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Identifying Promising Cowpea (*Vigna unguiculata* L. Walp) Genotypes for Grain yield and its Component Traits through Direct and Indirect Selection Suitable for *Rabi* Conditions

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Abstract

Identification of cowpea genotypes suited to unconventional *rabi* season, forms the prerequisite to initiate breeding programs for such conditions. To achieve this, a minicore set of 172 accessions (163 germplasm and nine checks) were evaluated in alpha design in *rabi* 2022. The genotypes were evaluated for nine quantitative yield and its attributing traits *viz.,* days to fifty *per cent* flowering (DFF), pod length (cm) (PL), pod width (cm) (PW), seeds per pod (SP), pods cluster^{-1} (PC), average pod weight (g) (APWT), pods plant^{-1} (PP), hundred seed weight (g) (HSW) and grain yield plant^{-1} (g) (GYP). Among the traits, largest variation was observed for PP, followed by GYP and the least for PW. Trait specific accessions were identified based on adjusted means of genotypes. Accessions promising for multiple traits were also identified. The accessions 144 (IC202779) and 362 (EC107163) were identified to be promising for three traits each *viz.,* PW, HSW, APWT and SP, PP, GYP, respectively. Indirect selection was exercised by deploying six selection indices considering all traits except GYP, which were then compared against direct selection (DS) for GYP, through relative selection efficiency (RSE). Consequently, Base Linear Phenotypic Selection Index (BLPSI) proved to be better in selecting promising genotypes for GYP, with higher RSE of 64.89 per cent against DS. However, DS had highest coincidence index with rank sum method, suggesting higher number of common genotypes between them.The genotypes 362 (EC107163) and 390 (EC738131) were selected by five and four out of six indices respectively, highlighting their superiority over others. These selected genotypes, after further evaluations during *rabi*, would serve as potential cultivar options and as parents for developing elite genotypes upon hybridisation and selection.

Keywords : *Rabi* cowpea, Direct selection, Indirect selection, Selection indices, Relative selection efficiency

Grain legumes form an important source of protein besides possessing considerable amount of carbohydrate and other micronutrients. Cowpea (*Vigna unguiculata* L. Walp) is one such food legume which is native to Central Africa (Harlan, 1971), however predominantly cultivated in arid and semi-arid tracts of the world. Highest production of cowpea is in Nigeria, accounting for nearly half of the Africa's production (FAO, 2019). In India, it is cultivated in 3.9 million hectares (Giridhar *et al.,* 2020; Pushpa *et al.,* 2023), majorly in states of Rajasthan, Karnataka, Kerala, Tamil Nadu, Maharashtra and Gujarat. However, cowpea is less preferred by the farmers over other legume crops primarily owing to its reduced yield potential especially in intensive farming systems (Poornima *et al.,* 2023).

In tropical India, cowpea is primarily grown as main crop in *kharif* or as rice fallow crop during late *kharif.* Cowpea being a tropical crop, enjoys ample sunshine, during (late) *kharif* and produce luxuriant vegetative growth before translating that to grain yield. In contrast, rabi conditions are characterised by low temperatures, increased photoperiods and low rainfall. Since the selection programs were oriented towards identifying superior genotypes suitable for *kharif* cultivation, the chosen genotypes may not exhibit similar performance during *rabi* season (Padulosil, 1997). Moreover, fallow crop or intercrop sown as part of cropping system in rabi could be able to harness the residual moisture effectively in the field, providing more returns to farmers. Hence, it becomes quintessential to breed for and identify genotypes suitable specifically for *rabi* season. To achieve this, available germplasm needs to be screened under *rabi* conditions to identify best yielding accessions, which may serve as a cultivar option or parents for developing better genotypes suitable for *rabi* season.

