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Genetic diversity assessment for morphological, yield and biochemical traits in genotypes of pumpkin

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Abstract

The investigations were conducted with the using of twenty one genotypes (15 F₁ hybrids and 6 parents) of pumpkin. The germplasms were evaluated for twenty one morphological, yield and biochemical traits viz., days to first male flower anthesis, days to first female flower anthesis, node number to first male flower, node number to first female flower, days to first fruit harvest, number of primary branches per plant, Equatorial circumference of fruit, polar circumference of fruit, Flesh thickness, internodal length (cm), vine length (m), average fruit weight (kg), number of fruits per plant, Fruit yield per plant (kg), dry matter content, total soluble solids, total sugars, reducing sugars, non-reducing sugars, ascorbic acid content and β -carotene. The evaluations were conducted consecutively three seasons during 2015-16. The study revealed that mean squares due to genotypes were significant for all the traits during all three seasons (E₁, E₂, E₃). However, the analysis of variance on the basis of pooled revealed that mean squares due genotypes, environments, overall sum found significant for all the traits except overall sum for traits viz., flesh thickness, dry matter content and total sugars content. The investigations further revealed that high phenotypic and genotypic coefficient of variation were observed for vine length, number of fruits per plant, fruit yield per plant, reducing sugars and β -carotene. High heritability coupled with high genetic advance were observed for number of fruits per plant, fruit yield per plant, reducing sugars, ascorbic acid and β -carotene indicated that the improvement of these traits through selection.

Keywords: PCV, GCV, fruit yield per plant, heritability and genetic advance

1. Introduction

Pumpkin (*Cucurbita moschata* Duch. ex. Poir) is one of the most important vegetable crop of cucurbitaceae family grown throughout the world not only for good sources of nutrition to the consumers but also for its higher returns to the farmers. It is originated from central Mexico. Pumpkin is a herbaceous annual, sexually propagated vegetable having an identical genomic formula $2n=2x=40$. The word pumpkin originates from the word *pepon*, which is a Greek word meaning for "large melon", something round and large.

Based on commercial significance the cultivated *Cucurbita* species rank collectively among the 10 leading vegetable crops worldwide. China and India lead the world production. Other major producers are U.S., Egypt, Mexico, Ukraine, Cuba, Italy, Iran and Turkey (Ferriol and Pico, 2008). The total area of pumpkin in India is 19760 hectare whereas, the total production is 0.42 million tonne (Anonymous 2016) [1]. Robinson and Decker-Walters (1999) [19] concluded that in genus *Cucurbita* there are 5 cultivated and 10 wild species. Seshadri and More (2009) [20] also stated that the recent recognition of synonyms and taxonomic changes have reduced the number of *Cucurbita* species to 15 or even less.

The color of pumpkins is derived from the orange pigments abundant in them. The main nutrients are lutein and both alpha and beta carotene, the latter of which generates vitamin A in the body. Pumpkins are very versatile in their uses for cooking. Most parts of the pumpkin are edible, including the fleshy shell, the seeds, the leaves, and even the flowers. In the United States and Canada, pumpkin is a popular Halloween and Thanksgiving staple. Pumpkin purée is sometimes prepared and frozen for later use.

The continuous variation exhibited by quantitative traits with which the breeders have to deal with, include the heritable and non-heritable components. Though, it is difficult to assess the genotype directly but it is possible through the assessment of phenotypic expression (which is an outcome of interplay of the genotype and environment) in the existing material and thus, the study of phenotypic variability for yield and its component traits is very important.

Materials and Methods

The experiments of the present research work were conducted during *Kharif*, (E₁) *Rabi* seasons (E₂) and summer-season (E₃) of 2015-16 at Main Experiment Station of Department of

Vegetable Science, at Narendra Deva University of Agriculture & Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.). The experimental material comprising selected parental lines *i.e.* Narendra Upkar (P₁), NDPK-120 (P₂), Narendra Agrim (P₃), NDPK-39-2 (P₄), Kashi Harit (P₅) and NDPK-11-3 (P₆) and their 15 offspring which developed through diallel mating were evaluated in randomized block design with three replications.

