15.41** ± 0.29	-3.08** ± 0.59	8.24** ± 1.91	5.74** ± 1.66	-2.31* ± 0.84	1.07 ± 3.24	-
MSL	71.22** ± 0.85	-11.48** ± 1.55	18.42** ± 5.04	13.55** ± 4.59	-12.65** ± 1.99	12.55 ± 8.21	-
NSMS	50.61** ± 0.65	1.29 ± 1.40	-7.50 ± 4.08	-10.14** ± 3.82	-4.64** ± 1.76	22.82** ± 6.81	-
SL	3.86** ± 0.04	-0.41** ± 0.09	-0.34 ± 0.26	-0.32 ± 0.24	-0.17 ± 0.11	1.71** ± 0.43	-
NSS	14.15** ± 0.12	-3.67** ± 0.27	0.52 ± 0.80	-0.64 ± 0.73	-2.77** ± 0.36	5.09** ± 1.35	-
TSW	4.44** ± 0.05	1.18** ± 0.11	-0.35 ± 0.34	-0.38 ± 0.30	-0.18 ± 0.16	1.54* ± 0.60	-
SYP	19.63** ± 0.41	-5.66** ± 0.85	2.73 ± 2.59	-0.42 ± 2.36	-7.39** ± 1.07	2.73 ± 4.35	-
OC	39.04** ± 0.06	0.00 ± 0.10	-1.22** ± 0.29	-1.85** ± 0.30	0.52** ± 0.09	5.43** ± 0.47	Duplicate
SLL	8.29** ± 0.30	-5.13** ± 0.53	3.57* ± 1.66	3.10* ± 1.59	-1.61* ± 0.63	-11.35** ± 2.62	Duplicate

*Significant at *P ≤ 0.05*, **Significant at *P ≤ 0.01*; Cross-I (RH 1222-28 × EC 766300); Cross-II (RH 1222-28 × EC 766123); DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)

Table 7. Estimates of heritability (both broad and narrow sense), genetic advance and potence ratio for seed yield and its component traits in Indian mustard

Traits	Narrow sense heritability (h^2 ns)		Broad Sense heritability (h^2bs)		Genetic advance (GA)		Potence ratio	
	Cross-I	Cross-II	Cross-I	Cross-II	Cross-I	Cross-II	Cross-I	Cross-II
DF	0.10	0.31	0.52	0.59	5.37	6.21	0.24	-0.62
DM	0.66	0.72	0.80	0.78	10.54	9.77	-0.39	-0.61
PH	0.74	0.76	0.86	0.77	34.94	24.93	-0.19	0.41
NPB	0.67	0.35	0.73	0.54	2.94	1.88	0.29	1.20
NSB	0.44	0.41	0.60	0.52	6.71	5.45	0.36	3.25
MSL	0.47	0.67	0.75	0.72	22.73	21.89	-6.09	-1.00
NSMS	0.27	0.15	0.62	0.74	13.13	17.28	-0.41	0.44
SL	0.20	0.16	0.53	0.72	0.61	1.05	1.13	-0.11
NSS	0.41	0.04	0.58	0.66	2.48	2.87	3.11	1.29
TSW	0.65	0.10	0.82	0.43	1.77	0.78	-0.17	0.02
SYP	0.05	0.27	0.56	0.68	6.41	9.92	0.56	1.81
OC	0.26	0.48	0.94	0.86	2.00	1.09	4.14	1.21
SLL	0.60	0.73	0.79	0.86	7.85	9.18	0.65	0.14

Cross-I (RH 1222-28 × EC 766300); Cross-II (RH 1222-28 × EC 766123); DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)

Table 8. Estimates of component of genetic variance (D & H), covariance (F), average degree of dominance ($\sqrt{H/D}$), ratio of $F/\sqrt{H \times D}$ and effective factors/minimum number of genes responsible for Sclerotinia stem rot resistance, seed yield and its component traits in Indian mustard

