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Photo thermal studies of rice genotypes with respect to agro meteorological indices

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Abstract
An investigation was carried out with thirty two genotypes of rice under direct seeded condition. D^2 statistics were used to explore and access the nature and magnitude of genetic divergence on the basis of grain yield and other important traits. The Mahalanobis D^2 analysis grouped 32 genotypes of rice into seven distinct clusters. Maximum numbers of 11 genotypes were present in cluster V and least of 1 genotype within cluster II & IV. The highest intra-cluster distance was observed in cluster VII with highest mean value for most of the traits along with better individual performance of genotypes indicating greater genetic divergence among the genotypes belonging to this cluster. Maximum inter-cluster distance was recorded between clusters III and VI followed by clusters VI and VII. Cluster VII showed highest mean performance for most of the yield attributing traits therefore, selection of parents based on these traits are highest contributor towards the genetic divergence explored in present study.

Keywords: Variability, rice, D^2 statistics, genetic divergence, cluster distance

1. Introduction
Asia is considered as the "rice bowl" of the world, since it produces and consumes more than 90 per cent of world rice (Prabhu, 2017) [11]. Being the staple food for more than 65% of the people, national food security hinges on growth and stability of its production (Shamim *et al*., 2012) [19]. Worldwide, rice is grown on 161 million hectare with an annual production of about 487.46 million tonnes (Statista 2017-18) [24]. In India, rice field covers an area of about 44.10 million hectares with production of 110.15 million tonnes (Directorate of economics statistics Gov. of Bihar 2017-18). Water is becoming a looming crisis in agriculture, more particularly in rice cultivation. By 2025, per capita water availability in many Asian countries is likely to decline by 15-54% as compared with 1990. Direct seeded rice (DSR) cultivation is one of the promising water saving rice production technology where the amount of irrigation water meets the demand for evaporation from soil and transpiration by the crops. In DSR technique, grain yield and water productivity increased by 2.94 and 14.43 % respectively with laser levelling as compared to transplanted rice (Jat *et al*., 2006) [7].
To save irrigation water, researchers are developing some alternative cultivation methods which can help to save water and enhance water productivity in rice cultivation. The estimation of genetic divergence in the available germplasm is important for successful selection of parents for hybridization purpose. Genetic diversity represents the heritable variation within and between populations of organisms. The success of plant breeding depends on the availability of genetic variation, knowledge about desired traits and efficient strategies that make it possible to exploit existing genetic resources. The pool of genetic variation within an intermating population is the basis for selection as well as for plant improvement. Genetic

distance estimates for population grouping can be estimated by different methods as it is crucial to understand the usable variability existing in the population. One of the approaches is to apply multivariate analysis. Several workers have emphasized the importance of genetic divergence for selection of desirable parents (Sanyal 2016, shridhar 2016, Patra 2017, Saravanan 2017, Shaikh 2017) [16, 20, 10, 17, 18].

Looking into the importance of varietal development in rice under direct seeded condition, the present investigation was undertaken to assess the magnitude of genetic divergence among the selected rice genotypes and in order to identify and classify the variations for grouping of the genotypes by taking into account several characteristics and relationship between them.

Materials and Methods

Field experiment was conducted in Rice Research Farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar. Weather data which includes maximum temperature, minimum temperature, rainfall, relative humidity, day length and bright sunshine hours were collected from the Meteorological department of Dr. Rajendra Prasad Central Agriculture University, Pusa, Bihar from the month of sowing (June) to the month of harvesting (October) 2017.

A total of thirty two genotypes of rice were taken up in the present study for sowing during the month of June, 2017. The observations were recorded on five randomly selected competitive plants from each plot in all three replications for ten quantitative traits *viz.*, days to fifty per cent flowering, days to physiological maturity, plant height, number of tillers per plant, number of panicles per plant, panicle length, 1000-grain weight, relative water content, spikelet fertility and grain yield per plant. The remaining seven characters were agro-meteorological indices *viz*., growing degree days, photo thermal unit, helio thermal unit, photo thermal index, heat use efficiency, relative temperature depression and critical temperature for reproductive stage were calculated from both morphological and meteorological data. All the collected data were subjected to Mahalanobis D^2 analysis (Rao, 1952) to assess the genetic divergence among the available genotypes. The genotypes were grouped into different clusters, intra and inter cluster distance, mean performances for characters and their contribution to the divergence were also compared.