Observations were recorded on 14 economic traits *viz.*, days to first female flower anthesis, days to first male flower anthesis, node number to first male flower appearance, node number to first female flower appearance, days to first fruit harvest, vine length (m), internodal length (cm), number of primary branches per plant, fruit weight (kg), number of fruits per plant, equatorial circumference of fruit (cm), polar circumference of fruit (cm), flesh thickness (cm), fruit yield per plant (kg), and seven biochemical traits namely ascorbic acid, reducing sugars (%), non-reducing sugars (%), total sugars (%), dry matter content, total soluble solids, β -carotene (mg/100g).

Statistical analysis

The average values for each genotype in each replication for the traits studied were used for further statistical analysis. A brief outline of the procedure adopted for the estimation of statistical parameters. Analysis of variance, the data for the component traits excluding capsanthin content was analysed as per the following model given by Panse and Sukhatme (1984) [17]. The calculated 'F' values were compared with the tabulated 'F' values at 5 % level of significance. If the calculated 'F' value was higher than the tabulated, it was considered to be significant. All the characters which showed significant differences among genotypes were further subjected to the analysis for the different parameters. The phenotypic, genotypic, environmental coefficients of variation, heritability in broad sense (h^2_{bs}) and the expected genetic advance (GA) for different characters content were calculated as suggested by Burton and De Vane (1953) [4] and Johnson *et al.* (1955) [11].

For categorizing the magnitude of different parameters, the following limits were used:

PCV and GCV and ECV	<10%	-	Low
	10-20%	-	Moderate
	>20%	-	High
Genetic advance (GA)	<15%	-	Low
	15-30%	-	Moderate
	>30%	-	High
Heritability	<60%	-	Low
	60%-80%	-	Moderate
	> 80%	-	High

Results and discussion

The analysis of variance (Table- 1.1, 1.2., 1.3.,1.4.) revealed that mean squares due to genotypes were significant for all the traits during all three seasons (E₁, E₂, E₃). However, the analysis of variance on the basis of pooled revealed that mean squares due to genotypes, environments, overall sum found significant for all the traits except overall sum for traits *viz.*, flesh thickness, dry matter content and total sugars content. Sufficient genetic variability for many traits has also been reported by earlier workers *viz.*, Chigwe and Saka (1994) [6]; Babu *et al.* (1996) [2]; Kumaran *et al.* (1997) [12]; Mohanty (2000) [15]; Gwanama *et al.* (2002) [10]; Dhatt and Singh

(2008) [7] and thereby, supporting the present findings.

The estimates (Table 2) of phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters during all three seasons *kharif*, 2015 (E₁), *rabi*, 2015-16 (E₂) and summer-season, 2016(E₃) and over environments (pooled).

The highest phenotypic as well as genotypic coefficients of variation (Table 2) were observed in case of number of fruits per plant, fruit yield per plant, reducing sugars, β -carotene during all three seasons (E₁, E₂, E₃) and over environments (pooled). While, reducing sugars and non-reducing sugars only high PCV during all three seasons (E₁, E₂, E₃) and over environments (pooled) suggest substantial variability for the traits thereby ensuring ample scope for improvement of these traits through selection Mohanty and Mishra (1999) [16]; Laxmi *et al.* (2002) [13] and Dhatt and Singh (2008) [7] also reported the high GCV as well as PCV. Whereas, moderate phenotypic as well as genotypic coefficients of variation were observed for node number to first male flower anthesis, number of primary branches per plant, internodal length, average fruit weight, dry matter content, total soluble solids, total sugars, ascorbic acids and node number to first female flower anthesis only PCV and non-reducing sugars only GCV during E₁, node number to first male flower anthesis, node number to first female flower anthesis, number of primary branches per plant, polar circumference of fruit, flesh thickness, internodal length, average fruit weight, dry matter content, total soluble solids, total sugars, ascorbic acids and reducing sugars only GCV during E₂. Whereas, the rest of characters showed low estimates phenotypic as well as genotypic coefficients of variation. However, the estimates of environmental coefficient of variation observed low for all the traits except vine length, reducing sugars and non-reducing sugars these traits showed moderate environmental coefficient of variation.

