



Study of genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* L.) for yield components

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Abstract

Analysis of data on 10 characters on 30 wheat genotypes. The wide range of different characters and comparison of mean of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the germplasm collection evaluated. Seed yield per plant showed very strong positive association with No. of primary branches, No. of secondary branches, no. of silqua/ plant, Silqua length, Seeds per silqua and 1000-seed weight (g). Most of the characters showing significant positive correlation with grain yield per plant such as No. of primary branches, No. of secondary branches, no. of silqua/ plant, Silqua length, Seeds per silqua and 1000-seed weight (g) were also positively correlated among themselves. Existence of significant positive associations among yield and important yield components suggested that selection would be highly effective and efficient in improving these traits due to possibility of correlated response. Path analysis identified, plant height, days to maturity, days to 50% flowering, no. of silqua/ plant, Silqua length, Seeds per silqua thousand seed weight and no. of secondary branches/plant as major direct contributor towards expression of grain yield per plant. The character identified above as important direct and indirect yield components merit due to consideration in formulating effective selection strategy for developing high yielding varieties in mustard.

Keywords: Mustard, Correlation, Path analysis

Introduction

Brassica juncea (L.) Czern. belongs to the Cruciferae (Brassicaceae) plant family, commonly known as the mustard family. The name crucifer is derived from the shape of the flowers that have four diagonally opposed petals in the form of a cross. *B. juncea* has pale green foliage, with a few hairs on the first leaves and leaf blades that terminate well up the petiole. Mature *B. juncea* plants grow to a height of one to two meters. The lower leaves are deeply lobed, while the upper leaves are narrow and entire. *B. juncea* is distinct from its close relatives *B. napus* and *B. rapa* in that the upper leaves of *B. juncea* are not clasping. The inflorescence is an elongated raceme and the flowers are pale yellow and open progressively upwards from the base of the raceme. The seed pods are slightly expressed and 2.5 to 5 cm in length exclusive of the beak. The beak is 0.5 to 1 cm long. Seeds are round and can be yellow or brown.

A plant breeding program may be divided into three main steps viz. developing germplasms with various genetic resources, selection of the best individual from the expanded resources and utilized the best selected individual to develop a suitable and superior variety. There is plenty of scopes to increase yield per unit of area through breeding unrivaled varieties. The knowledge on genetic variability heritability and genetic advance and character association is a prerequisite for starting a fruitful breeding program expecting to develop high yielding varieties. High heritability value indicates the strategy for selection of suitable character by the phenotypic performance

of the respective genotype and genetic advance showed the progress for the choice of the best individual.

Determination of correlation coefficient between the characters has considerable importance in selecting breeding materials. Path coefficient technique splits the correlation coefficient into direct and indirect effects via alternative aspects or pathways and in this way allows an essential examination of components that influence a given correlation and can be useful in detailing an efficient selection strategy. Therefore, the path coefficient analysis has been found to provide more particular data on the direct and indirect impact of each of the segment characters upon seed yield. Inter-varietal and inter-specific hybridization are essential for creating the variation or transfer gene of interest from wild species in rapeseed improvement programme. Genetic variability is one of the criteria for parent choice. Consideration of more diverse parents (inside the farthest point) in hybridization should build the possibility of acquiring the most extreme heterosis and give the full range of variability in segregating generations. Therefore, the present study has been undertaken with the following objectives:

- To estimate the mean and range of different traits.
- To study genotypic and phenotypic association among traits.
- To estimate path coefficient analysis of traits under study on seed yield.
- To estimate the genetic diversity among 30 genotypes.

Material and Methods

Thirty diverse genotypes of Indian mustard (*Brassica juncea* L. Czern & Coss) were grown during rabi season 2021-2022 at the research Farm of Department of Genetics & Plant Breeding, R. M. P. (PG) College, Gurukul Narsan, Haridwar, Uttarakhand. The thirty genotypes of Mustard were sown in a randomized block design with three replications at the research farm. These lines were grown in single row plot of 3-meter length. The spacing between row to row and plant to plant was 45 cm and 15 cm, respectively and maintained by thinning. Recommended agronomic practices were adopted to raise a good crop. The observations were recorded on five randomly selected plants for twelve traits, including. The phenotypic and genotypic coefficients of variation (GCV and PCV),

heritability in broad sense, genetic advance as % of mean, correlation coefficients at genotypic and phenotypic level, correlation and path coefficient analysis computed using standard statistical methods.