The weather parameters for crop growing period were obtained from the Agrometeorology Division, Rajendra Agricultural University, Pusa, Samastipur, Bihar. All energy requirement parameters were recorded at physiological maturity as follows:

Growing degree days was computed with 10^0c as base temperature on the basis of daily mean temperature with the help of following formula:

$$GDD = \frac{\sum (Tmax + Tmin)}{2} - T_b$$

Where, T max and T min are daily mean maximum and minimum temperature, T_b is the base temperature.

Photo-thermal unit (PTU) (degree-days hours) was calculated on the basis of GDD and day length with the formula given below:

PTU= GDD x Day length

Halio-thermal unit (HTU) (degree-days hours) was calculated on the basis of GDD and sunshine hours by the following formula:

HTU = GDD x Duration of sun shine hours

Photo-thermal index (PTI) (degree-days day^{-1}) was calculated using the following equation:

PTI = GDD/ Growth days

Heat use efficiency (HUE) (kg ha^{-1} degrees-day) was calculated with the help of seed yield (kg-^{1}ha) per GDD with the help of following equation:

HUE = Seed yield (kg ha$^{-1)}$/GDD

Relative temperature depression was calculated using the formula:

$$RTD = \frac{\sum Tmax - Tmin}{Tmax} \times 100$$

Where, Tmax and Tmin are daily mean maximum and minimum temperature

Relative water content (RWC) of the flag leaves was determined using the equation given by Barr and Weatherley (1962):

$$RWC = \frac{F.W - D.W.}{T.W. - D.W.} \times 100$$

Where,
F.W. = Fresh Weight of flag leaf (g)
D.W. = Dry Weight of flag leaf (g)
T.W. = Turgid Weight of flag leaf (g)

Critical temperature for reproductive stage (^{o} c)

Critical temperature for reproductive stage was measured by recording accumulated daily temperature till flowering and accumulated daily temperature till maturity and calculated using the equation as proposed by Arnold (1960):

$$CRT = \frac{\text{Accumlulated daily temp. till maturity - Accumulated daily temp. till flowering}}{\text{Number of days to maturity - number of days to flowering}}$$

$$\text{Accumlulated daily temp. till maturity} = \text{Sum of daily average temperature} \times \text{No. of days up to maturity}$$

$$\text{Accumulated daily temp. till flowering} = \text{Sum of daily average temperature} \times \text{No. of days up to flowering}$$

Results and Discussion

Analysis of variance showed significant differences ($p \leq 0.01$) among the genotypes for all the seventeen studied characters, suggesting the existence of sufficient amount of genetic variability among the genotypes (Table 1). The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. The results indicated high magnitude of variances for majority of the characters might favour selection and further utilization in future recombination breeding programme. Similar findings were reported by Chandramohan *et al.* (2016) [4], Khokhar and Sarial (2016) [8] and Raj *et al.* (2017) [12].

Table 1: Analysis of variance for thirty two genotypes of rice

Sl. No.	Characters	Mean sum of squares		
		Replication (d.f.=2)	Treatments (d.f.=31)	Error (d.f.=62)
1.	Days to 50% Flowering	31.01	230.26**	10.91
2.	Days to Physiological maturity	6.88	258.37**	12.46
3.	.Plant height (cm)	0.76	149.45**	22.19
4.	Panicle length (cm)	0.56	6.62**	1.91
5.	Number of tillers per Plant	1.34	12.79**	1.25
6.	Number of panicle per Plant	0.87	8.15**	1.47
7.	Spikelet fertility (%)	9.69	195.44**	3.26
8.	1000 grain weight (gm)	0.67	25.69**	0.86
9.	Growing degree days(Degree days)	16453.22	221275.31**	11163.76
10.	Helio-thermal unit (Degree-days hours)	244211.65	6272588.50**	319061.00
11.	Photo-thermal unit (Degree-days hours)	4185303.00	33346478.00**	1791952.75
12.	Photo-thermal index (Degree-days day^{1})	0.09	0.21**	0.11
13.	Heat use efficiency (Kg ha^{-1} degree days)	0.0001	0.15**	0.01
14.	Relative Temperature depression	0.04	0.13**	0.04
15.	Critical temperature for reproductive stage(^{0} C)	0.14	0.36**	0.09
16.	Relative water content (%)	3.86	202.50**	8.89
17.	Grain yield per plant (gm)	0.48	10.58**	0.81

Thirty two genotypes of rice under study were grouped into seven clusters using Mahalanobis D^2 analysis (Table 2).