Heritability and genetic advance

Heritability in broad sense of a character is important to the breeder since it indicates the possibility and extent to which improvement is possible through selection. It also indicates direction of selection pressure to be applied for a trait during selection because it measures relationship between parents and their progeny, hence widely used in determining the degree to which a character may be transmitted from parents to offspring. However, high heritability alone is not enough to make efficient selection in advanced generation unless accompanied by substantial amount of genetic advance (Burton, 1952) [5]. High estimate of heritability along with high genetic advance in per cent of mean provides good scope for further improvement in advance generations.

The result on heritability and genetic advance in per cent of mean of present investigation had been presented in Table 4.2. The heritability estimates (Table 2) for different traits ranged from 28.00 to 99.00 per cent. High estimates of heritability number of fruits per plant and fruit yield per plant during all three seasons (E₁, E₂, E₃) and over seasons (pooled). Days to first male flower anthesis, Days to first female flower anthesis, node number to first male flower appearance, node number to first female flower appearance, days to first fruit harvest, number of primary branches per plant, equatorial circumference of fruit, polar circumference of fruit, internodal length, dry matter content, total soluble solids, total sugars, reducing sugars, ascorbic acid and β -carotene during all three seasons (E₁, E₂, E₃) which revealed that these traits are governed by additive gene action and phenotypic

selection would be effective for improvement of these traits. The earlier researchers *viz.*, Dojode and Sulladmath (1986) [8]; Rana *et al.* (1986) [18] and Mohanty (2000) [15] also reported high heritability. However, number of fruits per plant had high estimates of heritability in over seasons. However, in pooled analysis the moderate estimates of heritability observed for days to first male flower anthesis, node number to first male flower appearance, node number to first female flower appearance, days to first fruit harvest, number of primary branches per plant, equatorial circumference of fruit, polar circumference of fruit, total soluble solids and β -carotene.

The estimates of high heritability coupled with high genetic advance as per cent of mean were observed for number of fruits per plant and fruit yield per plant during all three seasons (E_1 , E_2 , E_3) and over seasons (pooled) while, number

of primary branches per plant, reducing sugars, ascorbic acid and β -carotene during all three seasons (E_1 , E_2 , E_3). High heritability coupled with moderate genetic advance were observed for days to first female flower anthesis, node number to first male flower appearance, node number to first female flower appearance, equatorial circumference of fruit, polar circumference of fruit, average fruit weight and dry matter content during all three seasons (E_1 , E_2 , E_3) which indicating the additive gene action for these traits the phenotypic selection could be relied upon. Mangal *et al.* (1979) [14]; Rana *et al.* (1986) [18]; Kumaran *et al.* (1997) [12]; Bindu *et al.* (2000) [3]; have reported high heritability with high genetic advance and Mohanty and Mishra (1999) [16] reported moderate with high genetic advance and Dhatt and Singh (2008) [7] have reported high heritability accompanied by moderate to high genetic advance.

Table 1.1: Analysis of variance for growth, yield and biochemical attributes of pumpkin during *Kharif* season 2015 (E_1)

Source of Variation	d.f.	Days to first male flower anthesis	Days to first female flower anthesis	Node number to first male flower	Node number to first female flower	Days to first fruit harvest	Number of primary branches per plant	Equatorial circumference of fruit	Polar circumference of fruit	Flesh thickness	Internodal length (cm)
Replications	2.00	0.03	0.06	0.00	0.06	0.30	0.03	0.40	0.41	0.01	0.05
Genotypes	20.00	41.78**	39.83**	1.16**	9.46**	65.48**	7.33**	72.70**	50.18**	0.13**	3.86**
Error	40.00	0.26	0.68	0.06	0.32	0.73	0.07	2.99	3.23	0.03	0.08

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1.1: Contd

Source of Variation	d.f.	Vine length (m)	Average fruit weight	No. of fruits per plant	Fruit yield per plant	Dry matter content	Total soluble solids	Total sugars	Reducing sugars	Non-reducing sugars	Ascorbic acid	β -carotene
Replications	2.00	0.01	0.00	0.00	0.47	0.02	0.05	0.03	0.0324	0.04	0.10	0.08
Genotypes	20.00	2.54**	0.11**	1.19**	5.11**	2.16**	1.74**	1.36**	0.9435**	0.48**	3.57**	4.97**
Error	40.00	0.13	0.01	0.03	0.17	0.10	0.09	0.10	0.0740	0.05	0.05	0.05

