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Extent and pattern of genetic diversity for morpho-agronomic traits in Ethiopian highland pulse landraces: I. Field pea (*Pisum sativum* L.)

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Abstract

An experiment was conducted in 2001 at Holetta and Kulumsa, Ethiopia, to study the extent and pattern of genetic diversity in Ethiopian field pea (*Pisum sativum* L.) landraces. One hundred forty-eight germplasm accessions were grown in an alpha lattice design with 2 replications. Data on 12 traits were collected and analyzed. Differences among the accessions were significant for most of the traits (except number of seeds/pod) at each location even though differences pooled over location were mostly non-significant. The accessions were grouped into five clusters of different sizes. Accessions from the southern part of the country (Arsi) distributed overall clusters while those from the northern half (North and South Wello, North Gonder and North Shewa) fell into clusters C_1 to C_3. Cumulative effects of a number of characters dictated differentiation of the accessions into clusters. There was no definite relationship between geographic diversity and genetic diversity as overlapping was encountered in clustering pattern among accessions from different parts of the country. Accessions from different regions might have similar genetic background and those from the same origin might also have different genetic background. Therefore, geographic diversity should not necessarily be used as an index of genetic diversity and parental selection should be based on a systematic study of genetic diversity in a specific population. Genetic distances among most of the clusters were significant that crosses between parents selected out of them are expected to generate desirable genetic recombination. Selection should also consider the special advantages of each cluster and each accession within a cluster. Future germplasm collection, conservation and breeding efforts should focus not only on inter-regional diversity but also on intra-regional diversity.

Introduction

The center of origin for field pea (*Pisum sativum* L.) is believed to stretch from the Mediterranean to the Central Asia as well as in the high elevations of Ethiopia (Davies 1976; Hagedorn 1984). However, the exclusive origin and primary source of diversity of the crop is not well known (Davies 1976). The crop is known to grow in Ethiopia since antiquity (Dawit et al. 1994) and the country is considered as one of the centers of diversity (Hagedorn 1984; Hailu et al. 1991). The species *P. sativum* is known to dominate the production system in Ethiopia even though wild and primitive forms are also known to exist in the high elevations of the country (Hagedorn 1984; Amare and Adamu 1994).

Knowledge of the extent and pattern of genetic diversity is very crucial to develop effective breeding and germplasm collection and conservation strategies (Bartual et al. 1985; Dale et al. 1985; Rezai and Frey 1990; Jaradat 1991; Demissie and Bjørnstad 1997). Crosses between parents with maximum genetic divergence would be more responsive to improvement since they are likely to produce higher heterosis and desirable genetic recombination and segregation in their progenies (Arunachalam and Bandyopadhyay 1984; Reddy 1988; Singh 1990; Wallace and Yan 1998; Chahal and Gosal 2002). Crosses between parents with high inter-parental diversity may also help to develop varieties with broad genetic base (Russell 1978; Chandel and Joshi 1983; Singh 1990; Gemechu et al. 1997) and raises the yield ceilings imposed by a narrow genetic base (Chandel and Joshi 1983).

Landraces have considerable breeding values as they contain valuable adaptive genes to different circumstances (Nechit et al. 1988; Ceccarelli 1994; Bunder et al. 1996; Chahal and Gosal 2002). A large number of field pea landraces have been collected from the most important production complexes in Ethiopia (Dawit et al. 1994). Even though it is generally believed that field pea in general (Hagedorn 1984) and the Ethiopian landraces in particular (Harlan 1969; Van der Maesen et al. 1988; Engels and Hawkes 1991) have tremendous genetic diversity in both domesticated and wild relatives (Edwards 1991), the extent and pattern of genetic diversity in Ethiopian landraces is not yet systematically studied (Hailu et al. 1991).