Table 2: Clustering patterns on the basis of D2 statistics for thirty two genotypes of Rice under direct seeded condition

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	9	RAU1451-66-1-1-5-2, RAU1421-12-1-7-3, RAU1451-66-1-1-5-1, RAU1417-9-7-22-5-7-3, RAU1428-543-35-5-5, RAU1397-18-3-7-9-4-7, RAU1428-7-3-6, RAU1421-12-1-7-4-4, RAU1416-4-2-5-2-2
II	1	RAU1463-16
III	4	RAU1421-12-1-7-4-3, RAU1401-18-1-1-5, Rajendra Nilam, Rajendra Bhagwati (C)
IV	1	RAU1421-15-3-2-5-3-7
V	11	RAU1417-2-1-5-7-7, RAU1415-35-76-9-5-3-4, RAU1401-18-1-1, RAU1421-15-3-2-5-7-3, RAU1415-35-7-6-9-5-1, RAU1426-43-2-5-4, RAU1415-8-6-4-3-3, Prabhat, Richaria, Rasi, Turanta
VI	3	RAU1397-25-8-1-2-5-4, RAU1417-11-1-74-3-2, MTU-1010
VII	3	RAU96-P-1-2, Sahbhagi,Vandana,

The discrimination of 32 genotypes into seven discrete and different clusters indicated existence of substantial genetic diversity in the material to suggest that it would serve as good source for providing suitable diverse parents for hybridization programme aimed at isolating superior segregants of rice. The genotypes within each cluster were closer to each other than the genotypes in different clusters.Maximum number of genotypes *i.e.* 11 were grouped in cluster V followed by 9 genotypes in cluster I, 4 genotypes in cluster III, 3 genotypes each in cluster VI and VII, cluster II and IV were solitary *i.e.* monogenotypic. Similar findings were observed by Hegde and Patil (2002) [6], Chauhan and Singh (2003) [5], Rani *et al.*, (2017) [13]. The pattern of group constellation proved the existence of significant amount of variability. The clustering pattern of the genotypes revealed that the clustering did not follow any particular pattern of clustering with respect to the origin. Ushakumari and Rangaswamy, (1997) [23] and Sheikh *et al.*, (2017) [18]. Similar study based on D^2 statistic was also observed by Maji *et al.*, (2012) [9] and Sanyal *et al.*, (2016) [16].

The estimates of intra- and inter-cluster distances represented by D^2 values among seven clusters were computed and have been given in Table 3. The intra-cluster distance ranged from 0.00 for cluster IV to 42.19 for cluster VII.

Table 3: Mean intra and inter-cluster distances among seven clusters of Rice under direct seeded condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	12.5	17.32	35.83	17.86	28.46	104.09	74.62
Cluster II		0.00	39.37	17.35	27.66	89.26	73.59
Cluster III			21.34	37.14	62.43	170.80	60.06
Cluster IV				0.00	39.72	112.87	78.82
Cluster V					22.92	110.29	85.85
Cluster VI						36.09	163.00
Cluster VII							42.19

The maximum intra-cluster distance was observed in cluster VII (42.19) followed by cluster VI (36.09), cluster V (22.92) and so onindicating less differences in genotypes within same cluster. The maximum inter-cluster distance was recorded between cluster VI and III (170.80) exhibiting high degree of genetic diversity and thus genotypes in this cluster may be utilized for inter varietal hybridization programme for getting high yielding recombinants. Similarly, inter varietal crosses may be attempted between genotypes in cluster III and VI. Then the inter-cluster distance followed by between cluster VI and VII (163.00), cluster IV and VI (112.87). The minimum estimates for the inter-cluster distance were recorded between cluster I and II (17.32). This cluster being relatively less divergent and crossing between genotypes from this cluster cannot produce vigorous offspring (F_1progenies). The genotypes grouped into same cluster displayed the lowest degree of divergence from one another and in case crosses made between genotypes belonging to the same cluster, no transgressive segregants are expected from such combination. To realize much variability and high heterotic effect, parents should be selected from two clusters having wider inter-cluster distance. The intra-cluster group mean for seventeen traits revealed marked differences between the clusters with respect to cluster means for different characters (Table 4). On the basis of inter or intra-cluster distance ward's minimum variance dendrogram was obtained which clearly indicates arrangement of genotypes according to their genetic distance (Fig.1).