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1.2: Analysis of variance for growth, yield and biochemical attributes of pumpkin during *Rabi* season 2015-16 (E_2)

Source of Variation	d.f.	Days to first male flower anthesis	Days to first female flower anthesis	Node number to first male flower	Node number to first female flower	Days to first fruit harvest	Number of primary branches per plant	Equatorial circumference of fruit	Polar circumference of fruit	Flesh thickness	Internodal length (cm)
Replications	2.00	0.22	0.03	0.07	0.84	1.29	0.01	0.55	0.67	0.00	0.05
Genotypes	20.00	85.91**	71.68**	2.96**	7.02**	89.36**	5.97**	61.99**	110.45**	0.23**	2.76**
Error	40.00	0.22	0.62	0.11	0.46	0.89	0.05	0.95	1.40	0.01	0.05

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1.2: Contd

Source of Variation	d.f.	Vine length (m)	Average fruit weight	No. of fruits per plant	Fruit yield per plant	Dry matter content	Total soluble solids	Total sugars	Reducing sugars	Non-reducing sugars	Ascorbic acid	β -carotene
Replications	2.00	0.00	0.00	0.06	0.14	0.02	0.01	0.01	0.02	0.00	0.01	0.05
Genotypes	20.00	0.31**	0.11**	1.15**	3.32**	3.05**	2.58**	2.47**	1.26**	0.44**	6.23**	5.11**
Error	40.00	0.07	0.00	0.03	0.09	0.04	0.04	0.05	0.02	0.01	0.05	0.05

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1.3: Analysis of variance for growth, yield and quality attributes of pumpkin during summer season, 2016 (E_3)

Source of Variation	d.f.	Days to first male flower anthesis	Days to first female flower anthesis	Node no. to first male flower appearance	Node no. to first female flower appearance	Days to first fruit harvest	Number of primary branches per plant	Equatorial circumference of fruit	Polar circumference of fruit	Flesh thickness	Internodal length (cm)
Replications	2.00	0.03	0.67	0.00	0.09	1.21	0.03	0.74	0.32	0.02	0.06
Genotypes	20.00	41.78**	39.83**	1.16**	9.40**	80.69**	7.33**	72.70**	50.18**	0.13**	3.86**
Error	40.00	0.26	0.47	0.06	0.30	0.55	0.07	2.99	3.38	0.03	0.08

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1.3: Contd

Source of Variation	d.f.	Vine length (m)	Average fruit weight (Kg)	No. of fruits per plant	Fruit yield per plant	Dry matter content (%)	Total soluble solids	Total Sugars (%)	Reducing sugars (%)	Non-reducing sugars (%)	Ascorbic acid (mg/100g)	β -carotene (mg/100g)
Replications	2.00	0.00	0.00	0.00	0.02	0.11	0.01	0.06	0.03	0.02	0.01	0.07
Genotypes	20.00	2.54**	0.11**	1.19**	6.07**	2.16**	1.74**	1.36**	0.94**	0.53**	3.57**	4.97**
Error	40.00	0.14	0.01	0.03	0.30	0.12	0.12	0.10	0.07	0.06	0.09	0.05

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1.4: Analysis of variance for growth, yield and quality attributes of pumpkin during over seasons (pooled)

Source of Variation	d.f.	Days to first male flower anthesis	Days to first female flower anthesis	Node number to first male flower	Node number to first female flower	Days to first fruit harvest	Number of primary branches per plant	Equatorial circumference of fruit	Polar circumference of fruit	Flesh thickness	Internodal length (cm)
Replications	2.00	0.19	0.09	0.02	0.06	0.98	0.07	0.31	0.25	0.02	0.03
Environments	2.00	68326.73**	57694.41**	93.09**	704.09**	70174.26**	5.48**	338.59**	562.15**	0.00	40.85**
Interactions	4.00	0.05	0.33	0.03	0.46	0.91	0.00	0.69	0.58	0.00	0.06
Overall Sum	8.00	17081.75**	14423.79**	23.29**	176.27**	17544.26**	1.39**	85.07**	140.89**	0.01	10.25**
Genotypes	20.00	115.46**	84.07**	3.21**	16.68**	136.84**	15.91**	170.44**	132.88**	0.27**	5.94**
Error	160	6.94	8.85	0.31	1.42	12.88	0.64	6.35	11.74	0.05	0.62