Traits	Additive variance (D)		Dominance variance (H)		Average degree of dominance $(\sqrt{H/D})$		Covariance between D & H over all the loci (F)		$F/\sqrt{H \times D}$		Effective factors/ minimum number of genes	
	Cross-I	Cross-II	Cross-I	Cross-II	Cross-I	Cross-II	Cross-I	Cross-II	Cross-I	Cross-II	Cross-I	Cross-II
DF	5.25	15.91	41.73	29.44	2.82	1.36	+12.81	+8.75	0.87	0.40	0.21	2.49
DM	53.18	53.13	23.28	8.86	0.66	0.41	+2.22	-6.48	0.06	-0.30	1.13	4.44
PH	572.70	361.12	183.51	24.37	0.57	0.26	-9.07	-37.29	-0.03	-0.40	0.61	3.80
PB	5.12	2.03	0.90	2.11	0.42	1.02	-0.97	-0.51	-0.45	-0.25	0.21	0.27
SB	25.76	21.19	19.17	11.46	0.86	0.74	+8.69	-5.23	0.39	-0.34	0.04	0.45
MSL	201.68	286.95	245.36	48.97	1.10	0.41	-38.92	-63.51	-0.17	-0.54	0.08	0.02
NSMS	57.25	39.20	148.95	299.04	1.61	2.76	+11.17	-54.11	0.12	-0.50	0.27	0.39
SL	0.13	0.16	0.41	1.13	1.82	2.63	+0.14	+0.13	0.61	0.31	0.03	0.21
NSS	3.50	0.33	2.93	11.12	0.91	5.79	-0.57	+1.36	-0.18	0.71	0.45	0.85
TSW	1.41	0.16	0.75	1.01	0.73	2.52	+0.21	+0.04	0.20	0.10	1.72	11.43
SYP	2.81	27.10	63.06	81.75	4.74	1.73	+2.37	+6.10	0.18	0.13	1.16	0.06
OC	0.55	0.36	2.86	0.57	2.28	1.26	+0.33	+0.06	0.26	0.13	0.02	2.84
SLL	27.81	38.77	17.56	14.04	0.79	0.60	-12.26	-12.80	-0.03	-0.02	2.59	0.88

Cross-I (RH 1222-28 × EC 766300); Cross-II (RH 1222-28 × EC 766123); DF-Days to flowering, DM-Days to maturity, PH-Plant height (cm), NPB-Number of primary branches/plant, NSB-Number of secondary branches/plant, MSL-Main shoot length (cm), NSMS-Number of siliquae on main shoot, SL-Siliqua length (cm), NSS-Number of seeds/siliqua, TSW-1000 seed weight (g), SYP-Seed yield/plant (g), OC-Oil content (%), SLL-Stem lesion length (cm)

dominance variance, average degree of dominance, potence ratio, correlation between H and D across all loci, and effective factors/minimum number of genes responsible for sclerotinia stem rot resistance, seed yield, and its components. Additive genetic variance was found significantly greater than dominance genetic variance for sclerotinia stem rot resistance (stem lesion length), whereas dominance genetic variance was more prominent than additive variance for all the studied traits such as seed yield/plant, siliqua length, number of siliquae on main shoot, days to flowering and oil content in both crosses. For other variables like plant height, days to maturity and number of primary branches/plant in both crosses; 1000-seed weight and number of seeds/siliqua in Cross-I; and main shoot length in Cross-II, additive genetic variance was significantly greater than dominance variance. Days to flowering, siliqua length, number of siliquae on main shoot, seed yield/plant, and oil content all had estimates of average degree of dominance greater than one (>1), whereas stem lesion length, plant height, days to maturity and number of secondary branches/plant had estimates less than one (1). Furthermore, in the remaining characters, this estimate was cross-specific. Days to flowering, 1000-seed weight, siliqua length, oil content and seed yield/plant were all higher than zero and in a positive direction in both crosses; however, stem lesion length, number of primary branches/plant, plant height and main shoot length were also higher than zero, but in a opposite direction. This estimate was cross specific for the remainder of the characters. The estimations were less than unity and larger than zero for the majority of the yield attributing features in both crosses. The effective factors/minimum number of genes controlling yield and its component traits varied from 0.03 (for siliqua length in Cross-I) to 11.43 (for siliqua length in Cross-I). The effective factors/minimum number of genes controlling yield and its component traits varied from 0.03 (for siliqua length in Cross-I) to 11.43 (for siliqua length in Cross-I) (for 1000-seed weight in cross-II). Maximum effective factors were found for stem lesion length (2.59) followed by 1000-seed weight (1.72), seed yield/plant (1.16), and days to maturity (1.13) in cross-I, whereas maximum effective factors were found for 1000-seed weight (11.43) followed by days to maturity (4.44), plant height (3.80), oil content (2.84), and days to flowering (2.84) in cross-II (2.49) respectively.