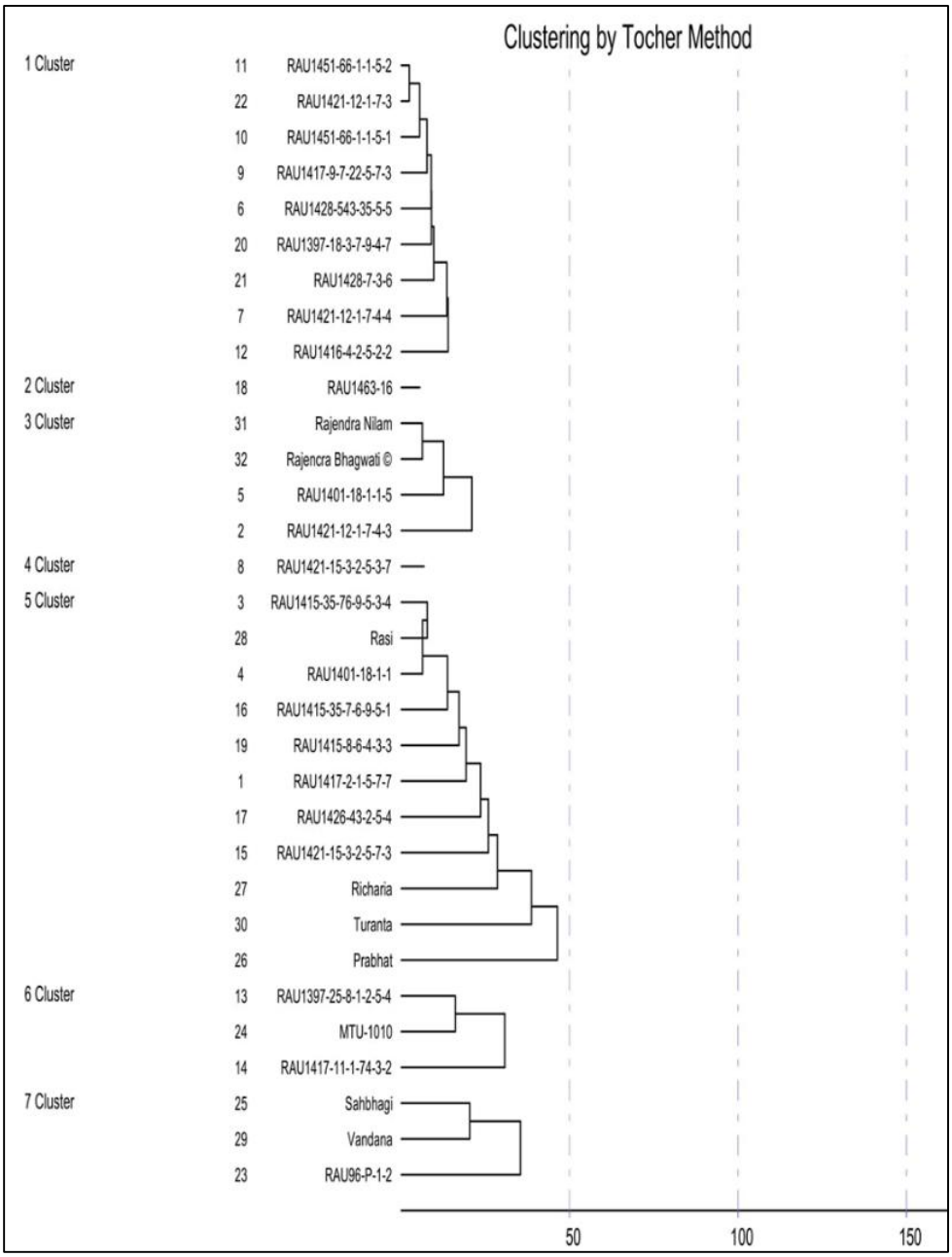

Fig 1: Clustering pattern of 32 genotypes of rice based on the D^2 statistic by Tocher method

