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ASSESSMENT OF GENETIC DIVERSITY IN CORE SET OF HORSE GRAM (*Macrotyloma uniflorum* Lam. Verdcourt) GERMPLASMS ACCESSIONS FOR YIELD ATTRIBUTING TRAITS AND POWDERY MILDEW DISEASE RESISTANCE

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ABSTRACT

A total of 277 core set accessions of Horse gram germplasms were evaluated under augmented design in Rabi 2022 for assessing variability and identifying high-yielding genotypes with determinate growth patterns, and to score for powdery mildew resistance. The 277 Horse gram germplasm accessions with six checks were characterized for nine qualitative traits and categorized them into different groups based on plant growth habit, plant growth pattern, leaf colour, leaf surface, stem colour, flower colour, pod shape, pod surface and seed colour. The semi-spreading type of growth pattern was more in the population (59.72%) followed by spreading types (21.91%). More variation was found in leaf characteristics like leaf colour and leaf surface. Dark green leaf colour (45.23%) and glabrous leaf surface (70.67%) dominated among the total accessions. In almost all the accessions the flower colour was light yellow (99.29%) and only two accessions including one check variety HGGP were found yellow. Maximum accessions had the cylindrical type of pod shape (84.45%). Nearly half of the accessions had glabrous pod surfaces (45.23%) and others had pubescent pod surfaces (54.77%). The seed colour of most of the accessions was found to be brown (67.49%) followed by black colour (25.80%), and a small number of accessions had grey colour. The variability for quantitative traits in the present investigation is characterised by phenotypic and genotypic variance for all the traits. Analysis showed that the Phenotypic coefficient of variation was higher compared to the genotypic coefficient of variation for all traits suggesting the influence of environment on the quantitative traits. Accessions with a determinate growth pattern were primarily affected by the disease and found to be susceptible. The accession IC-43497 and IC-71735 with desirable quantitative traits, and found to be good resistant against powdery mildew disease.

Keywords : *Macrotyloma uniflorum*, germplasm, Diversity, Quantitative traits, Powdery mildew disease.

Introduction

Horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] commonly known as *kulthi* or *Madras gram*, is one of India's traditional, underutilised, and ancient grain legume crops (Verdcourt, 1982). It is a drought-tolerant crop species from an eco-physiological point

of view, and it demonstrates several favourable characteristics like resistance to stress from heavy metals, salinity, and drought. Despite its significance, this crop has received disproportionately little attention and research (Fuller and Murphy 2018). Increased and continuous utilisation of genetic resources is essential

for improving genetic diversity and increasing the productivity of Horse gram. For this, it is necessary to extract dependable information on the degree and structure of genetic variability, the proportional contribution of genotypes, and the interaction between genotype and environment in terms of total phenotypic variability for economically significant quantitative features.

Horse gram has two different types of development habits: determinate and indeterminate. Its main stem stops growing but will not terminate in an inflorescence even when flowering begins in the lateral branches, in contrast to other legumes like the common bean (Campos *et al.* 2013), chickpea (Sandhu *et al.* 2010), and *Dolichos* bean (Keerthi *et al.* 2016), where the main meristem terminates in inflorescence in determinate genotypes (Ashwini *et al.* 2021). The majority of horse gram cultivars now being used for commercial production have indeterminate growth patterns. Determinate growth habit of horse gram enables high-density planting, which enhances crop productivity (Kim *et al.* 1995). In determinate genotypes, synchronous pod maturity reduces grain yield losses caused by pod shattering.

Among the numerous adversaries in agriculture, powdery mildew disease stands out as a common fungal intruder that relentlessly targets a range of crops. One such vulnerable candidate is horse gram, a significant leguminous crop crucial for its nutritional value and adaptability to various agro-climatic zones. As a testament to its impact, studies have revealed that powdery mildew can inflict substantial losses, with recorded yield reductions ranging from 20% to 50% in severe cases. Considering these aspects in horse gram, the present study was conducted to assess the spectrum of variation for grain yield and its component traits among the core set of horse gram germplasm and high-yielding genotypes from the core set accessions, followed by screening horse gram germplasm for powdery mildew disease resistance under field conditions.

Materials and Methods

Two hundred and seventy-seven indigenous germplasm accessions (Table 1) and six commercial check varieties (HGGP, Payiur-1, PHG-9, AK-21, Birsa Kulthi, DPI-2278) were evaluated during *Rabi* 2022 at the experimental plots of Dept. of Genetics and Plant Breeding (K Block), College of Agriculture GKVK Campus, University of Agricultural Sciences, Bangalore which comes under the Eastern dry zone with an altitude of 924m above mean sea level and at 13° 08' N latitude and 77° 57' E Longitude. The

material was acquired from NBPGR, DBT project on the enhancement of minor pulses and the Augmented block design (Federer, 1956) was used for evaluation. The accessions were sown in 10 compact blocks. Each block consisted of 28 accessions and 6 checks with border lines. The planting was done in a paired row system with row spacing of 45cm and 15cm between plants. Standard operating procedure (SOP) was followed throughout the crop production. The crop was irrigated regularly through drip pipes.