Selection of genotypes in variable population based on single target trait, may not lead to desirable genetic gain, especially for complex and less heritable traits like grain yield, which is often governed by large number of genes and highly influenced by environment. Under this premise, selection based on less complex traits like yield components, would enable us to identify genotypes promising for a single trait or a combination of traits. Thus, multi-trait selection facilitated through the use of multivariate selection indices aids in selection of superior genotypes for majority of traits *vis*-à-*vis* grain yield. Such selected trait specific accessions can serve as genetic stocks and putative parental lines for improving target trait, when complemented with another trait specific accession. Direct selection refers to selection of genotypes based on grain yield, whereas indirect selection emphasises selection for component traits except grain yield. Considering all the above constraints, the study is framed to address objectives *viz.,* to identify promising trait specific accessions suitable for *rabi* season from among cowpea mini core set, to construct and compare the efficiency of muti-trait selection indices against direct selection and to identify genotypes superior for multiple traits through selection indices.

MATERIAL AND METHODS

A set of 172 genotypes were selected from coreset of cowpea available with ICAR-NBPGR, New Delhi, and All India Coordinated Network Project (AICRN) on Potential crops, University of Agricultural Sciences, GKVK, Bengaluru, based on the principle of constructing mini core set with maximum representativeness and minimum redundancy, which was further validated (data not shown). This set comprised 163 germplasm accessions and nine checks (C1 to C9), where C1 (GC-3), C2 (DC-15), C3 (PL-3), C4 (PL-4) and C5 (RC-101) are the standards recommended by ICAR-NBPGR, whereas C6 (KBC-2), C7 (KBC-9), C8 (KBC-11) and C9 (PGCP-6) were developed at University of Agricultural sciences, Bangalore. These 172 genotypes were evaluated during late *rabi* 2022 for grain yield and its attributing traits, wherein the experiment was laid out in alpha design, with two replications. Sowing was taken up on 15th December 2021. Each genotype was sown in paired rows per replication with 45 cm between rows of same genotype and 90 cm between different genotypes. All the recommended agronomic and plant protection measures were followed to maintain healthy and productive crop.

Data was recorded on nine quantitative traits *viz.,* days to fifty per cent flowering (DFF), pod length (cm) (PL), pod width (cm) (PW), seeds pod^{-1} (SP), pods cluster^{-1} (PC), average pod weight (g) (APWT), pods plant^{-1}(PP), hundred seed weight (g) (HSW), grain yieldplant^{-1} (g) (GYP). Mean daily temperature during crop growth phase in rabi 2022 crop was recorded as 22.13°C. In each genotype, five random plants per replication were chosen for recording data on the above-mentioned traits. Data collected was analysed in R studio (R core team, 2021) with the package *agricolae*, using the function *PBIB. test* and adjusted means were calculated with variance component (VC) model. Based on the adjusted means, trait specific accessions for each the traits were identified. Genotypes which expressed lower mean values than trait grand mean minus twice of standard deviations (<GM+2σ) for flowering and higher values for other traits (>GM+2σ) are identified as superior accession (s) for each of the traits (Kirankumar *et al.,* 2023).

Multi-trait selection was performed to select accessions superior across all the traits except for GYP. Six multi trait selection criteria *viz.,* LPSI (linear phenotypic selection index) (Smith (1936); Hazel and Lush (1942); Hazel (1943)), BLPSI (Base linear phenotypic selection index) (Williams 1962), ESIM (Eigen selection index method) (Ceron-Rojas *et al*., 2008), rank sum (RS), FAI (factor analysis and ideotype-design) index (Rocha *et al*., 2018), MGIDI (Mean Genotype and ideotype distance index) (Olivoto *et al*., 2022) were deployed to select best genotypes for eight traits *viz.,* DFF, PL, PW, SP, PC, APWT, PP and HSW. Comparison of selection indices is based on relative selection efficiency (RSE) computed as selection differential (SD) for GYP in each of selection indices against SD obtained by selecting genotypes through direct selection (DS) on GYP. Selection differential is computed as difference between selected genotypes and total population and expressed as units of trait mean.

$$\text{SD} = \text{Mean of selected genotypes - Mean of all genotypes}$$

$$\text{RSE} = \frac{\text{SD obtained for GYP from indirect selection criteria}}{\text{SD obtained for GYP from direct selection}}$$