On the basis of cluster mean value, the genotypes having high cluster mean for traits namely, panicle length, number of tillers per plant, growing degree days, helio-thermal unit, photo-thermal unit and relative temperature depression were grouped in cluster VII. Similarly, maximum cluster mean value for number of panicles per plant, spikelet fertility, relative water content and grain yield per plant were grouped in cluster III. The genotypes having early flowering and early maturity were grouped in cluster IV along with high cluster mean for heat use efficiency. Cluster II constituted with genotypes having maximum cluster mean value for 1000-grain weight and photo-thermal index. Cluster V is useful for

selecting the genotypes for dwarfness since it has genotypes with minimum cluster mean value for plant height. The maximum critical temperature at reproductive stage were recorded in cluster VI with cluster mean value 30.48. These observations suggested that none of the clusters contained genotypes with all desirables traits, which could directly selected and utilized. Interestingly, most of the minimum and maximum cluster means were distributed in relatively distant clusters. Thus, hybridization between genotypes from different clusters is necessary for the development of desirable genotypes. Recombination breeding between genotypes of different clusters has also been suggested by Sood *et al.*, (2005) [21], Arivoli *et al.*, (2009) [1], Toshimenla *et al.*, (2016) [22]. It can be inferred that it is not the genetic diversity alone, which decides choice of suitable parents but cluster mean also plays significant role in it.

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Bose *et al.* 2011) [2]. Contribution towards genetic divergence is depicted in Fig. 2.

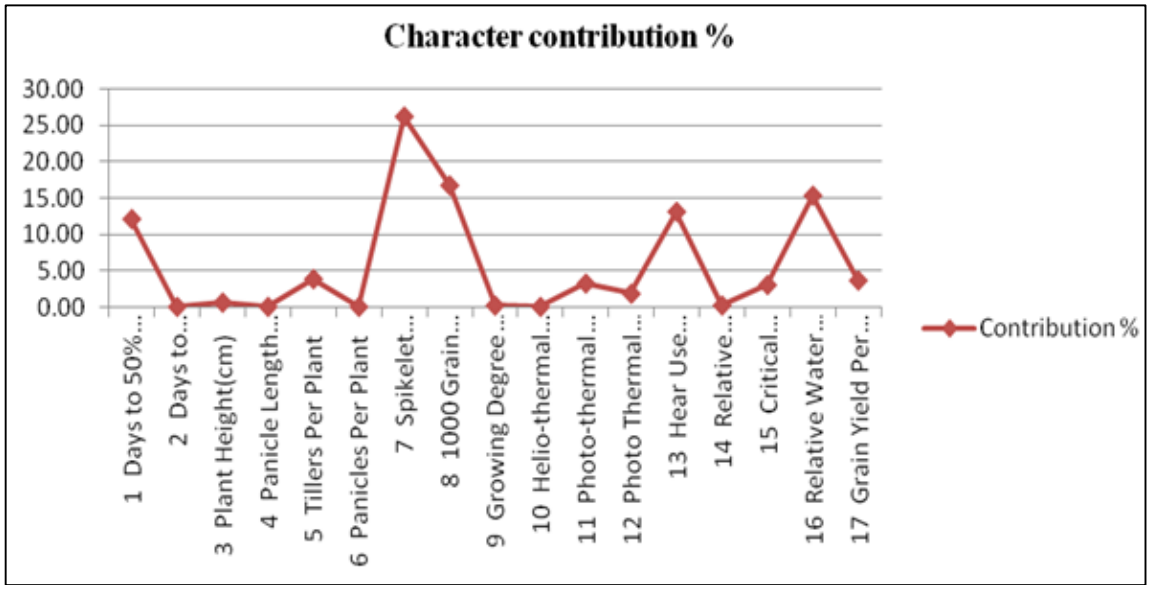

Fig 2: Character contribution (%) towards divergence of rice genotypes under direct seeded condition

