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Genetic variability studies and scope of improvement in sponge gourd under hot arid agro-climate

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Abstract

Fifteen landraces of sponge gourd were evaluated for 19 quantitative characters to study the genetic variability and association of the traits. The analysis of variance revealed considerable genetic variability in the evaluated germplasm. The GCV and PCV estimates were high for fruit yield/plant, number of fruits/plant and number of seeds/fruit indicating better scope for improvement through simple selection. These characters also depicted high estimates for heritability and genetic gain indicating additive type of gene action. Fruit yield/plant showed positive and significant association with number of fruits/plant and fruit weight. Among the genotypes tested for performance studies, AHSG-4 and AHSG-5 recorded the highest fruit yield potential under arid conditions. The genotype AHSG-4 exhibited earliness (53.84 days) for first marketable harvest.

Key words: *Sponge gourd, Luffa cylindrica, genetic variability and hot arid agro-climate.*

Introduction

Out of 9 species of *Luffa*, *L. acutangula*, *L. cylindrica* and *L. hermaphrodita* are native to India and are consumed as vegetable (Chandra, 2). Sponge gourd (*Luffa cylindrica* L.) is an important cucurbitaceous vegetable grown throughout the country. Despite its commercial importance, not much attempt has been made on its genetic improvement particularly to identify and develop genotype under stressed environmental conditions of arid region (Samadia, 7). Information on the magnitude of genetic variability available in the germplasm and knowledge of association between yield and its contributing traits are required to utilize the material potentially in breeding programme. Therefore, the present study was undertaken to assess the extent of genetic variability in the evaluated germplasm of sponge gourd and to assess the scope for improvement under hot arid agro-climate.

Materials and methods

The experimental material for the investigation comprised 15 land races collected from the tribal area of southern Rajasthan and northern Gujarat. The germplasm were evaluated at the experiment farm of Central Institute for Arid Horticulture, Bikaner (28° N latitude and 73° 18' E longitude and an altitude of 235 m above sea level) where the agro-climate is characterized by extremes of temperature (- 4° C in winter to 48° C in summer), low rainfall (150 - 300 mm in short spells from July - September), high vapour pressure deficit (30 mb in May-June), high solar radiation, high wind speed (12 - 16 km/hr) with dust storms, beside poor fertility and water holding capacity of the sandy soil. The experiment was laid during the rainy-winter season of 2003 and 2004 in a randomized block design with three replications. Seeds of each genotype were sown at 50 cm spacing on one side of the channel of 10 m length. The channels were spaced 2.5 m apart. Out of 15 - 18 plants maintained for each genotype, observations were recorded on five selected plants per replication for quantitative and qualitative characters. Recommended cultural practices were followed. Nineteen quantitative traits taken for presentation of results are days to appearance of first male flower (DFMF) days after sowing (DAS), days to appearance of first female flower, DAS (DFFF), node to first fruit set (NFS), days to first harvest, DAS (DFH), fruit length, cm (FL), fruit diameter, cm (FD), fruit weight, kg (FW), number of fruits/plant (NF/P), fruit yield/plant, kg (FY/P), vine length, m (VL), leaf length, cm (LL), leaf width, cm (LW), leaf size, cm^2 (LS), stamenned stalk length, cm (SSL), mature fruit length, cm (MFL), number of seeds/fruit (NS/F), seed length, cm (SL), seed width, cm (SW) and weight of 100 seeds, g (STW). The data were subjected to statistical analysis adopting standard procedures using computer based INDOSTAT packages.

Results and discussion

The analysis of variance revealed highly significant mean square estimates for all the 19 characters indicating sufficient variability in the germplasm. Wide range of variation was observed for all the characters (Table 1 and 2). The period of appearance of male and female flower ranged from 31.95 - 64.77 and 43.23 - 74.18 days after sowing (DAS), respectively. The first marketable fruit harvesting ranged from 53.84 - 83.61 days. Among the genotype, the earliest first harvest was recorded in AHSG-4 (53.84 days) followed by AHSG-15. The number of marketable fruits per plant ranged from 4.55 - 12.34 with a population mean of 8.06. The genotype AHSG-5, AHSG-4, AHSG-13, AHSG-3 AHSG-10, and AHSG-15 recorded higher number of fruits than the mean of population. Among the genotype evaluated, total marketable fruit yield/plant ranged from 0.384 - 1.421 kg with a population

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mean of 0.876 kg. The maximum fruit yield/plant was obtained in AHSG-5 (1.42 kg) followed by AHSG-4 (1.30 kg). On the basis of fruit quality characters, earliness and fruit yield, the genotype AHSG-4 was found to be the most potential. The germplasm under evaluation were diverse and thus have potential for further improvement for fruit yield and quality characters under high temperature conditions of arid region.