Among selection criteria mentioned above, four are weight free indices and the rest are weight based, where the breeder needs to assign weights to individual traits. In this case, equal weightage was given to eight traits subjected to analysis *viz.,* DFF, PL, PW, SP, PC, APWT, PP and HSW for LPSI, BLPSI, ESIM and MGIDI. Detailed description of LPSI, BLPSI and ESIM selection indices is provided in Ceron-Rojas and Crossa (2018) and explanation on FAI and MGIDI is provided by Rocha *et al.,* 2018 and Olivoto *et al.,* 2022, respectively. In rank sum (RS) method, ranks were assigned to the accessions for each of the traits (Pathy *et al.,* 2022), which were summed across traits, and further ranks were computed based on summed ranks. For DFF, ranks were given in ascending order, while it was *vice-versa* for other traits. FAI, MGIDI and ESIM are based on principal component analysis (PCA) and the number of principal components, having eigen value of more than one, were selected for further analysis. Analysis for LPSI, BLPSI and ESIM were performed in RindselR (Alvarado *et al*., 2018), ranksum was computed in MS Excel, while FAI and MGIDI were calculated through 'metan' package in R. Coincidence index (CI) was estimated according to Hamblin and Zimmermann (1986) given as:

$$CI = \frac{A - C}{M - C} \times 100$$

where CI is coincidence index, A is number of common selected genotypes in different methods; C is the number of expected genotypes selected by chance and M is the number of selected genotypes according to the selection intensity.

RESULTS AND DISCUSSION

Phenotypic data on nine quantitative traits were subjected to analysis of variance (ANOVA) and results manifested significant differences among genotypes for all the traits at 1 per cent level of significance (Table 1). These differences could be exploited by plant breeders to exercise selection for each of the traits and identify best ones. The adjusted means for each of the genotypes were taken for computing grand mean (GM) and these are indicated in Table 2. The mean DFF was 65.17 days, which is way higher as compared to *kharif* season. This can be expected in legumes owing to their higher photo and thermo sensitivity. A wide range of variation was observed for all the traits, highlighting substantial genetic diversity among the accessions constituting reduced representative core set. Standardised range is an unitless measure which compares variation across

TABLE 1

Analysis of Variance for nine quantitative traits among 172 cowpea genotypes constituting reduced representative core set

Source of variation	Degrees of freedom	DFF		PL		PW		SP		APWT		PP		PC		HSW		GYP	
		MSS	p value	MSS	p value	MSS	p value	MSS	p value	MSS	p value	MSS	p value	MSS	p value	MSS	p value	MSS	p value
Replication	1	3.98	0.26	4.20	0.25	0.03	0.18	1.41	0.09	0.14	0.09	4.97	0.09	0.51	0.08	0.14	0.24	32.38	0.02
Genotypes	171	40.56	<0.001	22.47	<0.001	0.04	<0.001	10.80	<0.001	0.82	<0.001	281.07	<0.001	0.29	<0.01	31.05	<0.001	31.05	<0.001
Block/rep	84	4.10	0.11	4.11	0.12	0.01	0.77	0.48	0.57	0.05	0.42	1.54	0.74	0.13	0.84	0.11	0.28	5.30	0.72
Residual	87	3.15		3.18		0.02		0.50		0.05		21.77		0.17		0.09		6.01	

DFF: Days to fifty per cent flowering, PL: Pod length (cm), PW: Pod width (cm), SP: Seeds pod^{-1}, APWT: Average pod weight (g), PP: Pod plant^{-1}, PC: Pods cluster^{-1}, HSW: Hundred seed weight (g), GYP: Grain yield plant^{-1}, MSS: Mean sum of squares, rep: replication.