Statistical Analysis

Data were recorded on five randomly selected plants from each line on nine qualitative traits based on visual rating/scoring (Plant growth habit, Plant growth pattern, Leaf colour, Leaf surface, Stem colour, Flower colour, Pod shape, Pod Structure and Seed colour, and on nine quantitative traits (Days to 50% flowering, Days to Maturity, Grain yield plant⁻¹(g), Number of Pods plant⁻¹, Number of seeds pod⁻¹, Number of Primary branches plant⁻¹, Plant height (cm)

Pod length (cm), and 100 seeds weight (g)) based on counting/measurement using an appropriate scale depending on the trait in all the lines, including check entries. The germplasm accessions were grouped into different classes based on qualitative traits. The number and *percentage* of accessions belonging to each class were counted and estimated. Variability among the accessions exhibiting different states of each of the qualitative traits was quantified by computing the percentage of accessions exhibiting different states.

The quantitative trait means values computed based on data on five randomly tagged plants in each germplasm accession and check entry were used for statistical analysis. ANOVA was performed for partition of the total variation among the germplasm accessions and check entries following Augmented block design (Federer 1956) using Statistical Package for Augmented block design (SPAD) developed by Indian Agricultural Statistics Research Institute (IASRI), New Delhi. The adjusted trait mean of each of the germplasm accessions was estimated (Federer 1956).

Genetic variability among the germplasm accessions was assessed using first-degree statistics such as absolute and standardised range, and second-degree statistics such as phenotypic variance (PV) and genotypic variance (GV) (Snedecor and Cochran 1989). Unit-independent phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were computed (Burton and De Vane, 1953) to enable comparison of PV and GV across traits. Genetic

parameters such as broad-sense heritability (h^2) (Lush, 1949) and expected genetic advance as *per cent* mean (GAM) were estimated (Johnson *et al.* 1955) using the adjusted trait mean of each of germplasm accessions.

Screening the germplasms for powdery mildew disease resistance

The plants in the experimental field were observed for symptoms like grey and white spots on the surface of plant leaves, stems, new growth, flowers, and even on top of pods, periodically at 15-day intervals of up to 100 days. Disease incidence was calculated based on the scale (0-Immune to 5-Highly Susceptible) as described by Bhaskar (2020).

Results and Discussion

Assessment of genetic variability for various qualitative and quantitative traits

The selection of a genotype with desired characteristics depends on the amount of variability present in the population or the material. Estimation of variability and heritability assists in the utilization of genetic variability in the population.

Variability for Qualitative Traits

The 277 Horse gram germplasm accessions with six checks were characterized for nine qualitative traits into different groups for plant growth habit, plant growth pattern, leaf colour, leaf surface, stem colour, flower colour, pod shape, pod surface and seed colour. Trait-wise classification of accessions and their *per cent* distribution into various groups is presented in Table 2 and Fig 1. The semi-spreading type of growth pattern was more in the population (59.72%) followed by spreading types (21.91%). More variation was found in leaf colour and leaf surface. Dark green leaf colour (45.23%) and glabrous leaf surface (70.67%) dominated among the accessions. In almost all the accessions the flower colour was light yellow (99.29%) and only two accessions including one check variety HGGP were found yellow. Maximum accessions had the cylindrical type of pod shape (84.45%). Nearly half of the accessions had glabrous pod surfaces (45.23%) and others had pubescent pod surfaces (54.77%). The seed colour of most of the accessions was found to be brown (67.49%) followed by black colour (25.80%), and a small number of accessions had grey colour. These results are in agreement with that of Visakha and Bindu (2022) and Chahota *et al.* (2013).

Variability for Quantitative Traits

The variability in the present investigation is characterised by phenotypic and genotypic variance for all the traits. The estimate of the coefficient of

variation is a measurement that employs the *per cent* of mean to express the variance that is being employed. The data gained are expressed as phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability (H_{bs}), and Genetic advance as *per cent* of mean (GAM). The descriptive statistics for nine quantitative traits are presented in Table 3.

