Genetic Diversity in Bread Wheat Germplasm under Reclaimed Sodic Soil Condition

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The genetic diversity in 300 wheat genotypes was assessed under reclaimed sodic soil condition for grain yield and its component traits using non-hierarchical Euclidean cluster analysis which grouped the genotypes in 11 different clusters. Cluster VII had highest intra-cluster D^2 values indicating maximum intracluster diversity. This cluster was also most distantly related to cluster VI than the other cluster combinations indicating most diverse genotypes for their further utilization in wheat improvement programme. Cluster VII showed highest mean values for grain yield per plant and tillers per plant.

Key Words: Wheat, Genetic divergence, Clusters analysis, Reclaimed sodic soil

Introduction

The salt affected lands occur in practically all climatic regions but the areas affected by soil salinity are not well defined and thus, global estimates vary widely (Flowers *et al.*, 1986). Of nearly 160 million hectares of cultivated land under irrigation worldwide, about one-third is already affected by salt, which makes salinity a major constraint to food production. It is considered as single largest soil toxicity problem in tropical Asia (Greenland, 1984). In India, nearly 7.0 million hectare area is affected by salts that cover the maximum area in the states of Uttar Pradesh, Gujarat and Haryana. The combination of salt affected soils and poor quality groundwater in wheat growing areas of the country severely limit wheat productivity. The salinity aspect was addresed at Cental Soil Salinity Research Institute (CSSRI), Karnal and the salt affected land was reclaimed for research purspose to generate suitable material for salt affected areas.

The germplasm is the reservoir of genetic variability and it needs to be churned properly for developing genotypes for different agro-climatic and soil conditions. For crop improvement purposes, the most widely used methodology is hybridization followed by selection in which diverse parents are used. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as bread wheat to recover transgressive segregates has also been repeatedly emphasized (Cox and Murphy, 1990) and therefore, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures such as D^2 statistic and non-hierarchical Euclidean cluster analysis (Mahalanobis, 1936; Spark, 1973). Keeping these in view, the wheat germplasm lines were evaluated with the objective to determine the magnitude of variability among the wheat germplasm for yield and component traits and to identify genetically diverse and agronomically desirable genotypes for their further exploitation in wheat improvement programme aimed at enhanced grain yield in salt affected conditions.

Materials and Methods

Three hundred genotypes maintained at the Division of Crop Improvement, CSSRI, Karnal (Haryana), constituted the material for the present study that included released varieties, genetic stocks, germplasm lines, doubled haploids and advanced breeding lines developed at various centres (Table 1). The material was evaluated under reclaimed sodic soil that is near to normal condition (pH value of 8.2) in augmented design with 12 blocks accomodating 25 test genotypes and 5 checks, namely, KRL 19, HD 2009, PBW 343, HD 4530 and *Kharchia* 65 in each block. The plot size was single row of 1 m with 23 x 5 cm spacing. All the recommended agronomic practices were followed to raise a good crop. The data were recorded on five randomly selected plants for plant height (cm), tillers per plant, spike length (cm), number of spikelets per spike, grain number per spike, 1000-grain weight and grain yield per plant (g) whereas the days to heading and days to maturity were recorded on plot basis. The data was analysed for adjusted mean values of 300 test genotypes for various traits in relation to the checks and estimates of error mean squares were obtained following Federer (1956) and used for subsequent statistical analysis. The non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) was done to estimate the intra and inter-cluster distances and to group the genotype into different clusters.

Results and Discussion

The analysis of variance showed significant differences

Table 1. Origin of genotypes/ culitvars/ advaced generation lines used as experimental material