Result and Discussion

Analysis of variance

The results of analysis of variance for various characters are presented in Table 1. The mean squares due to treatment for all the traits were highly significant, thereby suggesting the presence of considerable amount of variability among the 30 mustard genotypes with respect to the traits studied under present investigation.

Table 1: Analysis of variance for Ten characters in Indian Mustard (*Brassica juncea* L.)

S. No.	Characters	Mean sum of Square		
		Replication	Treatments	Error
		(d.f.= 02)	(d.f.=29)	(d.f.=58)
1	Days to 50% flowering	0.2205	3.8594**	2.790
2	Days to maturity	4.203	740.165**	10.816
3	Plant height (cm)	995.00	5586.30**	113.70
4	No. of primary branches	0.96	8.65**	0.45
5	Number of secondary branches	0.310	3.542**	1.217
6	Number of siliqua per plant	2.905	10.119**	0.621
7	Siliqua length	0.1575	0.7346**	3.137
8	Seeds per siliqua	0.259	12,355**	0.340
9	1000-seed weight (g)	1.021	0.656**	0.030
10	Yield per plant (g)	163.875	417.576**	39.387

*, **significant at 5% and 1% level of significance respectively

Variability, Heritability and Genetic advance

Significant variations were observed for most of the characters among 30 genotypes of *B. juncea*. The values of heritability,

genetic advance in the percentage of the mean, PCV and GCV for different yield related characters were shown in Table 2.

Table 2: The estimates of heritability, GCV, PCV, in 10 traits in Indian Mustard (*Brassica juncea* L.)

S. No.	Characters	Heritability (%)	Genetic advance (% mean)	Genotypic coefficient of variance	Phenotypic coefficient of variance
1	Days to 50% flowering	90.35	7.20	7.95	8.40
2	Days to maturity	82.70	7.05	2.65	2.95
3	Plant height (cm)	76.60	31.15	9.6	11.00
4	No. of primary branches	52.88	1.10	13.90	19.55
5	No. of secondary branches	52.90	3.25	22.55	34.30
6	No. of siliqua / plant	52.50	7.50	11.95	16.60
7	Siliqua length	87.40	1.10	14.55	15.50
8	Seeds per siliqua	66.65	1.70	9.25	12.85
9	1000-seed weight (g)	92.30	1.40	14.55	15.20
10	Seed yield/ plant (g)	86.60	6.15	18.35	19.70

Days to 50% flowering (50F)

The days to 50% flowering were observed the PCV (8.40) was slightly higher than the GCV (7.95) (Table2). Days to 50% flowering exhibited high heritability (90.35%) with genetic advance in the percentage of the mean (7.20) demonstrated that this attribute was controlled by non-additive gene (Table 2).

Days to maturity (DM)

The PCV (2.95) was higher than the GCV (2.65) (Table2),

which proposed that the environment has a significant role in the expression of this trait. Days to maturity demonstrates high heritability (82.70%) with the genetic advance in the percentage of the mean (7.05) indicated that this trait was controlled by the non-additive gene (Table 2).

Plant height

In this investigation, the PCV (11.00) value is slightly higher than GCV (9.60) value (Table 2). Plant height showed low

heritability (76.60%) with the genetic advance in the percentage of mean (31.15) (Table 2), uncovered the likelihood of the prevalence of the additive gene action in the inheritance of this trait and indicating that this trait could be improved through the selection process [Tyagi *et al.*, 2001] ^[16]. High variability in PH for *B. juncea*, L. was seen by [Afrin *et al.*, 2016] ^[1].

Number of primary branches per plant

The PCV (19.55) value is comparatively higher than the corresponding GCV (13.90) value indicating the apparent variation not only due to genotypes but also due to the considerable influence of the environment (Table 2). Varshney *et al.*, 1986 ^[17] also found significant differences in the Number of primary branches per plant. The Number of primary branches per plant displayed low heritability (52.80%) with the low genetic advance in the percentage of the mean (1.10), which uncovered that the non-additive gene controlled this trait. As a whole, the low heritability and the consequent low genetic advance indicated the lower plausibility of choosing genotypes for this attribute [Chowdhury *et al.*, 1987] ^[4]. However, some of the individual plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also found by [Ali *et al.*, 2016] ^[2].