TABLE 2

Descriptive statistics for nine quantitative traits among 172 cowpea genotypes constituting reduced representative core set

Statistic	DFF	PL	PW	SP	APWT	PP	PC	HSW	GYP
Grand mean	65.17	15.21	0.69	13.61	1.77	21.75	2.19	11.41	24.49
Coefficient of variation	2.72	11.71	17.78	5.18	12.41	6.12	18.63	2.69	10.10
Range	80-47.89	28.5-7.0	1.0-0.4	19-7	3.60-0.62	72.78-2.04	3.50-1.25	25.51-3.67	60.66-2.08
Standardised range	0.49	1.41	0.86	0.92	1.68	3.25	1.02	1.91	2.39

DFF: Days to fifty per cent flowering, PL: Pod length (cm), PW: Pod width (cm), SP: Seeds pod^{-1}, APWT: Average pod weight (g), PP: Pod plant^{-1}, PC: Pods cluster^{-1}, HSW: Hundred seed weight (g), GYP: Grain yield plant^{-1}

the traits. Accordingly, PP had highest variation followed by GYP, while the least was observed for DFF. Highest variation in PP during rabi might be because of significant flower drop in a few accessions, which are not adapted to the conditions. These differences would reflect in the trait GYP as well because of high correlation between these two traits.

Owing to high variations in these traits, it is imperative to select accessions promising for each of the traits. Therefore, trait specific accessions were identified considering grand mean and standard deviation as criteria and the accessions identified for each of traits is listed in Table 3. Consequently, 4, 4, 4, 7, 3, 5, 6, 6 and 9 trait-specific accessions were identified for DFF, PL, PW, SP, PC, APWT, PP, HSW and GYP, respectively (Table 3). These are the genotypes that are superior for each of traits considered in the study. Broadly, these promising accessions for each of the traits can serve as potential parents for trait specific breeding program. For instance, 524 (IC263015) was early flowering accession identified, which has high probability of throwing out superior early flowering transgressants, when combined with any of the other three trait specific accessions for DFF *viz.,* 102 (EC723684), 355 (EC738083), 399 (EC738260). This is rendered possible since the latter are exotic collections originating from different geographical regions thus possessing distinct set of genes regulating DFF, which could associate in segregating progeny to isolate and identify transgressants for early flowering. Such quantitative traitspecific germplasm accessions have been identified from core/mini-core collection in cowpea (Cobbinah, *et al.,* 2011). dolichos bean (Vaijayanthi *et al.,* 2016), common bean (Zeven *et al.* 1999), chickpea (Meena *et al.,* 2010; Parameshwarappa *et al.,* 2012; Meena and Kumar 2014) and groundnut (Upadhyaya *et al.* 2003).

Among trait specific genotypes selected, those superior for more than one trait were identified (Table 4). Consequently, three accessions *viz.,* 87 (EC244057), 143 (IC202774), 261 (IC400103) were promising for two traits and two *viz.,* 144 (IC202779) and 362 (EC107163) were promising for

TABLE 3

Promising trait specific accessions identified from among 172 cowpea genotypes constituting reduced representative core set

DFF	PL	PW	SP	APWT	PP	PC	HSW	GYP
102(EC723684)	307(IC-20658)	8(EC5269)	78(EC243943)	87(EC244057)	120(EC528420)	147(IC202791)	19(EC99573)	70(EC240983)
355(EC738083)	372(EC724239)	144(IC202779)	165(IC338865)	362(EC107163)	143(IC202774)	254(IC383461)	41(EC149457)	87(EC244057)
399(EC738260)	407(IC626138)	289(IC546525)	173(IC397942)	C2(DC-15)	144(IC202779)	264(IC413324)	143(IC202774)	98(EC244116)
524(IC263015)	518(EC724805)	505(EC725102)	242(IC548860)		171(IC361790)	312(IC-53351)	144(IC202779)	134(IC68786)
			249(IC372720)		225(IC278035)	362(EC107163)	256(IC397405)	238(IC334368)
			285(IC536609)		261(IC400103)	378(EC724745)	519(EC244046)	261(IC400103)
			300(NR-18-75)		371(EC724160)			274(IC426816)
								342(EC472282)
								362(EC107163)

DFF: Days to fifty per cent flowering, PL: Pod length (cm), PW: Pod width (cm), SP: Seeds pod^{-1}, APWT: Average pod weight (g), PP: Pod plant^{-1}, PC: Pods cluster^{-1}, HSW: Hundred seed weight (g), GYP: Grain yield plant^{-1}

Table 4

Accessions identified promising for more than one trait among 172 cowpea genotypes constituting reduced representative core set evaluated during *rabi* season