Centre	Entries (Total)	Name of the entries
Perth, Australia	54	BT-Schomburgk, Camm, Carnamah, Cunderdin, Ducula 4, Gamenya, Gutha, Kulin, Perenjori, Schomburgk, Spear, Westonia, 96W639-D-1-8, 96W639-D1-40, 96W639-D-1-53, 96W639-D-1-56, 96W639-D2-1, 96W639-D2-8, 96W639-D2-11, 96W639-D2-12, 96W639-D2-17, 96W639-D2-22, 96W639-D3-2, 96W639-D3-4, 96W639-D3-9, 96W639-D3-18, 96W 639-D3-19, 96W639-D3-29, 96W639-D4-10, 96W639-D4-24, 96W639-D5-2, 96W639-D5-5, 96W639-D5-6, 96W639-D5-9, 96W639-D5-10, 96W639-D5-15, 96W639-D5-17, 96W639-D5-20, 96W639-D5-21, 96W639-D5-26, 96W639-D5-30, 96W639-D5-31, 96W639-D5-33, 96W 639-D5-42, 96W639-D5-43, 96W 639-D5-44, 96W639-D6-2, 96W639-D6-5, 96W639-D6-12, 96W639-D6-18, 96W639-D6-29, 96W639-D6-34, 96W639-D6-36, 96W639-D6-37
CIMMYT, Mexico	04	BWIR7, BWMA8, WC1, WC6
CSAUA&T, Kanpur	24	K 78, K2008, K2021, K0101, K0103, K0111, K0123, K0124, K0142, K0209, K0224, K8027, K8034, K9107, KLP0265, KLP0268, KLP0317, KLP0318, KLP0319, KYZ0162, KYZ0165, KYZ0176, KYZ0294, KYZ0295
NDUA &T, Faizabad	22	NW1012, NW1014, NW1067, NW1076, NW2036, NW2069, NW2083, NW2095, NW(S)01-9, NW(S)02-4, NW(S)02-5, NW(S)02-6, NW(S)02-8, NW(S)02-11, NW(S)02-15, NW(S)03-1, NW(S)03-2, NW(S)03-3, NW(S)03-4, NW(S)03-5, NW(S)03-6, NW(S)03-7
CSSRI, Karnal	22	KRL1-4, KRL3-4, KRL35, KRL99, KRL100, KRL104, KRL105, KRL107, KRL113, KRL115, KRL117, KRL118, KRL119, KRL120, KRL121, KRL122, KRL123, KRL124, KRL125, KRL126, KRL127, KRL128
IARI, New Delhi	22	HD2189, HD2285, HD2329, HD2643, HD2687, HD2733, HD2781, HD2855, HD2859, HD2861, HD2864, HD2865, HD2866, HD2868, HD2885, HD2886, HDR77, PS701, PS703, PS705, PS708, PS711
IARI, Regional Station, Shimla	21	HS240, HS277, HS295, HS365, HS375, HS418, HS420, HS431, HS433, HS436, HS440, HS445, HS449, HS450, HS451, HS453, HS454, HS 455, HS 456, HS457, HS460
IARI, Regional Station, Indore	20	HI 977, HI1418, HI1454, HI1479, HI1500, HI1514, HI1516, HI1527, HI1530, HI1531, HI1532, HI1533, HI1535, HI1536, HI4672, HI8381, HI8498, HI8634, HI 8637, HI8638
IARI, Regional Station, Pusa	12	HP1731, HP1744, HP1761, HP1867, HP1871, HP1873, HP1875, HP1876, HP1877, HP1878, HP1879, HP1880,
IARI, Regional Station, Wellington	08	HW 3080, HW 4028, HW 5001, HW 5015, HW 5018, HW 5023, HW 5028, HW 5070
VPKAS, Almora	20	VL 616, VL 738, VL 802, VL 804, VL 829, VL 824, VL 830, VL 832, VL 852, VL 858, VL 859, VL 860, VL 861, VL 862, VL 864, VL 865, VL 866, VL 867, VL 868, VL 869
BHU, Varanasi	18	AKJ03-1, AKJ03-2, AKJ03-3, AKJ03-5, AKJ03-6, AKJ03-7, HUW206, HUW234, HUW468, HUW510, HUW524, HUW533, HUW549, HUW564, HUW567, HUW574, HUWJ2, HUWJ13
GBPUA&T, Pantnagar	14	UP2338, UP2425, UP2565, UP2584, UP2590, UP2592, UP2594, UP2596, UP2618, UP2619, UP2620, UP2623, UP2624, UP2625
RAU, Durgapura	13	Raj 1482, Raj 1555, Raj 3077, Raj 3765, Raj 3777, Raj 4037, Raj 4065, Raj 4067, Raj 4069, Raj 4077, Raj 4078, Raj 4085, Raj 4086
CCSHAU, Hisar	11	WH736, WH755, WH773, WH775, WH779, WH785, WH794, WH1008, WH1009, WH1010, WH1011
JNKVV, Jabalpur	09	MP1150, MP1155, MP1156, MP1160, MP1161, MP1165, MP1168, MP1169, MP4010
PAU, Laudhiana	06	PBW 175, PBW 373, PBW 396, PBW 498, PBW 502, PBW 509
Total	300	