The genetic variability parameters are represented in Table 4. Analysis showed that the Phenotypic coefficient of variation was higher compared to the genotypic coefficient of variation for all traits suggesting the influence of environment on the quantitative traits. The range of Phenotypic coefficient of variation was from 9.35% to 31.46%. This indicates that the effect of the environment is present to moderate extent. The range of genotypic coefficient of variation was from 5.57% to 30.89% in *rabi* 2022 indicating genotypic variability. The maximum values of PCV and GCV were recorded for Grain yield plant⁻¹ and the Number of pods plant⁻¹. However, the lowest values of PCV and GCV were recorded for days to maturity in *Rabi* 2022. These results are in agreement with the results obtained by Durga (2012) and Gomashe *et al.*, (2018).

The accessions were moderately variable for days to fifty *per cent* flowering, plant height, number of primary branches plant⁻¹ and pod length. Similar results were obtained by Priyanka *et al.*, (2021) for Days to fifty *per cent* flowering, Days to maturity and plant height suggesting more influence of environment on these characteristics. Among the traits studied narrow differences were observed among all the traits in *Rabi* 2022. Comparing expected genetic gains from selection based on an alternative selection strategy is one of the main applications of measuring heritability and the genetic parameters that compose the heritability estimate. The appropriate selection of genotypes for the trait of interest requires consideration of heritability and genetic advance as a percentage of the mean in addition to GCV values, which reflect genetic variability. In the present study, the broad sense heritability values ranged from 87.71% to 98.01%. 100 seeds weight had the lowest value while days to maturity had the highest value of broad sense heritability. A higher heritability value reflects a lesser influence of the environment on the trait. The above results are in agreement with Rakesh *et al.*, (2015).

The range of Genetic advance as *per cent* mean was from 11.39% to 62.57% and Days to maturity had the lowest value. Grain yield plant⁻¹ had the highest value. In an overall sense the moderate values of broad sense heritability and genetic advance as *per cent* mean

for a few of the traits indicates that those traits have more influence of environment or non-fixable genetic elements (Dominance and epistasis) and improvement of those traits can be through heterosis or production of transgressive segregants.

Analysis of Variance (ANOVA)

ANOVA is the diagnostic procedure to find different sources of variation pertinent to the outcomes of field experiments, like those presented in the current study. ANOVA was performed for nine quantitative traits evaluated in Horsegram germplasm accessions from *Rabi* 2022. The analysis of variance of the 277 accessions sown in Augmented block design during 2022 with six checks is presented in Table 5. The analysis of variance indicated significant genotypic differences for all the nine yield and yield-related traits which reflected the presence of high genetic variability among the accessions. For the blocks, the mean sum of squares was non-significant for all the traits except for plant height. For the majority of the quantitative features, highly significant mean squares revealed significant variation not just across the germplasm accessions but also between those accessions and the check varieties.

Identification of Trait-specific accessions

Quantitative trait-specific germplasm accessions have been identified in Horse gram germplasm by (Kirankumar *et al.* 2023; Priyanka *et al.* 2021), common bean (Meena *et al.* 2018), cowpea (Cobbinah *et al.* 2011). In the present study, some of the germplasms are comparable to superior to the checks for quantitative traits such as days to fifty *per cent* flowering, number of pods plant⁻¹, grain yield plant⁻¹, number of primary branches plant⁻¹, 100 seeds weight, Pod length, days to maturity, number of seeds pod⁻¹ and plant height. The trait-specific accessions have been identified which performed better as compared to the standard checks.

Days to flowering directly affect the length of maturity; this makes them a crucial adaptation feature, especially when crop growth is hindered by abiotic conditions like drought and severe temperatures. Early flowering and subsequent early maturity aid in reducing losses brought on by pod borer infestation and avoiding the impact of extreme low temperatures and drought (Rao *et al.* 1995). Short-duration cultivars provide added benefits for integration into multi-cropping systems, but achieving this advantage involves making a necessary trade-off in productivity. This trade-off occurs because short-duration cultivars utilize only a portion of the growing season, leading to a notable decrease in economic yield.

Some accessions were identified for multiple traits represented in Table 6. To enhance the pace of Horse gram breeding, these accessions may be recombined with advanced breeding lines and selection for economically important traits may be practiced. The accessions are suggested for preferential use in Pureline variety development and introgression breeding to generate variability for recovering farmer-acceptable varieties with consumer/end-user preferred traits.

Identification of Determinate and High-Yielding Genotypes

The previous studies of Chandana *et al.* (2022), Ashwini *et al.* (2021), and Chahota *et al.* (2013), it is clear that the need for identification of Horse gram accessions with determinate growth pattern is increasing in the farming community. In the present study, an attempt has been made to identify accessions which have determinate growth pattern and other yield attributing and quality traits like grain yield plant⁻¹, early to fifty *per cent* flowering, and brown seed colour which is generally preferred. Since, the presently available commercial variety with determinate growth pattern in Horse gram is Birsakulthi which has a mean yield of 6g plant⁻¹ and has early to fifty *per cent* flowering. These accessions can be used in further breeding programmes to breed for desired characteristics. Further, the accessions with determinate growth pattern are seen for other desired traits such as early to fifty *per cent* flowering and brown seed colour.