Number of secondary branches per plant (NSB)

The PCV value (34.30) is higher than the corresponding GCV value (22.55) (Table 2). It indicated the presence of considerable variability among the genotypes for this trait. Singh *et al.*, 1987 ^[15] found the highest GCV for the NSB while working on 24 genotypes of *B. napus* L. Varshney *et al.*, 1986 ^[17] found significant differences for the NSB. Moderately high heritability (52.90) along with the low the genetic advance in the percentage of the mean (3.25) (Table 2) revealed that the non-additive gene controlled this trait. As a whole, the moderately high heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes. Moderately high heritability coupled with low genetic advance was also found by [Rashid *et al.*, 2015] ^[10].

Number of silique per plant

The PCV (16.60) had a similar trend as GCV (11.95) (Table 2). The difference between the PCV (16.60) and GCV (11.95) indicated the existence of adequate variation among the genotype. The low heritability (52.50) with the genetic advance in the percentage of the mean (7.50) was observed for this trait, which uncovered that the non-additive gene controlled this trait. As a whole, the low heritability and the consequent low genetic advance indicated the lower plausibility of choosing genotypes for this attribute [Chowdhury *et al.*, 1987] ^[4].

Length of silique

Relatively medium PCV (15.55) and GCV (14.50) was found for this trait (Table 2). Silique length showed the high

heritability (87.40) with the low genetic advance in the percentage of the mean (1.10) indicated that this trait was controlled by non-additive gene (Table 2).

Number of seeds per silique

The value of PCV and GCV were 12.85 and 9.25 respectively for the number of seeds per silique (Table 2) which indicating that medium variation exists among the different genotypes. Number of seeds per silique showed high heritability (66.65%) coupled with the low genetic advance in the percentage of the mean (1.70) (Table 2) indicated that this trait was controlled by non-additive gene and choice for this character would be helpful [Lekh *et al.*, 1998] ^[7].

Thousand seed weight

The PCV (15.20) and GCV (14.55) were close to each other (Table 2). This trait had high heritability (92.30%), low genetic advance in the percentage of the mean (1.40) revealed that this trait was controlled by non-additive gene. High heritability for this trait was also observed by [Singh, 1987] ^[15].

Seed yield per plant

The value of PCV and GCV were 19.70 and 18.35 respectively for the number of seeds per silique (Table 2) which indicating that medium variation exists among the different genotypes. Seed yield per plant showed the high heritability (86.60%) with moderately the high genetic advance in the percentage of the mean (6.15) (Table 2) indicated that this trait was controlled by the additive gene and selection for this character would be effective [Lekh *et al.*, 1998] ^[7]. High heritability coupled with the high genetic advance for this trait was also observed by Rashid *et al.*, 2015] ^[10]. High heritability and genetic advance for Seed Yield/Plant were reported by [Singh, 1987] ^[15] while working with 22 genotypes of *B. napus* L.

The knowledge of variability is prerequisite for simultaneous selection and significant improvement of rapeseed genotypes. The NSB and number of silique per plant demonstrates the presence of broader variability suggesting that these traits could be the excellent candidate for developing new high yielding rapeseed varieties Ejaz-ul-hasan *et al.*, 2014] ^[5]. GCV is a good indicator that imparts information on the existence of genetic variability present in various quantitative traits, but it is lack of providing the clear picture about the heritable variation contributed to GCV [Awas *et al.*, 2015] ^[3]. In the current investigation, we found a cross-link between GCV and PCV for PH, NSP, SL, NSS, and SYP indicating that environment influenced less for the expression of these traits. The highest GCV and PCV value observed for traits- NPB, NSB, and NSP suggesting that selection for these traits would be rewarding to isolate more promising lines. Moderate GCV and PCV value were found for SL, NSS, and SYP indicating that vigorous selection method is utilized for the improvement of these parameters. The descriptors such as 50F, DM, PH, and TSW displayed low GCV and PCV value recommended breeder to find out the high variability source for these traits for the future improvement.