Genotypic and phenotypic coefficient of variation (GCV and PCV) study indicated that there is an ample scope of improvement of this crop (Table 2). In general, the estimates of PCV were higher than GCV for all the characters. A close correspondence between PCV and GCV values in respect of all the characters indicated that environment had very little influence on the expression of the character. The GCV which gives a picture of the extent of genetic variability in the population ranged from 4.31 (seed length) to 34.88 (fruit yield/plant). The GCV and PCV estimates were considerably high (>25%) for economic traits such as fruit yield/plant, number of fruits/plant and number of seeds/fruits indicating better scope of improvement through selection. Since the difference between GCV and PCV was very low, phenotypic selection should be better for fruit yield.

High heritability estimates were recorded in respect of all the characters. Though heritability estimates give a useful indication of the relative value of selection based on phenotypic expression, but reliable conclusion, cannot be dawn unless genetic advance is not taken into consideration along with heritability (Johnson *et al.*, 3). Genetic advance as percentage of mean in the present study ranged from 7.21 - 71.84%. High heritability value accompanied with high genetic advance for number of fruits/plant, fruit yield/plant and number of seeds/fruit indicates additive type of gene action. Simple selection, therefore, could be effective for the improvement of these traits. High heritability accompanied with low to moderate genetic advance for maturity, fruit and seed characters seems to be due to non-additive type of gene action and therefore simple selection for these characters will be less effective (Panse and Sukhatme, 5). The present studies on genetic variability components are in agreement with the results of Krishna Prasad and Singh (4), Singh *et al.* (8) and Ram *et al.* (6) in ridge gourd. The high variability and heritability along with high genetic gain for number of fruits and fruit yield per plant indicate that either the selected genotypes could be tested under multi-location trial or selected as a donor for these characters to be used in breeding programme.

The magnitude of genotypic correlations coefficients, in general, indicated higher than the phenotypic ones for most of the characters studied (Table 3), thereby establishing an inherent relationship among the characters. These results are in agreement with those of Abusaleha and Dutta (1) in ridge gourd and Ram *et al.* (6) in *Luffa*. Fruit yield/plant showed significant positive correlation with number of fruits/plant and fruit weight. Vine length exhibited positive and significant relationship with number of fruits and fruit yield/plant. Days to anthesis of first male flower, days to anthesis of first female flower and days to first harvest showed negative and non-significant association with fruit yield/plant. Positive and significant association had been observed between days to anthesis of male and female flower with days to first harvesting indicating mutual association of these characters.

Table1. Genetic variability studies for various characters in sponge gourd

Characters	Range		Mean	ECV (%)	GCV (%)	PCV (%)	h^2 (broad sense)	Genetic Advance (GA)	GA as percentage of mean (5 %SI)
	Minimum	Maximum							
DFMF	31.95	64.77	50.78	3.98	16.18	16.35	98.02	16.76	33.01
DFFF	43.23	74.18	60.24	4.11	12.95	13.17	96.74	15.81	26.24
NFS	17.27	29.23	24.99	5.84	13.45	13.87	94.07	6.61	26.88
DFH	53.84	83.61	69.88	3.07	10.90	11.05	97.42	15.49	22.16
FL	14.42	24.17	19.35	6.33	11.69	12.25	91.09	4.44	22.99
FD	3.18	4.25	3.62	2.22	10.58	10.68	98.55	0.78	21.65
FW	0.076	0.125	0.106	5.87	13.87	14.28	94.36	0.03	27.76
NF/P	4.55	12.34	8.06	7.89	28.00	28.37	97.42	4.59	56.93
FY/P	0.384	1.421	0.867	11.24	34.88	35.48	96.65	0.61	70.64
VL	2.71	3.54	3.17	6.36	9.72	10.39	87.51	0.59	18.73
LL	11.41	20.37	16.05	1.83	15.19	15.23	99.51	5.01	31.22
LW	13.83	28.28	20.79	1.38	21.08	21.09	99.86	9.02	43.35
LS	189.23	576.43	341.33	1.90	33.98	33.99	99.90	238.81	69.96
SSL	1.11	3.15	1.73	4.06	34.95	35.03	99.55	1.24	71.84
MFL	20.26	37.57	28.68	5.73	19.92	20.19	97.31	11.61	40.48
NS/F	123.49	405.25	246.94	3.53	32.59	32.66	99.61	165.51	67.02
SL	1.060	1.236	1.136	5.37	4.31	5.31	65.59	0.08	7.21
SW	0.530	0.913	0.765	7.05	13.91	14.50	92.12	0.21	27.51
STW	8.730	12.650	11.155	2.23	11.64	11.72	98.79	2.66	23.85

Table 2: Growth, flowering and fruit yield characters in evaluated sponge gourd germplasm