4. DISCUSSION

All crop improvement programmes have as their primary goal the development of high-yielding varieties. However, developing disease-resistant cultivars with high yielding potential is critical, since it is the most popular, economical and biologically safe mean of plant protection. The importance of disease resistant cultivars in food security underlines the fact that disease resistance breeding must be prioritized globally. Sclerotinia stem rot deteriorates oil quality as well decreases seed production in Indian mustard, enforces the high need of developing resistant cultivars with high yielding potential [3]. In order to design an effective breeding strategy for the development of a high yield potential and disease resistant cultivar against this devastating disease, the present study looked at the inheritance pattern and nature of gene actions determining sclerotinia stem rot resistance, seed yield and their component traits in two crosses of Indian mustard. According to Singh et al. [3], the maximum and minimum temperatures of 25 and 5–12°C along with high relative humidity (>80%) and high soil moisture are the optimal environmental conditions for disease infection and development. The meteorological data in supplemental Table 1 demonstrated that the experimental site's climatic conditions were highly favorable for sclerotinia rot disease growth. Analysis of variance indicates that there is adequate amount of genetic variation among generations for sclerotinia stem rot resistance and most of the yield and its component attributes except for days to flowering and number of secondary branches/plant in Cross-I. The most important phase in every crop improvement effort is selection in a desirable direction, which is only achievable if the plant material employed has a lot of genetic variety [4]. These findings also support the selection of parents for this study, which is required for generation mean analysis [5]. Manjunath et al. [6] and Lionneton et al. [7] found significant genotypic differences among various generations of Indian mustard crosses for seed yield and its component traits except for the number of secondary branches per plant.

The results of generation mean analysis showed that the genetic regulation of sclerotinia stem rot resistance, seed yield production, and its component traits in Indian mustard is dependent on the cross combination used. All gene effects such as additive, dominant, and epistatic played a critical role. In comparison to the scenario

corresponding to the basic additive-dominance model of heredity, this suggests that improving these features would be challenging [3]. In these circumstances, populations must be passed down to future generations to find the greatest fit model. Disi et al. [8] and Khan et al. [9] previously documented the presence of non-allelic interactions along with additive and dominant gene effects while determining the inheritance pattern of sclerotinia stem rot resistance in Brassica oilseeds. In diverse crossings of Indian mustard, Manjunath et al. [6] and Paul [10] showed the relevance of both additive and non-additive gene activities with varied inheritance patterns for seed yield and its components.

Sclerotinia stem rot susceptibility in F_1 plants from both crossings demonstrated that the resistance is recessive. The presence of increaser alleles and an associated pair of genes is shown by the relevance of additive component (d) and additive × additive (i) gene interactions for stem lesion length in both crossings. This shows that single plant selection for resistance enhancement might result in enhanced manifestation. In Cross-I, the importance of dominance gene activity indicates that both parents had heterozygous loci with dominant alleles for Sclerotinia stem rot resistance. Because duplicate epistasis exists in cross-II, the effective breeding approach will be one that can sweep up the genes to produce superior gene constellations that interact favorably. In oilseed rape, Khan et al. [11,12] discovered the function of dominant dominance type of gene effect for Sclerotinia rot resistance. Significant and negative indicators of the dominance (l) interaction revealed that it has beneficial impacts in terms of blooming commencement, maturity duration, and plant height reduction. Significant positive additive (d) and dominance (h) signs, on the other hand, imply that these estimations were influenced by parents who possessed alleles responsible for high levels of these qualities [1]. The duplicate epistasis was observed in one or both crosses, however, a recurrent selection technique might be useful for further improvement. Kant and Gulati [13] and Sachan and Singh [14] identified comparable sorts of gene action for days to flowering and maturity in Indian mustard. The insufficiency of all fitted models for the number of siliqua on main shoot, number of primary and secondary branches/plant, main shoot length and 1000-seed weight in both crosses suggested the presence of higher order interactions, linkage, or both. In such circumstances, accessible populations must be passed down to future generations in order to gain the best-fit model [15]. Individual and joint scaling tests, as well as all six genetic parameters in Cross-I, except the mean (m) effect for number of secondary branches/plant, indicate that the simple additive–dominance model is adequate; the nonallelic interaction effect is absent, and generation means are solely dependent on the gene's additive–dominance effect [5]. On the other hand, the substantial and positive estimates of the dominance (h) and additive × additive (i) interactions, revealed that their impacts were rising for the number of secondary branches/plant in cross-II as well as main shoot length in both crosses.