GCV along with the heritable components estimation would render the outcome for proper selection for utilizing them in the future breeding program. Genetic and environmental factors are the contributors to the observed variation in a population. Genetic factors are the only heritable portion from generation after generation. We cannot solely confirm the expected genetic gain in the next generation unless we consider heritability in conjunction with the genetic advance because it provides reliability for the selection of the trait of interest from the variable entries. Characters have high heritability and high genetic advance as a percentage of mean is considered as a powerful genetic tool in the selection round of the best genotype. These characters are governed by the additive gene action and have a less chance to influence by the environment. We found high heritability coupled with high genetic advance

as a percentage of the mean for the trait NSB and NSP. Thus these traits have a less tendency to guide by the environment. Three types of heritability were found in corn- low (0-20%), medium (20-60%) and high (above 60%) [Robinson *et al.*, 1949] ^[12].

Correlation coefficient

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. The correlation coefficient between pairs of the attribute for F₃ materials of *B. juncea* is shown in (Table 3).

Table 3: Phenotypic correlation coefficients for 10 characters of Indian mustard varieties

S. No.	Characters	1	2	3	4	5	6	7	8	9	Seed Yield/Plant
1	Days to 50% flowering		0.008	0.298**	-0.1599	-0.0890	-0.209*	-0.450**	-0.220*	-0.602**	-0.24*
2	Days to maturity			-0.1159	0.1341	0.0903	0.1602	0.1823	0.1838	0.1176	0.169
3	Plant height (cm)				-0.0548	-0.0648	0.1504	-0.220*	-0.291**	-0.1880	0.130
4	No. of primary branches					0.347**	0.377**	0.212*	0.377**	0.405**	0.357**
5	No. of secondary branches						0.596**	0.1302	0.339**	0.224*	0.453**
6	Number of siliqua/plant							0.268**	0.222*	0.306**	0.573**
7	Siliqua length								0.394**	0.285**	0.325**
8	Seeds per siliqua									0.276**	0.396**
9	1000-seed weight (g)										0.472**

*, **significant at 5% and 1% level of significance respectively

Days to 50% flowering showed a highly significant and positive correlation with Plant height (0.298**) indicated that if Days to 50% flowering increased then Plant height also increased. It also exhibited interaction with Days to maturity (0.008). However, it had significant and negative correlation with Number of siliqua / plant (-0.209*), siliqua length (-0.450**), seed per lsiliqua (-0.220*), 1000 seed weight (-0.602**) and seed yield / plant (-0.24*). It had also negative correlation with no of primary branches (-0.1599) and no. of secondary branches (-0.0890) Insignificant association of these traits indicated that environmental factors largely influenced the associations between these traits.

Days to maturity showed insignificant and positive correlation with no of primary branches (0.1341), no. of secondary branches (0.0903), Number of siliqua / plant (0.1602), siliqua length (0.1823), seed per lsiliqua (0.1838), 1000seed weight (0.1176) and seed yield / plant (0.1696) (Table 2). It had negative correlation with plant height (-0.1159) (Table 2). In significant association of these traits indicated that environmental factors largely influenced the associations between these traits. [Parveen *et al.*, 2007] ^[9] also revealed that DM had an insignificant and positive interaction with SYP.

Plant height showed highly significant and negative interaction with selliqua length (-0.220*) and seed / siliqua (-0.291**) (Table 2). This result suggested that selection for one trait, would result into negative/ adverse correlated response in other trait, which had negative correlation. The significant positive correlation between PH and selliqua length and seed / siliqua was found by [Khan and Khan, 2003] ^[6].

Number of primary branches per plant showed positive and significant interaction with no. of secondary branches (0.347**), Number of siliqua / plant (0.377**), siliqua length (0.212*), seed per lsiliqua (0.377**), 1000 seed weight (0.405**) and seed yield / plant (0.357**) (Table 2). Highly significant positive associations between PH and other characters indicate that the same gene governed the traits and simultaneous improvement would be effective. These findings are showing similar to the reports of [Varshney *et al.*, 1986] ^[17].