Screening germplasm for Powdery Mildew Disease Resistance Under Field Conditions.

According to Sudhagar *et al.* (2022), Horse gram has been identified as a viable crop for the future, however tight self-pollination restrictions, a lack of genetic variety for economic features, and a relative lack of research on germplasm characterisation highlight the need for accelerated breeding efforts. Among the other diseases Horse gram during winter is majorly affected by powdery mildew which can cause losses up to 80%. In this present study, we have screened the core set accessions for powdery mildew disease resistance under field conditions during *Rabi* 2022 Table 7.

The results have shown that the disease screening the accessions with determinate growth pattern were predominantly affected by the powdery mildew while the accessions with indeterminate growth pattern performed well even after disease incidence as these types have more vegetative growth phase. It was found that the line IC-43497 having brown seed colour with a mean grain yield plant⁻¹ of 10.7g was immune to

powdery mildew disease and the line IC-71735 having a black seed colour with mean grain yield plant⁻¹ of 9.74g was resistant to disease under field conditions. These genotypic accessions which have been identified as immune, resistant and moderately resistant types which can be selected for developing powdery mildew disease resistant varieties.

Table 1 : List of Horse gram core set accessions procured from NBPGR, New Delhi.

Sl. No.	Accessions	Sl. No.	Accessions	Sl. No.	Accessions	Sl. No.	Accessions
1	IC-261296	51	IC-145347	101	IC-1835	151	IC-316320
2	IC-113896	52	IC-139347	102	IC-320913	152	IC-269629
3	IC-385622	53	IC-489215	103	IC-142025	153	IC-120770
4	IC-23497	54	IC-261278	104	IC-68587	154	IC-208514
5	IC-426464	55	IC-145325	105	IC-94595	155	IC-426471
6	IC-19429	56	IC-145309	106	IC-208471	156	IC-521467
7	IC-421755	57	IC-398703	107	IC-49552	157	IC-120839
8	IC-570764	58	IC-139374	108	IC-347177	158	IC-89043
9	IC-342972	59	IC-71785	109	IC-139446	159	IC-139476
10	IC-47137	60	IC-123021	110	IC-45725	160	IC-385916
11	IC-424462	61	IC-145321	111	IC-208478	161	IC-425088
12	IC-56130	62	IC-68597	112	IC-71798	162	IC-23448
13	IC-22782	63	IC-385918	113	IC-113758	163	IC-208507
14	IC-139410	64	IC-45700	114	IC-22805	164	IC-53450
15	IC-120826	65	IC-55061	115	IC-425073	165	IC-266888
16	IC-33765	66	IC-561037	116	IC-26138	166	IC-139524
17	IC-71763	67	IC-26840	117	IC-321299	167	IC-23432
18	IC-371987	68	IC-256867	118	IC-343900	168	IC-19446
19	IC-71815	69	IC-22756	119	IC-94585	169	IC-208472
20	IC-53618	70	IC-364123	120	IC-257875	170	IC-470243
21	IC-71771	71	IC-470209	121	IC-23840	171	IC-145252
22	IC-22824	72	IC-32729	122	IC-261293	172	IC-470211
23	IC-42194	73	IC-385836	123	IC-120820	173	IC-27602
24	IC-89009	74	IC-105546	124	IC-208506	174	IC-342687
25	IC-489185	75	IC-145246	125	IC-561043	175	IC-548801
26	IC-344192	76	IC-16175	126	IC-22813	176	IC-262880
27	IC-257373	77	IC-26132	127	IC-53637	177	IC-56137
28	IC-626489	78	IC-276110	128	IC-23464	178	IC-53622
29	IC-22762	79	IC-426552	129	IC-22792	179	IC-105588
30	IC-139560	80	IC-426503	130	IC-470252	180	IC-22776
31	IC-89012	81	IC-45733	131	IC-71781	181	IC-512218
32	IC-32834	82	IC-426514	132	IC-277642	182	IC-201111
33	IC-120802	83	IC-426455	133	IC-261300	183	IC-19432
34	IC-43497	84	IC-343386	134	IC-622773	184	IC-283868
35	IC-145301	85	IC-139352	135	IC-470300	185	IC-23458
36	IC-393385	86	IC-145337	136	IC-470275	186	IC-406378
37	IC-320970	87	IC-425085	137	IC-105522	187	IC-369745
38	IC-89016	88	IC-208475	138	IC-113761	188	IC-139525
39	IC-341248	89	IC-203207	139	IC-123033	189	IC-395654
40	IC-400120	90	IC-120772	140	IC-45750	190	IC-283572
41	IC-23502	91	IC-257694	141	IC-53611	191	IC-113756
42	IC-33124	92	IC-541465	142	IC-71754	192	IC-396007
43	IC-89036	93	IC-337229	143	IC-148337	193	IC-32848
44	IC-145279	94	IC-330562	144	IC-139336	194	IC-145249
45	IC-277643	95	IC-312385	145	IC-362586	195	IC-71735
46	IC-88999	96	IC-343849	146	IC-23481	196	IC-94618
47	IC-45698	97	IC-22766	147	IC-213929	197	IC-139376
48	IC-277619	98	IC-120842	148	IC-23460	198	IC-426454
49	IC-120829	99	IC-19433	149	IC-520825	199	IC-145295
50	IC-343896	100	IC-47122	150	IC-45715	200	IC-526965