Geographical separation with physical barriers and genetic barriers to crossablity is believed to give rise to genetic diversity among genetic materials (Singh 1990). However, whether differences in geographic origin (source) necessarily imply genetic distance in parental selection for hybridization is still a matter of some controversy. Joshi and Dhawan (1966) suggested the concept that geographic diversity may serve as an index of genetic diversity in parental selection. Others argue that genetic divergence was not apparently related to geographic diversity in some crops (Durga Prasad et al. 1985; Sindhu 1985; Nadaf et al. 1986; Rezai and Frey 1990; Katule et al. 1992). If the former holds true, it is logical to expect that the physical barriers might have resulted in distinct genetic diversity of field pea accessions growing in different parts of Ethiopia as the country of great geographical diversity with high and rugged mountains (EMA 1988). The objectives of this experiment were, therefore, to estimate the extent and pattern of genetic diversity among the Ethiopian field pea landraces, the relative contribution of various morpho-agronomic traits to the total diversity in the accessions and to study the association of geographic origin with genetic diversity.

Materials and methods

One hundred forty-eight random samples of field pea accessions collected in collaboration with the Institute of Biodiversity Conservation and Research (IBCR) from the most important production complexes of Ethiopia were considered in this study (Figure 1). The materials were collected from different agro-ecologies varying in altitude, rainfall, temperature and soil type. The list of the test accessions is given along with their geographical origins in Table 1. The accessions were evaluated at two locations, Holetta (09°00′ N, 38°30′ E) and Kulumsa (08°01′ N, 39°09′ E) in Ethiopia during the year 2001. Holetta, with an altitude of 2400 m above sea level (m asl) and average annual rainfall of 1000 mm, represents the major high-altitude production areas of the country while Kulumsa, with an altitude of 2200 m asl and average annual rainfall of 800 mm, represents the major mid-altitude production areas. Holetta is characterized by a red-brown clay soils with a pH 5.7 and Kulumsa by a dark-clay loam soil with a pH 6.0. The trials were laid down in an alpha lattice design with two replications. Undamaged clean seeds of each accession selected to a reasonably uniform size by hand sorting were planted on the seedbeds. Each plot consisted of two rows 4 m long with a spacing of 20 cm between rows and 5 cm between plants. The trial was managed following research recommendations specific to each location. Data were collected either on plot basis or from randomly selected 10 plants on:

1. days to flowering,
2. days to maturity,
3. grain filling period (days to maturity minus days to flowering),
4. plant height (cm),
5. ascochyta blight (*Mycosphaerella pinodes* Lib.) (1–9 scale),
6. number of nodes/plant,