among the blocks and checks for all the traits (Table 2). The traits studied showed wide range among the genotypes under reclaimed sodic soil conditions. The coefficient of variation (%) was also estimated to get the comparative values of variability present for the traits under study and it indicated the maximum variability for grain yield/plant followed by tillers per plant, spike length and grain number/ spike (Table 2). On the other hand, lower CV values were observed for days to maturity and heading, number of spikelet per spike and 1000-grain weight indicating less variability for the trait compared to other traits (Singh and Chatrath, 1993; Singh *et al.*, 2001; Munns and James, 2003; Pawar *et al.*, 2003). However, there is still ample scope for selection of superior genotype for these traits. The best performing genotypes for various traits were screened on the basis of their performance and the promising genotypes for more than two characters were identified for their further utilization in wheat improvement programme. These genotypes were HD 2886 (for early heading, spike length, grain number and 1000-grain weight), HD 2861 (for early heading, plant height and 1000-grain weight), Raj 4077 (for early heading, spike length and 1000-grain weight), HW 5015 (for plant height, grain number and yield per plant) and NW 2069 (for spike length, grain number and yield per plant).

Based on Non-hierarchical Euclidean cluster analysis, all the 300 genotypes were grouped into 11 clusters (Table 3) as the sequential F test revealed the appropriateness

Table 2. Analysis of variance, general mean, range and coefficient of variation for nine characters under reclaimed sodic soil conditions

Traits	Mean sum of squares (MSS)			Mean	Range	Coefficient of variation (%)
Source of variation	Blocks	Checks	Error			
Degree of freedom	11	04	44			
Days to heading	133.01**	146.98**	2.47	94.7	78 - 116	6.05
Days to maturity	13.54**	23.75**	2.64	140.7	136 - 145	1.06
Plant height (cm)	333.04**	3012.45**	34.21	90.7	67.5 - 134.2	10.79
Spike length (cm)	8.91**	38.15**	0.22	11.3	6.8 - 15.6	12.74
Spikelets/ spike	6.50**	20.14**	0.75	19.7	15 - 26	8.61
Tillers/ plant	7.19**	2.76**	0.72	5.6	3.2 - 9.0	14.87
Grains/ spike	92.29**	356.09**	31.87	62.0	36 - 87	12.60
1000-grain weight (g)	37.91**	41.67**	5.80	39.7	26.9 - 45.6	9.79
Grain yield/ plant (g)	39.16**	21.15**	3.11	10.3	2.0 - 16.8	26.60

** Significant at 1% level

Table 3. Clustering pattern of 300 bread wheat genotypes on the basis of non-hierarchical Euclidean cluster analysis under reclaimed sodic soil condition