201	IC-470230	221	IC-590835	241	IC-330563	261	IC-282588
202	IC-280032	222	IC-320852	242	IC-33152	262	IC-426539
203	IC-201115	223	IC-261298	243	IC-139558	263	IC-316309
204	IC-139334	224	IC-561016	244	IC-24344	264	IC-470254
205	IC-26128	225	IC-361650	245	IC-71778	265	IC-436596
206	IC-427526	226	IC-23447	246	IC-33072	266	IC-145329
207	IC-120753	227	IC-71725	247	IC-71758	267	IC-71803
208	IC-470264	228	IC-19498	248	IC-262058	268	IC-273744
209	IC-65462	229	IC-341228	249	IC-520826	269	IC-261020
210	IC-23482	230	IC-33056	250	IC-23841	270	IC-23462
211	IC-22816	231	IC-66134	251	IC-26127	271	IC-520828
212	IC-208474	232	IC-123035	252	IC-208513	272	IC-561015
213	IC-361648	233	IC-417914	253	IC-214721	273	IC-426533
214	IC-53641	234	IC-489252	254	IC-121636	274	IC-280768
215	IC-470216	235	IC-470295	255	IC-277651	275	IC-26840
216	IC-277659	236	IC-123029	256	IC-541010	276	IC-353815
217	IC-49509	237	IC-333338	257	IC-68595	277	IC-16170
218	IC-424465	238	IC-71769	258	IC-88990		
219	IC-1102	239	IC-570766	259	IC-145293		
220	IC-590834	240	IC-145265	260	IC-120831		

Table 2 : Variability for qualitative traits, their frequency and per cent distribution among Horse gram germplasm core set accessions

S.No.	Trait	Classification	Frequency	Percentage(%)
1	Plant growth habit	Spreading	62	21.91
		Semi-spreading	169	59.72
		Trailing	52	18.37
2	Plant growth pattern	Determinate	147	51.94
		Indeterminate	136	48.06
3	Leaf colour	Pale green	28	9.89
		Green	127	44.88
		Dark green	128	45.23
4	Leaf surface	Glabrous	200	70.67
		Pubescent	83	29.33
5	Stem colour	Light yellow	97	34.28
		Green	122	43.11
		Purple	64	22.61
6	Flower colour	Light yellow	281	99.29
		Yellow	2	0.71
7	Pod shape	Flat	44	15.55
		Cylindrical	239	84.45
8	Pod surface	Glabrous	128	45.23
		Pubescent	155	54.77
9	Seed colour	Brown	191	67.49
		Black	73	25.80
		Grey	19	6.71

Table 3: Descriptive statistics for the year 2022.

Sl. No.	Characters	Range		Mean $\pm$ SEM
		Min	Max	
1	Days to 50% flowering	30.43	56.93	43.68 $\pm$ 0.29
2	Days to maturity	90.82	126.48	109.65 $\pm$ 0.37
3	Grain yield plant ⁻¹ (g)	2.36	15.10	8.73 $\pm$ 0.14
4	Number of pods plant ⁻¹	19.23	92.56	49.36 $\pm$ 0.81
5	Number of seeds pod ⁻¹	3.73	6.38	5.12 $\pm$ 0.03
6	Number of primary branches plant ⁻¹	2.17	8.03	4.7 $\pm$ 0.05
7	Plant height (cm)	19.14	52.16	27.79 $\pm$ 0.25
8	Pod length (cm)	3.81	6.28	4.86 $\pm$ 0.03
9	100 seeds weight (g)	4.31	4.23	3.18 $\pm$ 0.06