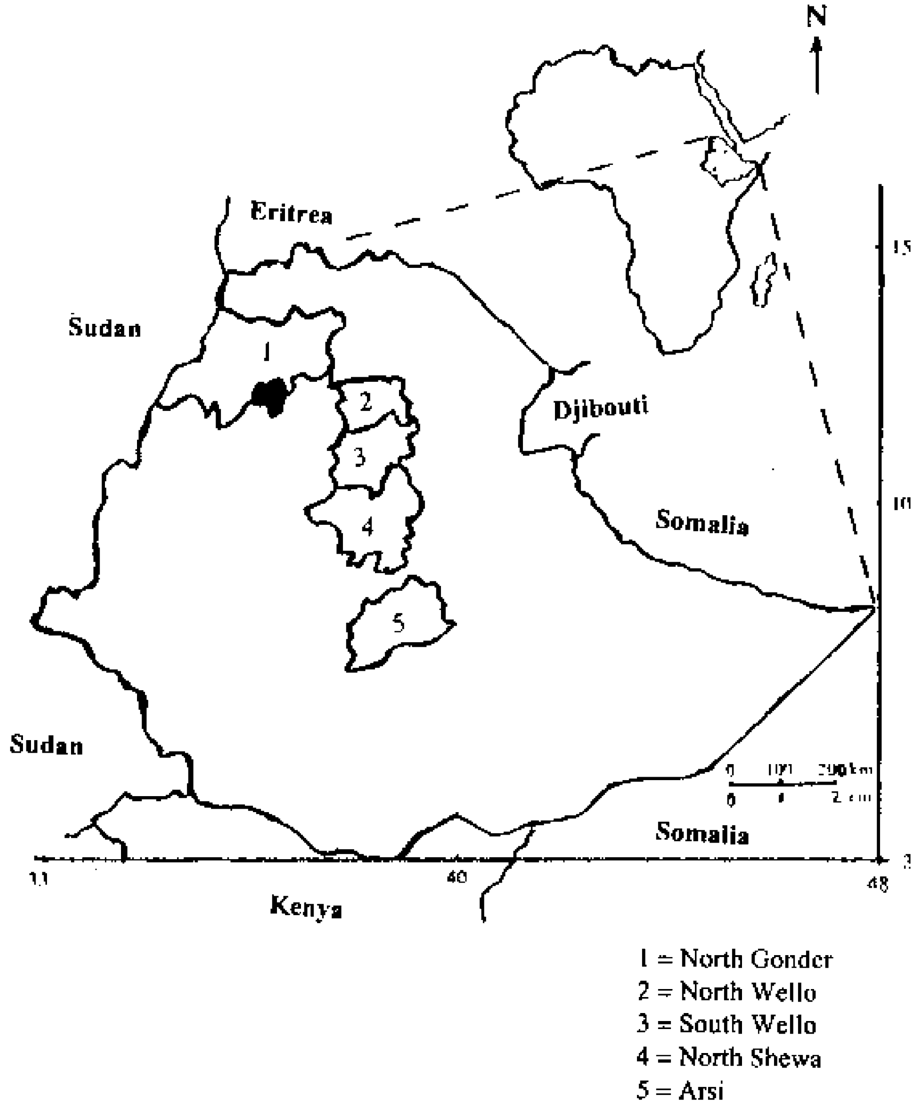

Figure 1. Map of Ethiopia showing geographical locations from where the accessions of were collected (all boundaries are approximate and not official).

7. number of podding nodes/plant,
8. number of pods/podding nodes,
9. number of pods/plant,
10. number of seeds/pod,
11. 1000 seed weight (g),
12. grain yield/plot (g).

The SAS computer package (SAS Institute 1996) was used to test for presence of outliers and normality of residuals. The total variability for each trait was quantified using pooled analyses of variance over location using the following model:

$$p_{itjk} = \mu + l_t + r_{i(t)} + b_{j(i)(t)} + g_k + (gl)_{kt} + e_{itjk}$$

where p_{itjk} is the phenotypic observation in the i^{th} replication, t^{th} location, j^{th} incomplete block within replication i and location t and from the k^{th} accession, μ is the grand mean, l_t is the effect of location t, $r_{i(t)}$ is the effect of replicate i within location t, $b_{j(i)(t)}$ is the effect of the incomplete block j within replication i and location t, g_k is the effect of the k^{th} accession, $(gl)_{\text{kt}}$ is the effect of interaction of the k^{th} accession and the t^{th} location and e_{itjk} is the random error.

Table 1. Origin of accessions.