Cluster	Number of genotypes	Genotypes
I	32	VL 824, VL 862, VL 867, VL 868, HD 2329, UP 2565, UP 2590, Raj 1555, Raj 3077, MP 1156, MP 4010, WH 775, WH 779, WH 785, KO 123, KO 124, KO 224, NW 2083, HS 365, HI 1516, HI 1479, HUW 510, HW 4028, HD 2285, HP 1871, PBW 175, NW (S) 3-1, Raj 4078, KRL 100, KRL 115, BT-Schomburgk, HD 2643
II	38	HD 2733, KO 209, HI 8498, HI 8381, HI 8634, HI 4672, HI 8638, HI 8627, HUW-567, HUW-533, HUW 549, PS 701, HP-1731, HP-1879, PBW 373, 96W 639-D-1-53, 96W 639-D-1-56, 96W 639-D2-11, 96W 639-D2-12, 96W 639-D2-22, 96W 639-D3-18, 96W 639-D4-24, 96W 639-D5-5, 96W 639-D5-6, 96W 639-D5-9, 96W 639-D5-10, 96W 639-D5-15, 96W 639-D5-17, 96W 639-D5-20, 96W 639-D5-26, 96W 639-D5-43, KRL 119, KRL 124, KRL 125, KRL 126, KRL 128, 96W 639-D5-42, Ducula 4
III	30	VL 860, HD 2687, UP 2584, Raj 4037, Raj 4069, MP 1169, K 78, NW 1012, NW 1014, NW 2036, HS 418, HI 1514, HI 1531, HI 1454, HI 1418, HUW-574, HUW-234, HD 2861, HD 2864, HD 2855, Spear, PBW 509, WH 1011, NW (S) 3-4, NW (S) 2-11, KRL 120, KRL 1-4, AKJ-03-5, Gutha, Schomburgk
IV	33	VL 859, VL 861, UP 2596, UP 2625, Raj 1482, MP 1165, HS 440, HS 451, HS 453, HS 455, HS 460, HI 1532, HI 1535, HU\V 468, HUW 206, HW 3080, HW 5001, BWIR 7, 96W 639-D5-2, 96W 639-D5-21, KRL 107, KRL 121, KRL 127, N\V (S) 02-8, AKJ-03-1, 96W639-D5-44, Cunderdin, Perenjori, Camm, Westonia, Kulin, Raj 4067, HD 2859
V	19	KO 103, K 9107, K 2021, N\V 1076, HS 436, HS 445, HI 1527, PS 703, PS 711, HP 1878, HP 1876, HP 1880, KLP 318, KO 111, NW (S) 3-7, Raj 4086, 96W 639-D5-33, KRL 123, HUWJ 13
VI	14	VL 858, VL 864, VL 865, VL 866, 96W 639-D2-1, 96W 639-D2-8, 96W 639-D3-4, 96W 639-D3-23, 96W 639 D4-10, 96W 639-D5-31, 96W 639-D6-2, 96W 639-D6-34, 96W 639-D6-36, 96W 639-D6-37
VII	16	HD 2865, HI 1500, HP 1867, NW (S) 3-2, Raj 4077, BWMA 8, KRL 104, KRL 3-4, NW (S) 02-4, NW (S) 02-15. KLPO 265, KLPO 268, KYZO 295, K 142, WCl. 96W639-Dl-40
VIII	18	Gameny, HS 449, HS 450, HS 454, HS 456, HS 457, HI 1530, 96W 639-D-1-8, 96W 639-D3-2, 96W 639-D5-30, 96W 639-D6-5, 96W 639-D6-12, 96W 639-D6-18, 96W 639-D6-29, KRL 117, WC 6, 96W 639-D2-17, Carnamah
IX	47	VL 852, VL 830, UP 2592, UP 2619, UP 2620, UP 2624, UP 2425, Raj 3765, Raj 3777, MP 1150, MP 1155, MP 1160, MP 1168, WH 736, WH 794, KO 101, NW 2095, HS 295, HS 420, HS 431, HS 433, HUW-524, HW 3070, HW 5022, HW 5023, H\V 5018, HD 2886, PS 705, PS 708, HP 1873, HP 1761, HP 1875, HP 1744, PBW 498, PBW 502, UP 2338, KLP 317, KLP 319, WH 1009, NW (S) 3-6, Raj 4085, NW (S) 1-9, 96W 639-D3-9, KRL 99, HUWJ 2, KYZ 294, AKJ-03-6
X	27	K 2008, K 8034, NW 2069, HS 240, HS 277, HS 375, HI 1536, HI 1533, HUW-564, KRL 35, HW 5015, WH 755, WH 1008, \VH 1010, NW (S) 3-3, NW (S) 3-5, KRL 105, KRL 113, KRL 122, NW (S) 02-5, NW(S) 026, KYZ 162, KYZ 165, AKJ-03-2, AKJ-03-3, AKJ-03-07, 96W 39-D3-19
XI	26	VL 832, VL 869, VL 616, VL 738, VL 802, VL 804, VL 829, HD 2189, HD 2885, HD 2866, HD 2868, HD 2781, HDR 77, UP 2594, UP 2618, UP 2623, Raj 4065, MP 1161, WH 773, K 8027, NW 1067, HI 977, HP 1877, PBW 396, KRL 118, KYZ 176
Total	300	

of 11 clusters for all the genotypes under consideration. The cluster strength varied from 14 to 47 genotypes in these clusters out of which cluster IX was the biggest accommodating 47 genotypes followed by cluster II with 38 genotypes and cluster IV with 33 genotypes. The pattern of distribution of these germplasm lines into different clusters indicated that the genotypes of same origin were grouped into different cluster that suggested that geographical diversity is not similar to those of genetic diversity and the clusters accomodated the genetically more similar genotypes.