Min. = Minimum Max. = Maximum SE_m = Standard error of mean

Table 4: Genetic variability parameters for different traits of Horse gram

Sl. No.	Characters	PCV (%)	GCV (%)	H _{bs}	GAM (%)
		2022	2022	2022	2022
1	Days to 50% flowering	11.68	11.52	97.18	23.42
2	Days to maturity	5.63	5.57	98.01	11.39
3	Grain yield plant ⁻¹ (g)	31.46	30.89	96.42	62.57
4	Number of pods plant ⁻¹	27.28	26.35	93.32	52.51
5	Number of seeds pod ⁻¹	9.35	8.8	88.63	17.09
6	Number of primary branches plant ⁻¹	18.09	17.49	93.56	34.91
7	Plant height (cm)	15.41	14.78	92.06	29.26
8	Pod length (cm)	10.26	9.69	89.16	18.88
9	100 seeds weight (g)	12.28	11.51	87.71	22.23

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

H_{bs} = Broad sense heritabilityGAM = Genetic advance as *per cent* mean**Table 5:** Analysis of variance (ANOVA) for yield and yield attributing traits

Source of Variation	df	Mean Sum of squares								
		DF	DM	GYP	NPP	NSP	PB	PH	PL	TW
Block (Ignoring Treatment)	9	55.6**	48.15**	19.07**	371.19**	0.24**	1.7**	40.84**	0.3**	0.27**
Accessions (Eliminating Block)	282	27.8**	48**	6.16**	244.68**	0.23**	0.72**	18.72**	0.24**	0.14**
Accessions Adjusted Check	5	120.67**	254.39**	18.68**	615.06**	0.28**	2.84**	79.18**	0.28**	0.14**
Accession Adjusted Test Vs Check	277	26.13**	44.28**	5.88**	205.5**	0.23**	0.68**	37.63**	0.24**	0.14**
Accession (Ignoring Block)	282	29.55**	49.53**	6.18**	249.97**	0.24**	0.77**	49.91**	0.25**	0.15**
Block Adjusted Check	5	120.67**	254.39**	19.68**	514.06**	0.28**	2.84**	79.18**	0.28**	0.14**
Block Adjusted Accessions	276	23.61**	38.12**	5.93**	181.24**	0.23**	0.72**	38.33**	0.25**	0.14**
Block Adjusted Test Vs Check	1	915.26**	2072.43**	30.8*	893.49**	1.44**	5.08**	160.39**	1.26**	1.44**
Block Eliminating Accessions	9	0.82	0.39	0.32	5.52	0.03	0.09	3.59*	0.04	0.03
Residuals	45	0.67	0.76	0.21	12.11	0.03	0.05	1.45	0.03	0.02
SE										
Control Tr means		0.92	0.99	0.52	3.94	0.18	0.24	1.37	0.19	0.15
Two test accessions Same Block		0.37	0.39	0.21	1.56	0.07	0.1	0.54	0.07	0.06
Two test accessions Different Block		1.25	1.33	0.7	5.32	0.25	0.33	1.84	0.25	0.20
Test Vs Check		1.15	1.23	0.65	4.92	0.23	0.3	1.71	0.23	0.19
CD										
Control Tr means		1.86	1.99	1.05	7.94	0.37	0.49	2.75	0.37	0.30
Two test accessions Same Block		0.74	0.79	0.41	3.13	0.15	0.19	1.09	0.15	0.12
Two test accessions Different Block		2.51	2.68	1.42	8.71	0.5	0.66	3.71	0.51	0.41
Test Vs Check		2.33	2.48	1.31	9.91	0.46	0.61	3.44	0.47	0.38

*** Significant at P= 0.001; ** Significant at P= 0.01; * Significant at P= 0.0

DF – Days to 50% flowering, DM- Days to Maturity, GYP – Grain yield plant⁻¹(g), NPP- Number of pods plant⁻¹, NSP- Number of seeds pod⁻¹, PB- Number of Primary Branches, PH- Plant height (cm), PL- Pod Length (cm), TW- 100 seeds weight (g), SE - Standard errors, CD - Critical differences**Table 6:** Promising accessions identified for multiple traits in a core set of Horse gram germplasm