Accessions	Number of traits for which accession is promising	Traits for which accession is promising
87 (EC244057)	2	SP, GYP
143 (IC202774)	2	APWT, HSW
144 (IC202779)	3	PW, HSW, APWT
261 (IC400103)	2	APWT, GYP
362 (EC107163)	3	SP, PP, GYP

DFF : Days to fifty per cent flowering, PL: Pod length (cm), PW: Pod width (cm), SP: Seeds pod^{-1}, APWT: Average pod weight (g), PP : Pod plant^{-1}, PC: Pods cluster^{-1}, HSW: Hundred seed weight (g), GYP: Grain yield plant^{-1}

three traits. Majority of the accessions, thus identified, were superior for traits which are highly correlated. For example, 144 (IC202779) was promising for PW, HSW and APWT and 261 (IC400103) for APWT and GYP. However, 362 (EC107163) was identified to be superior for SP, PP and GYP, where SP and PP are not correlated in general. This accession tends to possess superior genes for two distinct component traits for GYP and could serve as putative parent for improvement of GYP, when combined with complementary trait specific accessions like 144 (IC202779) or 143 (IC202774). Since these latter accessions are indigenous collections, the genetic diversity existing between them and 362 (EC107163) can be tapped to recover superior transgressants for GYP.

Six different selection criteria *viz.,* RS, FAI, MGIDI, SHI, BLPSI and ESIM were deployed to identify best accessions based on multiple yield component traits DFF, PL, PW, SP, PC, APWT, PP and HSW. These traits formed the basis for selecting genotypes through indirect selection. Whereas, trait specific genotypes for GYP were the basis for direct selection. Selection intensity was fixed at 5 per cent and selection differential and RSE were estimated for each of the indices. GYP mean of accessions selected directly was 52.17 g and this is taken as standard to compare the indices (Fig. 1). The highest mean was

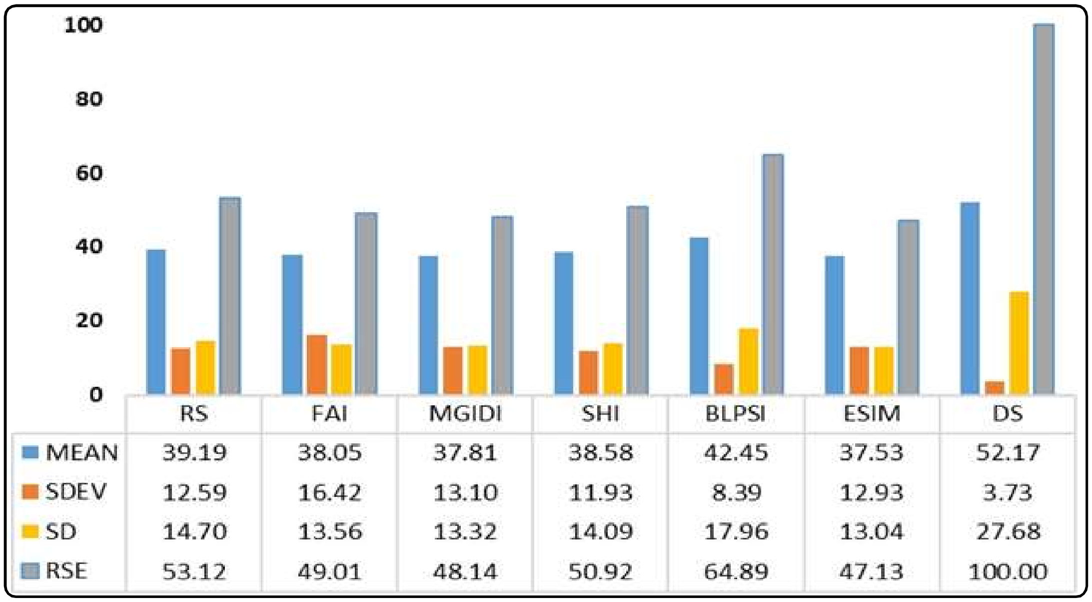

Fig. 1 : Comparative statistics of six indirect selection indices and direct selection (DS) for GYP