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 1.4: Contd

Source of Variation	d.f.	Vine length (m)	Average fruit weight	No. of fruits per plant	Fruit yield per plant	Dry matter content	Total soluble solids	Total Sugars (%)	Reducing sugars (%)	Non-reducing sugars (%)	Ascorbic acid	β -carotene
Replications	2.00	0.00	0.00	0.03	0.05	0.05	0.01	0.08	0.05	0.02	0.02	0.20
Environments	2.00	31.76**	6.60**	1.27**	73.64**	2.01**	2.50**	1.18**	5.89**	3.16**	7.09**	5.68**
Interactions	4.00	0.00	0.00	0.02	0.29	0.05	0.03	0.01	0.02	0.02	0.05	0.00
Overall Sum	8.00	7.94**	1.65**	0.33**	18.57**	0.54	0.64**	0.32	1.49**	0.80**	1.80*	1.47**
Genotypes	20.00	3.29**	0.33**	3.30**	13.71**	4.29**	4.30**	2.10**	1.55**	0.60**	7.40**	11.55**
Error	160	0.35	0.01	0.05	0.24	0.45	0.28	0.45	0.24	0.13	0.79	0.47

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 2: Estimates of variability parameters for growth, yield and quality traits in pumpkin during three seasons (E₁, E₂, E₃) and over seasons (pooled)

Component of variation \ Traits		Days to first male flower anthesis	Days to first female flower anthesis	Node number to first male flower appearance	Node no. to first female flower appearance	Days to first fruit harvest	Number of primary branches per plant	Equatorial circumference of fruit	Polar circumference of fruit	Flesh thickness	Internodal length (cm)
PCV (%)	E ₁	9.06	8.52	14.80	10.49	7.73	18.57	9.36	9.10	9.77	14.92
	E ₂	5.47	5.15	15.82	13.91	4.66	15.80	9.07	14.32	11.17	15.56
	E ₃	9.21	8.52	14.80	10.43	8.75	18.57	9.31	9.01	9.76	15.33
	Pooled	7.25	6.82	15.63	11.34	6.48	17.63	9.26	10.83	10.25	15.30
GCV (%)	E ₁	8.98	8.30	13.77	9.98	7.60	18.29	8.81	8.28	7.19	14.49
	E ₂	5.45	5.08	15.01	12.64	4.59	15.59	8.87	14.05	10.55	15.15
	E ₃	9.12	8.37	13.77	9.96	8.67	18.29	8.76	8.17	7.19	14.86
	Pooled	5.78	4.75	11.14	8.37	4.66	15.02	7.98	7.92	6.03	10.69
ECV (%)	E ₁	1.23	1.89	5.43	3.23	1.39	3.20	3.16	3.77	6.62	3.59
	E ₂	0.47	0.82	4.99	5.80	0.80	2.59	1.91	2.76	3.69	3.52
	E ₃	1.25	1.59	5.43	3.11	1.24	3.20	3.14	3.80	6.60	3.77
	Pooled	4.38	4.89	10.97	7.65	4.51	9.23	4.71	7.40	8.29	10.94
h ² (broad sense) (%)	E ₁	98.00	95.00	87.00	91.00	97.00	97.00	89.00	83.00	54.00	94.00
	E ₂	99.00	97.00	90.00	83.00	97.00	97.00	96.00	96.00	89.00	95.00
	E ₃	98.00	97.00	87.00	91.00	98.00	97.00	89.00	82.00	54.00	94.00
	Pooled	63.00	49.00	51.00	54.00	52.00	73.00	74.00	53.00	35.00	49.00
Genetic advance (% of mean)	E ₁	18.32	16.68	26.38	19.56	15.40	37.12	17.08	15.53	10.89	28.97
	E ₂	11.18	10.33	29.34	23.66	9.33	31.67	17.86	28.40	20.51	30.40
	E ₃	18.62	16.94	26.38	19.58	17.67	37.12	16.99	15.25	10.92	29.67
	Pooled	9.48	6.82	16.34	12.72	6.90	26.36	14.15	11.92	7.31	15.39
General Mean	E ₁	41.45	43.51	4.40	17.48	61.14	8.50	54.72	47.75	2.60	7.75
	E ₂	98.15	95.81	6.50	11.70	118.18	9.01	50.85	42.91	2.60	6.27
	E ₃	40.78	43.29	4.40	17.50	59.64	8.50	55.01	48.36	2.60	7.56
	Pooled	60.13	60.87	5.10	15.56	79.65	8.67	53.53	46.34	2.60	7.19