Traits	Accessions
Early to Fifty <i>per cent</i> flowering, Grain yield plant ⁻¹ (g)	IC-120772, IC-421755, IC-23482, IC-424465, IC-261298, IC-145265, IC-23841, IC-261020, IC-23462, IC-139560, IC-277619, IC-145321, IC-55061
Late to fifty <i>per cent</i> flowering, Grain yield plant ⁻¹ (g)	IC-208507, IC-398703, IC-353815, IC-277643, IC-343386
Number of Pods plant ⁻¹ , Number of Seeds pod ⁻¹ , 100 Seeds weight (g)	IC-470295, IC-139560, IC-470209
Number of Pods plant ⁻¹ , Number of Seeds pod ⁻¹	IC-470295, IC-139560, IC-43497, IC-470209
Early to Fifty <i>per cent</i> flowering, Number of Pods plant ⁻¹ , Number of Seeds pod ⁻¹ , Grain yield plant ⁻¹ (g), 100 seeds weight(g)	IC-261298, IC-139560
Late to fifty <i>per cent</i> flowering, Grain yield plant ⁻¹ (g), 100 seeds weight, Number of Pods plant ⁻¹ , Number of Seeds pod ⁻¹	IC-398703, IC-353815
Grain yield plant ⁻¹ , 100 seeds weight	IC-277643, IC-385918, IC-145295, IC-590835

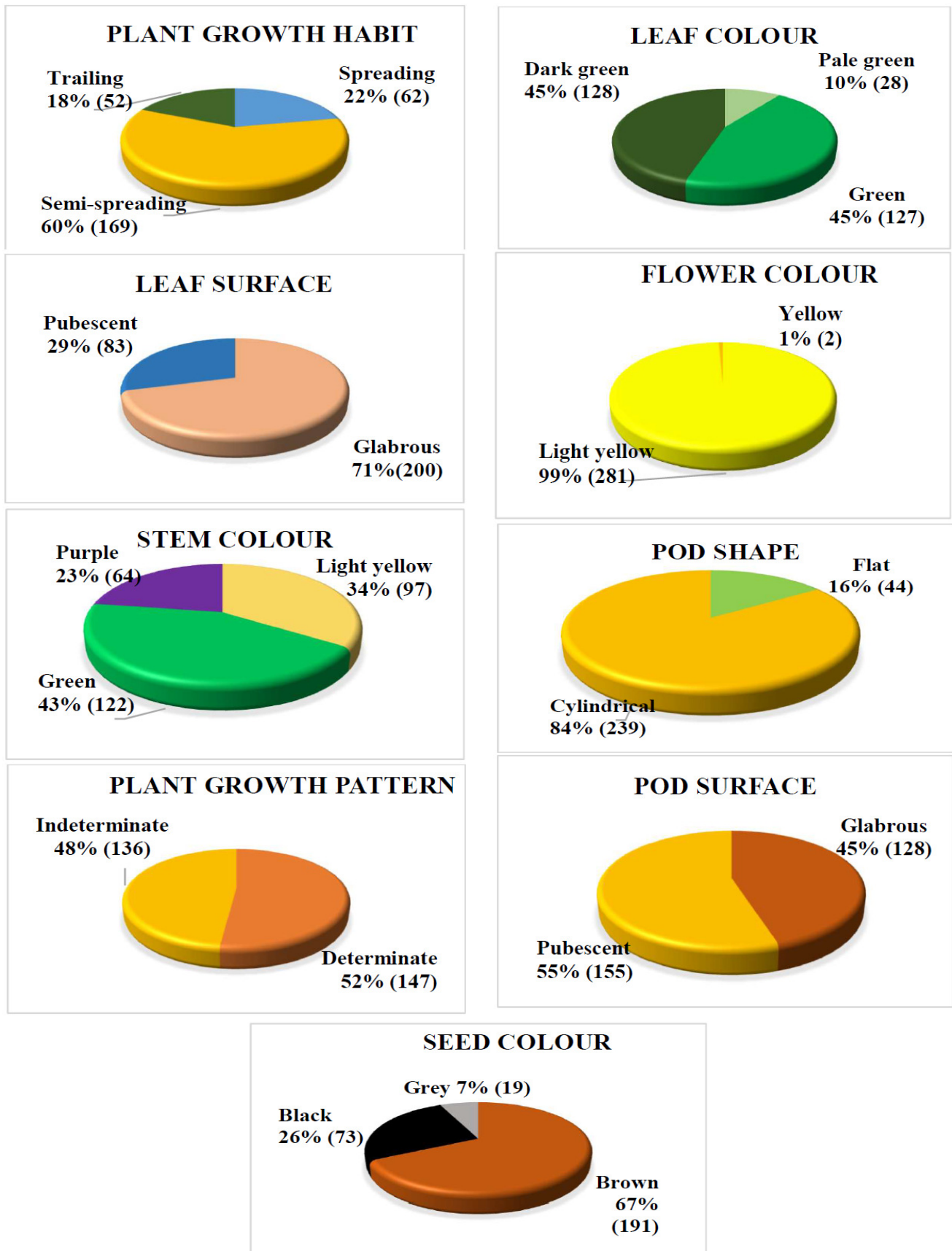


Fig. 1: Pie diagram depicting the variability for qualitative traits of Horse gram core set accessions