observed in BLPSI followed by RS and the least in ESIM. Similar trend was observed for SD and RSE. The RSE of BLPSI was 64.89 per cent of DS, while ESIM, FAI and MGIDI had less than 50 per cent RSE. Standard deviations among selected accessions in each of the indices revealed that direct selection had lowest deviations followed by BLPSI, while large deviations were observed in FAI. Large means and low standard deviations of BLPSI suggests that selection of accessions targeted higher GYP values with little deviations around mean. Larger standard deviations imply selection of genotypes with inconsistent GYP, pulling down the mean values. Similar results were obtained in the previous studies on chickpea (Talekar *et al.,* 2023).

FAI and MGIDI are based on the principle of factor analysis, which assumes the presence of underlying factors that contribute to the correlation between observed traits. Index scores based on FAI were derived from varimax rotation of factor loadings, whereas genotypes are selected based on distance between ideotype and genotypes in MGIDI. Based on the principal component analysis (PCA), three PCs were selected with eigen value of more than one, which explained a cumulative variation of more than 65 per cent (Fig. 2). As seen from the Table 5, PW, APWT, PP and HSW had higher loadings in factor 1, PL and SP for factor 2 and DFF and PC for factor 3. PC and SP had the highest communalities (Table 5), where DFF recorded lowest, with a mean communality of 65.13 per cent. This suggests that the factors explained 80 per cent of the variation in PC and SP, whereasonly 42 per cent of variation in DFF was explained by these common factors, implying that DFF is least correlated with the other traits studied. FAI is a weight free index, where the factor scores are used as weight to derive the scores for genotypes. In contrast, weights have to assigned for traits in MGIDI, to construct the ideotype, to select the genotypes closer to ideotype based on the scores. Among the selected accessions, 390 and 50 had smallest contributions for factor 1, inferring the superiority of these accessions for PW, APWT, PP and HSW. Similarly, for PL and SP (factor 2), 362 and C2 were identified to be the best among selected ones. However, some of the accessions *viz.,* 192, 354 and C2 selected through MGIDI indirect selection had lower GYP, resulting in reduced SD upon selection.

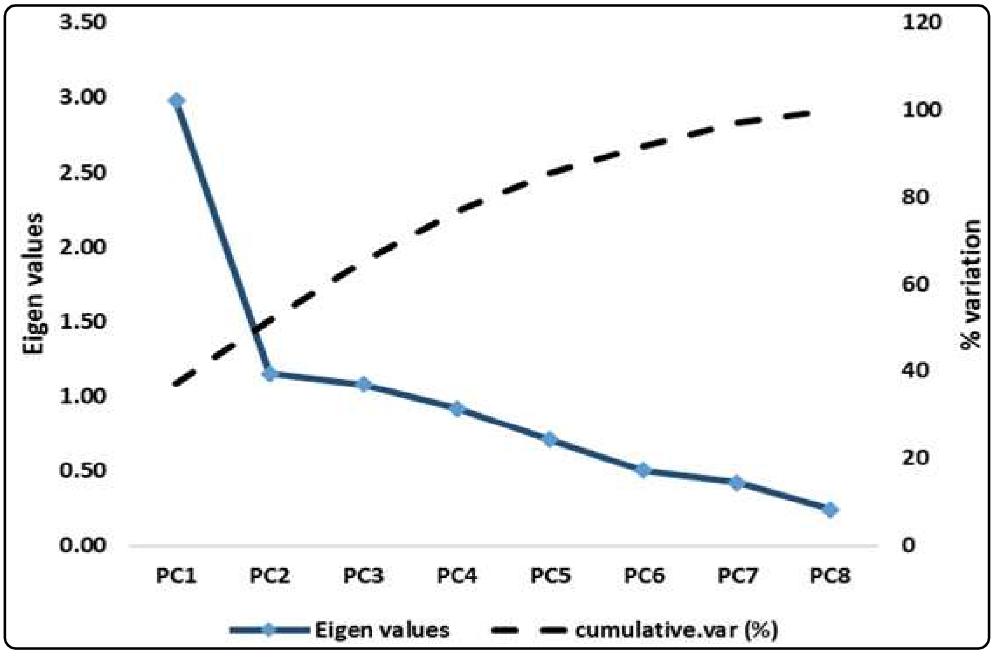

Fig. 2 : Extracted principal components (PCs) along with eigen values and cumulative variation explained