The Number of secondary branches per plant showed a significant and positive correlation with Number of siliqua / plant (0.596**), seed per siliqua (0.339**), 1000 seed weight (0.224**) and seed yield / plant (0.453**) (Table 2). Highly significant positive associations between PH and other characters indicate that the same gene governed the traits and simultaneous improvement would be effective [Varshney *et al.*, 1986] ^[17]. whereas the insignificant and positive interaction was found in siliqua length (0.1302) Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. [Tyagi *et al.*, 2001] ^[16] reported that NSS had a positive and insignificant effect on SL.

Number of Siliqua / plant showed a highly significant and positive correlation with siliqua length (0.268**), seed per lsiliqua (0.222*), 1000seed weight (0.306**) and seed yield / plant (0.573**) (Table 2). Highly significant positive associations between Number of Siliqua/ plant and other

characters indicate that the same gene governed the traits and simultaneous improvement would be effective. These findings are showing similar to the reports of [Varshney *et al.*, 1986]^[17]. Siliqua length showed a highly significant and positive correlation with seed per siliqua (0.394**), 1000seed weight (0.285****) and seed yield / plant (0.325**) (Table 2) indicated that the traits were governed by same gene and simultaneous improvement would be effective. [Nasim, 1994]^[8] reported that if SL increased then seed per siliqua, 1000seed weight and seed yield / plant will increase.

Seed/ Siliqua showed a highly significant and positive correlation with 1000seed weight (0.276**) and seed yield / plant (0.396**) (Table 2) indicated that the traits were governed by same gene and simultaneous improvement would be effective. [Nasim, 1994]^[8] reported that if Seed/ Siliqua increased then 1000seed weight and seed yield / plant will increase.

Thousand seed weight showed insignificant and positive interaction with Seed yield/plant (0.472**) (Table 2) indicated

that the traits were governed by same gene and simultaneous improvement would be effective. [Saini and Kumar, 1995]^[13] reported that if Thousand seed weight then seed yield / plant will increase.

Path coefficient analysis

Association of character determined by correlation coefficient may not provide an exact picture of the relative importance of the direct and indirect influence of each of yield components on seed yield per hectore. To find out a clear view of the inter-relationship between SYP and other yield attributes, direct and indirect effects were worked out using path analysis at the phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable, and all other characters were causal (independent) variables. Estimation of the direct and indirect effect of path coefficient analysis for *B. juncea* L. is presented in Table 4.

Table 4: Phenotypic path analysis of 10 traits on seed yield of 30 genotypes of Indian mustard

S. No.	Characters	1	2	3	4	5	6	7	8	9	Yield / plant
1	Days to 50% flowering	0.0596	0.0005	0.0178	-0.0095	-0.0053	-0.0125	-0.0269	-0.0132	-0.0359	-0.24*
2	Days to maturity	0.0003	0.0384	-0.0044	0.0051	0.0035	0.0061	0.007	0.0071	0.0045	0.1696
3	Plant height (cm)	0.0721	-0.028	0.2416	-0.0132	-0.0156	0.0364	-0.0533	-0.0703	-0.0454	0.1307
4	No. of primary branches	0.0055	-0.0046	0.0019	-0.0343	-0.0119	-0.013	-0.0073	-0.0129	-0.0139	0.357**
5	No. of secondary branches	-0.0127	0.0129	-0.0092	0.0495	0.1427	0.0851	0.0186	0.0485	0.032	0.453**
6	No. of siliqua / plant	-0.059	0.0451	0.0423	0.1062	0.1677	0.2813	0.0755	0.0626	0.0863	0.5737**
7	Siliqua length	-0.0548	0.0222	-0.0268	0.0258	0.0158	0.0327	0.1216	0.048	0.0348	0.3253**
8	Seeds per siliqua	-0.0511	0.0425	-0.0673	0.0872	0.0786	0.0514	0.0912	0.2312	0.064	0.3966**
9	1000-seed weight (g)	-0.2084	0.0407	-0.0651	0.1404	0.0776	0.1062	0.0989	0.0958	0.346	0.4724**
	Partial R ²	-0.0148	0.0065	0.0316	-0.0123	0.0646	0.1614	0.0396	0.0917	0.1635	

Path coefficient analysis revealed that days to 50% flowering had a positive direct effect (0.067) on grain yield/plant. Days to 50% flowering showed a positive indirect effect on Days to Maturity (0.056) and Plant height (0.016) and negative effect on No. of primary branches (-0.095), No. of secondary branches (-0.056), No. of siliqua / plant (-0.012), Siliqua length (-0.029), Seeds per siliqua (-0.012) and 1000-seed weight (g) (-0.039) (Table 3).