Due to presence of the strong positive dominance (h) impact for main shoot length, selection should be postponed until heterozygosity in both populations is diminished. Previous findings by Manjunath et al. [6] and Kabdal and Singh [16] found similar gene activity for the number of primary and secondary branches/plant as well as main shoot length in one or both crosses. The opposite sign of h and l indicated that number of seeds per siliqua, siliqua length and seed yield per plant were governed by duplicate epistasis in cross-I. However, these traits were unable to show any type of digenic epistasis in cross-II due to the presence of linkage and/or higher order interactions. In both crosses, the dominant dominance (l) interaction led to increase the length and quantity of seeds per siliqua. In the inheritance of 1000-seed weight, the additive (d) impact and dominant dominance (l) interaction performed a major favourable contribution. Early generation selection of preferred segregants may be possible if additive gene activity is present. Our findings for these features are in line with those of Akanksha et al. [17], Kabdal and Singh [16], and Singh and Singh [18]. The duplicate kind of gene activation, as well as the considerable and positive additive × additive (i) interaction, influenced oil content. This means that future generations may be able to get transgressive segregants with high oil content. Kant and Gulati [13] in Indian mustard and Wang et al. [19] in oilseed rape found a nearly identical inheritance pattern for oil content. On the other hand, Manjunath et al. [6] limelighted the role of higher order interaction in enhancing oil content. For certain qualities, the size of the various genetic components was uneven. The dominance (h) and dominance × dominance (l) gene effects expressed opposite signs for most

of the traits, indicating duplicate epistasis. The opposing signs of h and l counterbalanced each other's effects, resulting in less heterosis and an indication of mostly scattered alleles at the interacting loci [20]. These findings are consistent with those of Kemparaju et al. [21], Kabdal and Singh [16], Singh et al [22], Patel et al. [23] and Ishaq et al. [24].

Trait heritability refers to the proportion of phenotypic variations that may be explained by heritable genetic variables. A trait's heritability must be estimated in order to maximise the selection response [25]. Broad-sense heritability is a measure of a trait's overall heritability, which includes all conceivable sources of heritable variation (additive, dominance, epistatic, and maternal effects). Most of the examined characteristics have high broad-sense heritability (> 0.60), indicating that there are few environmental influences on their expression and that genetic variation accounts for the majority of variance. As a result, phenotype-based selection will be useful in increasing these characteristics. Xing et al. [26] in oilseed rape and Mehla et al. [27] in Indian mustard showed strong broad-sense heritability for most yield-attributing traits, which is similar to our findings. Disi et al. [8] and Khan et al. [11,12,9] also reported moderate broad-sense heritability for sclerotinia stem rot resistance in Brassica. In overall genetic variations, only additive genetic variance responses to selection process [25]. Narrow-sense heritability refers to the percentage of phenotypic variation caused by additive genetic factors, as well as the degree of similarity between relatives [28]. In our study, high narrow-sense heritability (> 0.50) was found in one or both crosses for days to maturity, number of primary branches/plant, main shoot length, plant height, 1000-seed weight and stem lesion length indicating that these traits may have a better chance of improving when selection pressures are applied in a desirable direction. In oilseed rape, Xing et al. [26] and Wang et al. [19] observed moderate to high narrow sense heredity for yield component characteristics, while Singh and Singh [18] found low to moderate narrow sense heritability for same traits in Indian mustard. Moderate to high narrow sense heredity was observed for sclerotinia rot resistance in previous studies of Baswana et al. [29] in cauliflower and Castano et al. [30] in sunflower crop.

The degree of achieved gain for a character under a certain selection pressure is explained by genetic advance. High genetic advance combined with high narrow sense heritability estimates is more consistent and expressive than the former alone, and it also provides more opportunities for selection during early segregating generations, resulting in significant character improvement. In this work, strong narrow sense heritability combined with moderate genetic advancement in stem lesion length, plant height, and main shoot length allowed for the production of disease-resistant plants with long main shoot length. Previous studies like Awasthi et al. [31], Paul [10], and Singh and Singh [18] all reported almost identical results for one or more characters. Although the traits like siliqua length, number of siliquae on main shoot, number of seeds/siliqua and oil content had high broad-sense heritability, low narrow-sense heritability, (3) and genetic advance in both crosses, suggesting that these traits are primarily controlled by non-additive gene action, and the selection for these traits would not be effective for improving yield due to early segregating generations. As a result, selection should be postponed until heterozygosity in these populations is diminished [32]. The occurrence of non-allelic interaction for these parameters may explain their higher broad-sense heritability and lower +narrow-sense heritability. Overall, greater heritability and genetic advance estimates for yield component traits suggest that indirect selection for yield via these component traits might be more successful rather than direct selection for seed yield [33].