TABLE 5

Rotated factor loadings for traits and communalities extracted from factor analysis

Trait	FA1	FA2	FA3	Communalities	Assigned factor
DFF	-0.26	0.22	0.55	0.42	FA3
PL	-0.53	0.6	-0.07	0.64	FA2
PW	-0.66	0.36	0.1	0.58	FA1
PC	0.1	-0.11	0.88	0.8	FA3
SP	0.12	0.88	0.07	0.8	FA2
APWT	-0.69	0.52	0.12	0.77	FA1
PP	0.67	0.13	0.2	0.46	FA1
HSW	-0.86	0.07	0.07	0.74	FA1

DFF: Days to fifty per cent flowering, PL: Pod length (cm), PW: Pod width (cm), SP: Seeds pod^{-1}, APWT: Average pod weight (g), PP: Pod plant^{-1}, PC: Pods cluster^{-1}, HSW: Hundred seed weight (g), GYP: Grain yieldplant^{-1}; FA1, FA2 and FA3 are factors extracted through PCA

Different indices employed in the study varied in the selection of genotypes and to compare the indices consistent with each other, coincidence index (CI) was estimated (Table 6). Accordingly, CI matrix resulted in identifying SHI and BLPSI, as highly consistent with value of 0.88, wherein eight out nine selected accessions were jointly selected by both of them. Least CI (0.06) was observed among SHI and RS, FAI, MGIDI and also BLPSI and RS, FAI, MGIDI. This highlights the diversity among the employed indices in selecting accessions. Higher values of CI were observed between weight-based indices (SHI and BLPSI) and between Factor analysis-based indices *viz.,* FAI and MGIDI. High CI among such indices directs the researcher to use any of those indices, if not others, to select best genotypes to avoid redundancy. RS recorded highest CI with DS, highlighting the efficiency of the former in selecting the best ones. This could possibly due to the fact that ranking of genotypes were directly based on phenotypic values, which contribute to the yield ultimately (Pathy *et al.,* 2022 and Vinu *et al.,* 2024).

TABLE 6

Matrix of Coincidence index (CI) among evaluated selection indices

	FAI	MGIDI	SHI	BLPSI	ESIM	DS
RS	0.53	0.41	0.06	0.06	0.30	0.41
FAI		0.65	0.06	0.06	0.18	0.30
MGIDI			0.06	0.06	0.06	0.18
SHI				0.88	0.18	0.18
BLPSI					0.18	0.30
ESIM						0.18

RS: Rank sum, FAI: Factor analysis index, MGIDI: Mean Genotype Ideotype Distance Index, SHI: Smith Hazel Index, BLPSI: Best linear Phenotypic selection index, ESIM: Eigen selection index method, DS: Direct selection

Fixed selection intensity of 5 per cent resulted in identification of nine genotypes per index, making a total of 54 selections across six indices. As discussed with respect to CI, certain genotypes were selected by more than one index, thereby downsizing 54 selections to 28 unique genotypes. Frequency of these 28 genotypes being selected by more than one index is depicted in the graph (Fig. 3). Eight of these 28 genotypes (indicated by * in the graph) were identified as GYP trait specific accessions based on DS. The accession 362 (EC107163) was selected by highest number of five different indices, whereas 11 accessions were selected by only one of the indices. This genotype was also selected through DS.