Genotype	DFMF	DFFF	NFS	DFH	FL	FD	FW	NF/P	FY/P	VL
AHSG 001	64.77	74.18	28.93	83.61	14.42	3.18	0.07	7.57	0.57	3.26
AHSG 002	52.11	61.04	26.69	73.47	21.49	4.15	0.08	4.69	0.38	2.82
AHSG 003	52.32	61.47	26.36	68.29	17.34	3.83	0.10	9.45	0.97	2.89
AHSG 004	31.95	43.23	26.59	53.84	21.49	4.15	0.12	10.44	1.30	3.51
AHSG 005	57.68	66.54	29.23	75.04	19.26	3.53	0.11	12.34	1.42	3.54
AHSG 006	52.75	63.26	25.57	73.60	18.26	3.77	0.10	7.82	0.85	3.54
AHSG 007	54.95	67.47	26.36	77.24	22.23	3.55	0.11	7.96	0.94	3.54
AHSG 008	48.36	55.92	26.03	64.92	24.17	4.25	0.12	7.96	0.98	3.45
AHSG 009	53.67	63.02	21.45	71.48	19.27	2.82	0.09	4.55	0.42	2.75
AHSG 010	51.21	55.01	19.54	66.54	19.26	3.54	0.11	9.37	1.08	2.81
AHSG 011	54.12	64.54	25.50	72.21	18.37	3.48	0.11	4.61	0.51	2.71
AHSG 012	53.67	62.46	25.46	74.72	18.27	3.50	0.10	6.25	0.67	3.25
AHSG 013	51.83	60.58	22.30	69.80	17.36	3.53	0.09	10.34	0.99	3.46
AHSG 014	49.05	59.34	21.57	67.94	18.47	3.26	0.09	8.40	0.77	2.85
AHSG 015	33.34	45.53	17.27	55.47	20.60	3.87	0.12	9.13	1.10	3.17
CD at 5 %	3.30	4.14	2.40	3.89	2.04	0.15	0.01	1.04	0.16	0.33

Table 3: Genotypic (above) and phenotypic (below) diagonal correlation among various characters in sponge gourd

CHR	DFMF	DFFF	NFS	DFH	FL	FD	FW	NF/P	FY/P	VL	MFL	NS/F	SL	SW	STW
DFMF	**1.000**	0.998	0.504	0.986	-0.552	-0.548	-0.589	-0.248	-0.437	-0.123	-0.438	-0.429	0.382	0.001	-0.090
DFFF	0.968	**1.000**	0.543	1.004	-0.548	-0.573	-0.597	-0.302	-0.488	-0.057	-0.547	-0.420	0.307	-0.117	-0.120
NFS	0.418	0.533	**1.000**	0.550	-0.072	0.182	-0.152	0.034	-0.018	0.397	-0.213	-0.037	-0.036	-0.447	0.047
DFH	0.959	0.979	0.529	**1.000**	-0.503	-0.514	-0.596	-0.340	-0.509	0.006	-0.511	-0.486	0.234	-0.095	-0.088
FL	-0.511	-0.509	-0.076	-0.475	**1.000**	0.636	0.661	0.005	0.295	0.264	0.330	0.007	-0.376	0.108	0.651
FD	-0.536	-0.552	0.179	-0.508	0.606	**1.000**	0.467	0.237	0.389	0.336	0.581	0.190	-0.353	-0.272	0.276
FW	-0.566	-0.565	-0.139	-0.583	0.586	0.455	**1.000**	0.408	0.689	0.384	0.209	0.539	-0.036	0.050	0.384
NF/P	-0.257	-0.287	0.026	-0.328	-0.018	0.229	0.395	**1.000**	0.938	0.615	0.374	0.346	0.420	0.285	0.118
FY/P	-0.438	-0.464	-0.019	-0.496	0.247	0.378	0.687	0.933	**1.000**	0.627	0.390	0.471	0.309	0.244	0.279
VL	-0.098	-0.027	0.384	-0.001	0.203	0.322	0.394	0.567	0.594	**1.000**	-0.011	0.016	-0.003	0.113	0.242
MFL	-0.426	-0.537	-0.211	-0.516	0.291	0.570	0.210	0.369	0.386	-0.005	**1.000**	0.125	0.043	-0.008	-0.098
NS/F	-0.425	-0.413	-0.036	-0.475	0.002	0.186	0.522	0.344	0.464	0.011	0.123	**1.000**	0.012	-0.097	0.137
SL	0.311	0.245	-0.009	0.210	-0.231	-0.274	-0.049	0.315	0.214	-0.045	0.001	0.023	**1.000**	0.744	0.369
SW	-0.004	-0.124	-0.427	-0.091	0.093	-0.264	0.041	0.282	0.238	0.077	-0.005	-0.089	0.558	**1.000**	0.450
STW	-0.088	-0.112	0.043	-0.086	0.614	0.276	0.373	0.120	0.277	0.235	-0.095	0.137	0.274	0.432	**1.000**

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