The potency ratio is a common metric for identifying the type and direction of dominance. Our potence ratio data showed that both crosses had over-dominance in the desired direction for oil content, number of seeds/siliqua and siliqua length in Cross-I, and main shoot length, number of primary branches/plant and seed yield/plant in cross-II. This suggests that these features have the potential to improve oil and seed production productivity through heterosis breeding. Singh and Singh [18] observed partial to over dominance for number of seeds per siliqua and seed output per plant in one or more crosses of Indian mustard over several years, while complete dominance for number of primary branches/plant.

The recapitulation of heritability and genetic advance are validated by estimations of additive and dominant genetic components, as well as average degree of dominance. In the inheritance

of days to flowering, siliqua length, number of siliquae on main shoot, oil content and seed yield/plant in both crosses, higher values of H over D and greater than unity values for average degree of dominance confirmed high level of dominance as well as preponderance of non-additive gene action, while the opposite is true for sclerotinia stem rot resistance and remaining yield component traits in one or the other cross. Positive F estimates (F > 0) indicate that dominant alleles are more common than recessive alleles in the inheritance of siliqua length, seed yield/plant, and oil content in both populations. Negative F estimates indicated that recessive alleles were relevant for sclerotinia stem rot resistance, main shoot length, number of primary branches/plant, and plant height. Near-zero F estimates for 1000-seed weight indicated a balanced distribution of dominant and recessive alleles, both of which were helpful for improving this characteristic.

The average degree of dominance is crucial for practical plant breeding, particularly when dealing with quantitative characteristics that are influenced by several loci. As a result, (H/D) is a far better predictor of average degree of dominance across all loci. Non-allelic interaction, on the other hand, distorts average degree of dominance estimations [34]. Estimates of dominance variance (H) may be attributed to the repulsion phase of linkage when (H/D) approaches unity, making it impossible to distinguish between actual and pseudo-overdominance. As a result, our findings do not support the occurrence of actual over-dominance for the qualities described above. The F/(HD) estimates refer to the degree as well as the sign of dominance for all genes regulating a specific trait, and it was significantly less than unity for all of the characteristics investigated in this study. The high difference between F and (H/D) indicates that dominant alleles were disseminated in all of the parents utilised in the current experiment for developing populations, which is consistent with prior observations on inheritance patterns in Indian mustard [10,18].

Estimation of effective factors/minimum number of genes influencing quantitative features has significant significance in crop breeding operations. This enables the development of a breeding plan for the introduction of certain desirable characteristics into an otherwise exceptional genetic background. Effective factors/minimum number of genes for sclerotinia stem rot resistance varied from 0.88 (in cross-II) to 2.59 (in Cross-I), implying that resistance is governed by a small number of genes with large impact and a few minor effect genes. Vleugels and Bockstaele [35] identified three primary genes responsible for red clover resistance to *Sclerotinia trifoliorum*, whereas one or more genes may be responsible for partial soybean resistance to sclerotinia stem rot [36]. For seed yield and its component qualities, effective factors/minimum number of genes were often low and extremely varied. Depending on the features and crossings studied, these estimates varied from 0.03 to 11.43. This is similar to prior published gene number estimates (0.001-0.75) for various yield components by Paul [9]; (1 to 6) by Paul et al. [37,17] in Indian mustard, but slightly higher. Furthermore, our estimations were slightly lower than Singh and Singh [18], who analyzed several sets of crosses in Indian mustard and found 5-7 genes for seed yield/plant and 1-4 genes for yield components.

5. CONCLUSION

Based on the overall findings, this study infer that sclerotinia stem rot resistance and the majority of yield-related attributes were regulated by additive, non-additive as well as duplicate epistasis genetic components. For the enrichment of sclerotinia stem rot resistance along with high seed and oil yield, reciprocal recurrent selection procedures require repeated crossing, such as diallel selective mating followed by intermating among desirable F_2 segregants. The intermating among the selected segregants helps to break undesirable connections. Consequently, the breeding tactics would be likely to successfully recover desired recombinants in later generations. Since, duplicate epistasis was observed in most of the examined parameters, heterosis breeding would be equally effective in improving these traits.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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