Table 2: Contd

Component of variation	Vine length (m)	Average fruit weight	No. of fruits per plant	Fruit yield per plant	Dry matter content	Total soluble solids	Total sugars	Reducing sugars	Non-reducing sugars	Ascorbic acid	β -carotene	
PCV (%)	E ₁	27.72	11.25	24.22	27.18	12.61	13.63	15.26	22.54	21.16	17.79	25.48
	E ₂	15.99	13.99	23.95	28.69	14.50	15.72	18.68	20.05	23.26	21.18	23.14
	E ₃	25.61	10.40	22.27	25.18	12.17	13.02	14.48	20.61	22.60	17.55	23.80
	Pooled	25.40	11.66	23.44	26.99	13.11	14.15	16.27	21.00	22.33	19.07	24.10
GCV (%)	E ₁	25.77	10.00	23.47	25.86	11.80	12.68	13.65	20.12	18.37	17.44	25.12
	E ₂	11.78	13.28	23.04	27.52	14.21	15.32	18.16	19.54	22.58	20.92	22.80
	E ₃	23.67	9.11	21.42	23.42	11.24	11.75	12.97	18.40	19.36	16.93	23.46
	Pooled	17.71	10.72	21.94	25.05	9.16	11.07	8.76	12.89	11.83	13.22	20.48
ECV (%)	E ₁	10.24	5.14	5.98	8.37	4.45	5.00	6.83	10.16	10.50	3.53	4.28
	E ₂	10.81	4.39	6.52	8.12	2.87	3.53	4.38	4.50	5.59	3.28	3.97
	E ₃	9.77	5.03	6.08	9.27	4.67	5.61	6.43	9.29	11.66	4.64	4.03
	Pooled	18.21	4.59	8.24	10.04	9.38	8.81	13.71	16.58	18.94	13.74	12.70
h ² (broad sense) (%)	E ₁	86.00	79.00	94.00	91.00	88.00	87.00	80.00	80.00	75.00	96.00	97.00
	E ₂	54.00	90.00	93.00	92.00	96.00	95.00	95.00	95.00	94.00	98.00	97.00
	E ₃	85.00	77.00	93.00	86.00	85.00	81.00	80.00	80.00	73.00	93.00	97.00
	Pooled	49.00	85.00	88.00	86.00	49.00	61.00	29.00	38.00	28.00	48.00	72.00
Genetic advance (% of mean)	E ₁	49.33	18.33	46.85	50.68	22.76	24.30	25.15	36.99	32.85	35.20	51.00
	E ₂	17.88	25.98	45.67	54.38	28.70	30.76	36.37	39.22	45.14	42.57	46.26
	E ₃	45.08	16.42	42.44	44.85	21.37	21.83	23.94	33.83	34.16	33.63	47.62
	Pooled	25.44	20.30	42.32	47.90	13.18	17.85	9.71	16.30	12.92	18.89	35.86
General Mean	E ₁	3.48	1.87	2.65	4.96	7.02	5.86	4.73	2.68	2.06	6.22	5.10
	E ₂	2.43	1.42	2.66	3.77	7.04	6.00	4.95	3.28	1.67	6.86	5.70
	E ₃	3.78	2.04	2.90	5.92	7.34	6.25	4.98	2.93	2.06	6.37	5.46
	Pooled	3.23	1.78	2.74	4.88	7.13	6.03	4.89	2.96	1.93	6.48	5.42

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