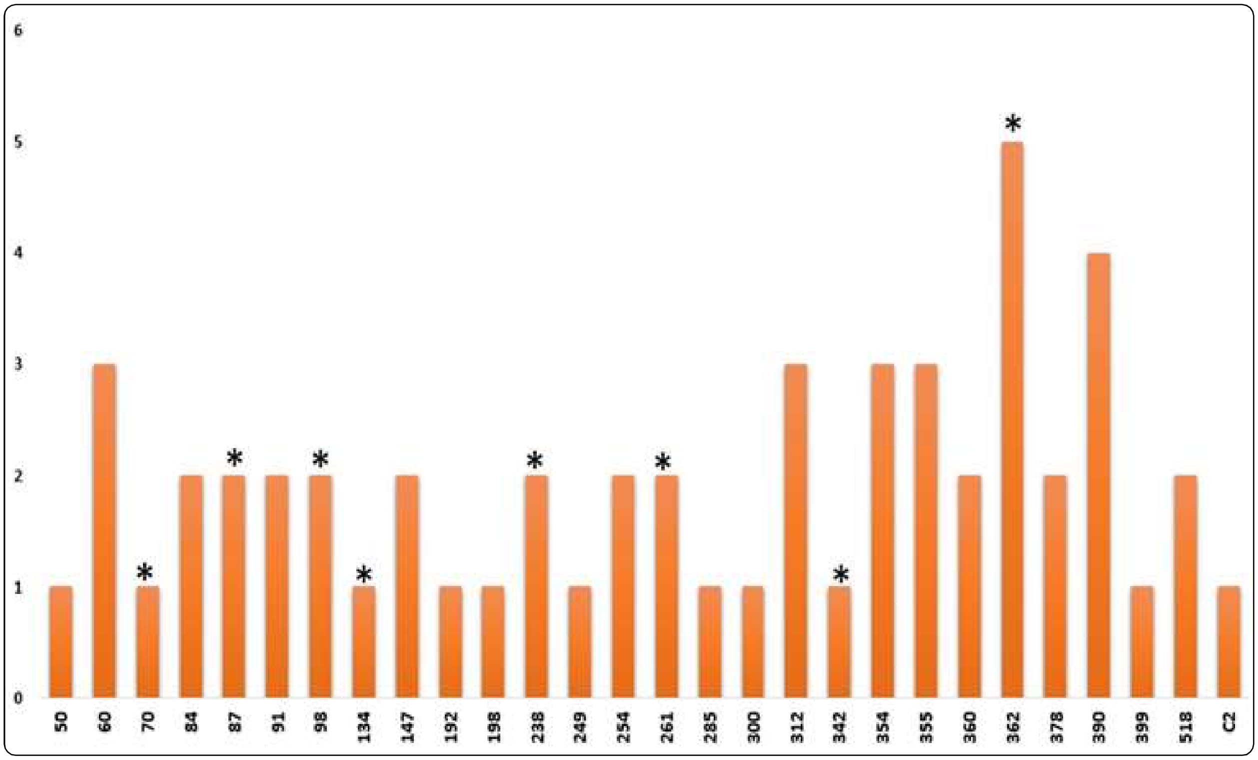

Fig. 3 : Frequency of promising cowpea accessions identified through indirect selection six different selection indices

Accession number	Accession	Accession number	Accession	Accession number	Accession	Accession number	Accession
50	EC240665	134	IC68786	261	IC400103	360	EC-738122
60	EC240841	147	IC202791	285	IC536609	362	EC107163
70	EC240983	192	IC560918	300	NR-18-75	378	EC724745
84	EC244025	198	IC590841	312	IC-53351	390	EC738131
87	EC244057	238	IC334368	342	EC472282	399	EC738260
91	EC244065	249	IC372720	354	EC-724805	518	EC724805
98	EC244116	254	IC383461	355	EC-738083	C2	DC-15

*Indicates trait specific accessions for GYP through direct selection

Another genotype 390 (EC738131) follows 362, being selected by four indices, but was not a part of GYP trait specific accessions.

A total of 172 genotypes (163 germplasm accessions and nine checks) were evaluated for nine agronomic traits in *rabi* 2022 and promising accessions for each of the traits were identified. Genotype 362 (EC107163) found to be promising for three traits *viz.,* SP, PP, GYP. Selection indices deployed as indirect selection for all the component traits except yield, proved BLPSI as best index for selecting genotypes for GYP based on its relative selection efficiency. Accessions selected through BLPSI also had low standard deviations for GYP. Five selection indices included the accession 362 in their selection, which was also selected through DS. This accession could offer potential parental source for future breeding programs.

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