The cluster mean values were estimated for various traits (Table 4) and it was observed that out of 11 clusters, only six cluster had the higher mean values for the traits in desired direction. Cluster VII has shown higher mean values for grain yield per plant, 1000-grain weight and tillers per plant. Cluster X had higher mean for spikelets per spike and grain number per spike whereas, cluster I had shown superiority for early flowering and dwarf plant types. Early maturity and longer spikes were observed in cluster V and cluster XI, respectively.

The intra and inter-cluster distances (Table 5) were estimated to identify the diverse groups of genotypes. The intra-cluster distance ranged from 2.000 to 2.436 and it was

Table 4. Cluster means and coefficient of variance for nine characters under reclaimed sodic soil condition

Cluster No.	Character	Days to heading	Days to maturity	Plant height (cm)	Spike length (cm)	Spikelets / spike	Tillers / plant	Grains / spike	1000-grain weight (g)	Grain yield / plant (g)
I	Mean ± SD	88.51± 3.78	140.09±1.16	83.36±7.85	10.78±1.02	17.62±1.00	5.39±0.62	55.57±8.15	41.55±2.67	8.28±1.72
	C.V. (%)	4.27	0.82	9.41	9.46	5.67	11.50	14.66	6.42	20.77
II	Mean±SD	98.60±3.14	140.66±1.17	90.37±8.05	9.39±0.95	19.28±1.06	5.41±0.51	58.83±5.90	40.69±2.69	9.66±1.45
	C.V. (%)	3.18	0.83	8.90	10.11	5.49	9.44	10.02	6.61	15.01
III	Mean±SD	90.84±3.40	141.64±0.76	85.66±6.14	10.82±0.85	18.32±1.42	6.04±0.64	62.39±6.20	40.97±2.69	11.83±1.97
	C.V. (%)	3.74	0.53	7.16	7.85	7.75	10.59	9.93	6.56	16.65
IV	Mean±SD	96.53±5.00	142.00±0.96	86.26±4.92	11.47±0.94	20.37±1.36	5.31±0.60	67.67±3.91	33.67±2.20	9.13±2.34
	C.V. (%)	5.17	0.67	5.70	8.19	6.67	11.29	5.77	6.53	25.73
V	Mean±SD	92.80±4.29	138.76±0.85	92.06±7.29	11.43±0.96	18.97±1.48	6.27±0.59	60.29±5.18	40.90±2.36	12.63±1.94
	C.V. (%)	4.62	0.61	7.91	8.39	7.80	9.40	8.59	5.77	15.36
VI	Mean±SD	104.21±6.14	139.32±1.21	97.52±7.42	10.98±0.99	20.55±0.84	4.53±0.63	63.09±5.49	37.28±3.94	5.83±2.11
	C.V. (%)	5.89	0.86	7.60	9.01	4.08	13.90	8.70	10.64	36.19
VII	Mean±SD	90.56±4.45	140.85±0.88	107.78±11.98	11.46±1.40	18.78±1.07	6.72±0.71	54.83±8.01	43.37±0.90	13.10±2.33
	C.V. (%)	4.91	0.62	11.11	12.21	5.69	10.56	14.60	2.07	17.78
VIII	Mean±SD	99.08±3.08	114.58±0.94	101.50±7.89	10.50±0.86	20.81±1.14	6.30±1.05	63.57±5.00	36.01±3.49	9.61±1.88
	C.V. (%)	3.10	0.66	7.77	8.19	5.47	16.66	7.86	9.69	19.56
IX	Mean±SD	92.55±3.90	140.11±1.24	86.92±7.22	12.50±1.26	20.87±1.21	5.01±0.52	67.14±4.98	41.54±2.57	11.03±2.11
	C.V. (%)	4.21	0.88	8.30	10.08	5.79	10.37	7.41	6.18	19.21
X	Mean±SD	97.53±4.61	139.97±1.43	93.03±8.96	12.00±1.17	21.73±1.13	6.15±0.63	71.75±5.99	37.23±3.07	12.98±2.10
	C.V. (%)	4.72	1.02	9.63	9.75	5.20	10.24	8.34	8.24	16.17
XI	Mean±SD	95.66±4.89	142.15±1.25	93.65±7.68	12.66±1.02	19.72±1.36	5.20±0.52	56.83±6.60	42.42±2.22	8.37±1.93
	C.V. (%)	5.11	0.87	8.20	8.05	6.89	10.00	11.61	5.23	23.05