The highest contribution in manifestation of genetic divergence was exhibited by spikelet fertility (26.21) which isshown as highest peak in the line diagram followed by 1000-grain weight (16.73), relative water content (15.32), heat use efficiency (13.10) and days to fifty per cent flowering (12.10) suggesting, these five characters contributed maximum towards genetic divergence. The greatest diversity in the present materials is due to these contributing characters which will offer a good scope for improvement of yield through rational selection of parental genotypes. These characters can be used for choice of parents in the hybridization programme. The contribution of days to fifty per cent flowering, 1000-grain weight and yield in divergence has also been observed by Chandra *et al*., (2007) [3] and Chandramohan *et al*., (2016) [4].

Similar findings were recorded for traits like days to fifty per cent flowering, 1000-grain weight in their maximum contribution towards genetic divergence by Patra *et al*., (2017) [10]. The contribution of various characters towards the expression of genetic divergence should be considered as criterion for choosing parents for crossing programme for the improvement in such character Sandhya *et al*. (2015) [15]. Based on the above results, the genotypes *viz*., RAU1421-12-1-7-4-3 and MTU-1010for hybridization programme can be selected from cluster III and VI with highest inter cluster distance. These clusters are suggested to provide a broad spectrum of variability in segregating generations. Also, selection of the genotypes *viz*., RAU 1421-12-1-7-4-3, RAU 1463-16,RAU1401-18-1-1-5, RAU 1421-15-3-2-5-3-7and RAU 1421-15-3-2-5-3-7within the cluster might be based on the traits viz., spikelet fertility % in cluster III, 1000-grain weight in cluster II, relative water contentin cluster III, heat use efficiency in cluster IV and days to fifty per cent flowering in cluster IV which have contributed more in the divergence and the rest of the traits are negligible. Thus, the crossing of genotypes belonging to cluster separated by high inter cluster distances and differing markedly for characters having high contribution towards total genetic divergence would be more fruitful for isolating superior segregates in segregating generations.

Conclusion

Diversity analysis has identified few characters that plays prominent role in classifying the variation existing in the available germplasm. The analysis identified spikelet fertility, 1000-grain weight, heat use efficiency, relative water content and days to fifty per cent flowering are the most important for classifying the variation. Thus, the results of diversity analysis used in the study have revealed the high level of genetic variation existing in the germplasm and explains the traits contributing for this diversity. Hence, the results will be of greater benefit to identify parents for improving various morphological traits analyzed in this study.

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Table 4: Cluster mean values of seven clusters for different quantitative characters of Rice under direct seeded condition

	DFF	DPM	PH (cm)	PL (cm)	TPP	PPP	SF (%)	TGW (gm)	GDD	HTU	PTU	PTI	HUE	RTD	CT (^{0} C)	RWC	GY/P (g)
Cluster I	70.52	91.15	88.18	21.84	9.81	7.78	82.85	23.07	2712.47	14079.98	34834.68	29.75	1.58	20.57	29.83	71.26	12.84
Cluster II	76.33	96.33	87.13	21.89	8.67	6.33	78.00	26.38	2869.57	14886.99	36712.48	29.79	1.56	20.62	30.43	74.64	13.47
Cluster III	79.67	101.00	94.14	23.98	12.92	9.58	85.42	24.05	2996.91	15610.23	38241.70	29.67	1.72	20.68	30.00	80.63	15.50
Cluster IV	63.00	83.67	93.87	22.57	11.00	8.33	82.00	26.24	2487.52	12928.08	32045.24	29.73	1.96	20.49	30.07	75.12	14.65
Cluster V	75.67	96.42	85.32	21.71	8.85	6.61	83.09	24.82	2865.93	14903.74	36841.50	29.61	1.33	20.63	30.06	63.22	11.39
Cluster VI	78.11	99.67	86.10	22.46	9.89	7.56	58.44	21.65	2930.99	15293.88	37433.46	29.42	1.32	20.68	30.48	66.62	11.58
Cluster VII	98.11	120.78	101.70	24.65	12.78	9.56	83.22	26.21	3581.98	18666.21	45592.93	29.66	1.37	21.12	29.54	75.50	14.75

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