Table 7: Reaction of Horse gram core set for Powdery Mildew

Reaction	Grade	Accessions
Immune	0	IC-43497, IC-89016, IC-105498, IC-45700, IC-55061, IC-470209, IC-385836, IC-16175, IC-426503
Resistant	1	IC-89012, IC-145301, IC-393385, IC-320970, IC-23502, IC-33124, IC-89036, IC-277643, IC-45698, IC-277619, IC-489215, IC-261278, IC-145325, IC-139374, IC-71785, IC-123021, IC-145321, IC-68597, IC-385918, IC-561037, IC-26840, IC-256867, IC-22756, IC-32729, IC-145246, IC-26132, IC-276110, IC-426552, IC-45733, IC-426514, IC-426455, IC-343386, IC-208471, IC-71798, IC-145337, IC-142025, IC-68587, IC-26138, IC-120820, IC-22813, IC-53637, IC-261300, IC-470275, IC-105522, IC-123033, IC-45750, IC-203203, IC-208472, IC-470243, IC-145252, IC-406378, IC-32848, IC-145249, IC-71735, IC-94618, IC-139410, IC-426454, IC-139334, IC-26128, IC-120753, IC-320852, IC-71815, IC-424463, IC-333338, IC-71769, IC-139560, AK-21
Moderately resistant	2	IC-113896, IC-426464, IC-22782, IC-33765, IC-371987, IC-71771, IC-32834, IC-49290, IC-400120, IC-145279, IC-88999, IC-145309, IC-364123, IC-105546, IC-49552, IC-347177, IC-139352, IC-425085, IC-321299, IC-261293, IC-23464, IC-22792, IC-470252, IC-71781, IC-113761, IC-53611, IC-71754, IC-148337, IC-213929, IC-23460, IC-520825, IC-45715, IC-398703, IC-470211, IC-27602, IC-342687, IC-56137, IC-512218, IC-201111, IC-19432, IC-369745, IC-139525, IC-139376, IC-145295, IC-526965, IC-470230, IC-280032, IC-201115, IC-427526, IC-65462, IC-23482, IC-53641, IC-261298, IC-561016, IC-71763, IC-23447, IC-33056, IC-66134, IC-123035, IC-417914, IC-470295, IC-330563, IC-33152, IC-139558, IC-33072, IC-26127, IC-214721, IC-541010, IC-68595, IC-88990, IC-145293, IC-120831, IC-426539, IC-145329, IC-71803, IC-280768, IC-22762, PHG-9, Paiyur-1
Moderately susceptible	3	IC-89009, IC-489185, IC-257373, IC-19429, IC-421755, IC-570764, IC-120826, IC-22824, IC-42194, IC-120802, IC-139347, IC-94595, IC-45725, IC-208478, IC-120772, IC-541465, IC-337229, IC-19433, IC-47122, IC-1835, IC-320913, IC-113758, IC-425073, IC-343900, IC-257875, IC-23840, IC-208506, IC-561043, IC-277642, IC-622773, IC-139336, IC-316320, IC-208514, IC-426471, IC-89043, IC-385916, IC-19446, IC-22776, IC-283868, IC-23458, IC-395654, IC-283572, IC-113756, IC-470264, IC-22816, IC-208474, IC-361648, IC-470216, IC-590834, IC-71725, IC-19498, IC-139371, IC-489252, IC-570766, IC-24344, IC-71778, IC-262058, IC-23841, IC-208513, IC-277651, IC-282588, IC-470254, IC-436596, IC-273744, IC-261020, IC-23462, IC-520828, IC-353815, IC-16170, HGGP, DPI2278
Susceptible	4	IC-626489, IC-385622, IC-342972, IC-424462, IC-343896, IC-208475, IC-203207, IC-330562, IC-94585, IC-362586, IC-23481, IC-269629, IC-120770, IC-521467, IC-120839, IC-139476, IC-23448, IC-53450, IC-139524, IC-23432, IC-262880, IC-105588, IC-396007, IC-277659, IC-49509, IC-424465, IC-1102, IC-590835, IC-341228, IC-123029, IC-121636, IC-316309, IC-561015, IC-426533, IC-26840, Birsa Kulthi
Highly susceptible	5	IC-261296, IC-56130, IC-344192, IC-23497, IC-47137, IC-53618, IC-341248, IC-120829, IC-145347, IC-139446, IC-257694, IC-312385, IC-343849, IC-22766, IC-120842, IC-22805, IC-470300, IC-425088, IC-208507, IC-266888, IC-548801, IC-53622, IC-361650, IC-145265, IC-71758, IC-520826

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