Table 5. Estimates of average intra and inter-cluster distances for eleven clusters under reclaimed sodic soil condition

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**(2.208)**	2.471	2.134	3.617	2.656	4.030	3.639	3.986	3.012	4.389	2.816
II		**(2.000)**	2.289	2.862	2.660	2.822	3.491	2.467	2.925	3.390	2.677
III			**(2.031)**	2.900	2.206	**4.435**	2.805	3.044	2.600	3.225	2.658
IV				**(2.051)**	3.675	3.166	4.613	2.308	2.716	2.693	2.909
V					**(2.052)**	4.086	2.433	3.204	2.516	2.678	3.294
VI						**(2.322)**	**5.131**	3.179	3.504	3.864	3.370
VII							**(2.436)**	3.378	3.798	3.850	3.339
VIII								**(2.262)**	3.365	2.471	3.038
IX									**(2.167)**	2.342	2.423
X										**(2.376)**	3.660
XI											**(2.218)**

Values in parenthesis are intra-cluster distances

Table 6. Potent genetic donors in bread wheat identified from cluster VI and VII for different characters under reclaimed sodic soil condition

Genotypes	Cluster	Traits (#)	Days to heading	Days to maturity	Spike Length (cm)	Spikelets / spike	Tillers / plant	Grains / spike	1000-grain weight (g)	Yield/plant (g)
KLPO 268	VII	06		*	*	*		*	*	*
2-K-142	VII	06	*	*		*	*	*	*	
WC 1	VII	05		*	*		*		*	*
Raj 4077	VII	05	*		*	*	*		*	
KYZO 295	VII	04		*	*				*	*
NW(S)3-2	VII	04	*		*		*		*	
VL 866,	VI	04		*	*	*		*		
KLPO 265	VII	03	*						*	*
KRL 104	VII	03					*		*	*
NW(S)02-15	VII	03					*		*	*
HP-1867	VII	03	*				*		*	
96W639-D2-1	VI	03		*		*		*		
96W639-D6-37	VI	03		*		*			*	
96W639-D6-2	VI	02		*		*				
VL 865	VI	02		*	*					
96W639-D6-36	VI	02		*		*				
96W639-D1-40	VII	02					*		*	
BWMA 8	VII	02					*		*	
Best check			HD 2009 (87 days)	HD 2009 (140 days)	KRL 19 (11.9cm)	PBW 343 (20)	Kh. 65 (6.40)	KRL19 (67)	PBW343 (42.3g)	PBW343 (11.4g)

maximum in cluster VII that indicated maximum diversity among the member genotypes of the cluster VII. On the other hand, least value was observed for cluster II (2.000) and cluster III (2.031) that indicated presence of narrow genetic variation within these clusters. The magnitude of inter-cluster distances measure the extent of genetic diversity between the cultivars of the different clusters which ranged from 2.134 between clusters I and III to 5.131 between clusters VI and VII. The maximum inter cluster distance between cluster VI and VII indicated the maximum diversity between these clusters and suggested the selection of genotypes from these clusters for their further utilization in hybridisation programme through combination breeding.

As clusters VI and VII are distantly related, the genotypic performance among the members of these two groups was evaluated and the promising genotypes for various traits were identified. The better performing genotypes than the respective checks were screened and the donor genotypes for two or more characteristics identified (Table 6). Among them, KLPO 268, 2-K-142, WC 1 and Raj 4077 were most promising genotypes for more than four traits and these can be more extensively utilized in wheat programmes aimed to improvement of genotypes for reclaimed sodic soil conditions.

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