Days to maturity had a positive direct effect (0.046) on grain yield/plant. This trait had a positive indirect effect through Days to 50% flowering (0.034), No. of primary branches (0.031), No. of secondary branches (0.022), No. of siliqua / plant (0.071), Siliqua length (0.006), Seeds per siliqua (0.008) and 1000-seed weight (g) (0.006) (Table 3) revealed that DM had a positive direct effect on yield. On the other hand, DM had negative indirect effect via Plant height (-0.022).

Plant height had a positive direct effect (0.241) on yield per plant. Also had a positive indirect effect via the days to 50% flowering (0.072) and No. of siliqua / plant (0.045) (Table 3). Plant height showed negative indirect effect on days to Maturity (-0.028), No. of primary branches (-0.014), No. of secondary branches (-0.017), Siliqua length (-0.067), Seeds per siliqua (-0.080) and 1000-seed weight (g) (-0.044).

The No. of primary branches had a negative direct effect on yield per plant (-0.044) (Table 3). This trait had a positive indirect effect via days to 50% flowering (0.006), plant height (0.002). On the other hand, the negative indirect effect was found on days to maturity (-0.046), No. of secondary branches (-0.039), No. of siliqua / plant (-0.024), Siliqua length (-0.003), Seeds per siliqua (-0.019) and 1000-seed weight (g) (-0.021). Singh, *et al.*, 1991^[14] reported that the NPB had the direct positive effect on seed yield.

The number of secondary branches had a positive direct effect (0.197) on grain yield/Plant. It had a positive indirect effect via days to maturity (0.019), No. of primary branches (0.055), No. of siliqua / plant (0.057), Siliqua length (0.019), Seeds per siliqua (0.056) and 1000-seed weight (g) (0.054) (Table 3). Rashid, (2007)^[11] observed that the NSB had a direct effect on SYP. On the other hand days to 50% flowering (-0.017), and plant height (-0.008) had negative indirect effect on the NSB.

The No. of siliqua / plant had a positive direct effect (0.267) on seed yield. This trait had a positive indirect effect on days to maturity (0.052), plant height (0.043), No. of primary branches (0.102), No. of secondary branches (0.177), Silqua length (0.085), Seeds per siliqua (0.077) and 1000-seed weight (g) (0.096) (Table 3). This trait had a negative indirect effect via Days to 50% flowering (-0.048).

Siliqua length had a direct positive effect (0.134) on grain yield /plant. This trait had indirect positive effect on days to maturity (0.039), No. of primary branches (0.038), No. of secondary branches (0.018), No. of siliqua / plant (0.027), Seeds per siliqua (0.097) and 1000-seed weight (g) (0.038). On the other hand, Siliqua length showed indirect negative effect via Days to 50% flowering (-0.038) and plant height (-0.034).

The Seeds per siliqua had a direct negative effect (0.245) on grain yield /plant. This trait had an indirect positive effect on days to maturity (0.025), No. of primary branches (0.079), No. of secondary branches (0.086), No. of siliqua / plant (0.014), Siliqua length (0.088) and 1000-seed weight (g) (0.084). On the other hand, Siliqua length showed indirect negative effect via Days to 50% flowering (-0.061) and plant height (-0.066). Path coefficient analysis revealed that TSW had positive direct effect on yield per plant (0.361) followed by positive indirect effect via days to maturity (0.067), No. of primary branches (0.207), No. of secondary branches (0.053), No. of siliqua / plant (0.124), Siliqua length (0.072), and Seeds per siliqua (0.081). On the other hand, Siliqua length showed indirect negative effect via Days to 50% flowering (-0.305) and plant height (-0.049).

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