SN[1]	Accession	Zone[2]	Locality	Altitude (m asl)
1	FPColl-30/99	N.W.	Betehor	2800
2	FPColl-31/99	N.W.	Betehor	2810
3	FPColl-32/99	N.W.	Yewetet	2800
4	FPColl-33/99	N.W.	Yewetet	2800
5	FPColl-34/99	N.W.	Kon	2820
6	FPColl-35/99	N.W.	Yedogit Michael	2820
7	FPColl-36/99	N.W.	Woteye Giorgis	2400
8	FPColl-37/99	N.W.	Yekorit	2350
9	FPColl-38/99	N.W.	Terara	2460
10	FPColl-39/99	N.W.	Woteye Giorgis	2590
11	FPColl-40/99	N.W.	Gurba Giorgis	2700
12	FPColl-41/99	N.W.	Mushmender	Farm store
13	FPColl-42/99	N.W.	Chegoma	2820
14	FPColl-43/99	N.W.	Chinga	2850
15	FPColl-44/99	N.W.	Yilana	2900
16	FPColl-45/99	N.W.	Boda	2960
17	FPColl-47/99	N.W.	Goshmeda	2490
18	FPColl-48/99	N.W.	Goshmeda	2200
19	FPColl-49/99	N.W.	Goshmeda	2200
20	FPColl-50/99	S.W.	Gishen	Farm Store
21	FPColl-51/99	S.W.	Kundi	Farm Store
22	FPColl-52/99	S.W.	Ababoru	Market
23	FPColl-53/99	S.W.	Grume	2870
24	FPColl-54/99	S.W.	Tenta Michael	2780
25	FPColl-55/99	S.W.	Gendit	2800
26	FPColl-57/99	S.W.	Godo (Chacha)	Farm store
27	FPColl-98/99	N.G.	Gonder Zuria	2500
28	FPColl-99/99	N.G.	Gonder Zuria	2500
29	FPColl-100/99	N.G.	Degoma	2500
30	FPColl-101/99	N.G.	Gind Metaya	2300
31	FPColl-102/99	N.G.	Ambezu	2660
32	FPColl-103/99	N.G.	Ambezu	2660
33	FPColl-104/99	N.G.	Koseye	2800
34	FPColl-105/99	N.G.	Wondgate	2900
35	FPColl-106/99	N.G.	Amba Giorgis	2840
36	FPColl-107/99	N.G.	Hiywet bademа	2700
37	FPColl-108/99	N.G.	Baldergie	2600
38	FPColl-110/99	N.G.	Workdemo	2680
39	FPColl-111/99	N.G.	Gedebeye	2700
40	FPColl-112/99	N.G.	Chemelgie	2640
41	FPColl-114/99	N.G.	Shimelako	2580
42	FPColl-115/99	N.G.	Kuara	2600
43	FPColl-116/99	N.G.	Tentanie	2680
44	FPColl-117/99	N.G.	Dildiye	2800
45	FPColl-119/99	N.G.	Kumbel	2960
46	FPColl-120/99	N.G.	Miljgebsa	3000
47	FPColl-21/99	N.G.	Aman amba	3100
48	FPColl-122/99	N.G.	Afaf	2700
49	FPColl-123/99	N.G.	Limalimo afaf	2700
50	FPColl-125/99	N.G.	Arba Tensa	2660
51	FPColl-126/99	N.G.	Dequa	2600
52	FPColl-127/99	N.G.	Abay	2500
53	FPColl-128/99	N.G.	Chenchit	2540
54	FPColl-129/99	N.G.	Birkach	2500
55	FPColl-130/99	N.G.	Selamgie	2300
56	FPColl-13 1/99	N.G.	Selamgie	2300
57	FPColl-132/99	N.G.	Woken	2620
58	FPColl-182/99	N.S.	Zanjera	2740
59	FPColl-183/99	N.S.	Kinbo Ager	2800
60	FPColl-184/99	N.S.	Arathside	2800
61	FPColl-185/99	N.S.	Keyit	2840
62	FPColl-186/99	N.S.	Aba mute	2900
63	FPColl-187/99	N.S.	Liymush	2900
64	FPColl-188/99	N.S.	Gudo Beret	2960
65	FPColl-189/99	N.S.	Ezawiene	2940
66	FPColl-190/99	N.S.	Kuromider	2780
67	FPColl-19 1/99	N.S.	Tiftef Dingay	2890
68	FPColl-192/99	N.S.	Bash	2820
69	FPColl-193/99	N.S.	Kitela	2820
70	FPColl-194/99	N.S.	Angawa	2840
71	FPColl-195/99	N.S.	Emego	2820
72	FPColl-196/99	N.S.	Gedembo	2820
73	FPColl-197/99	N.S.	Chiroche Amba	2820
74	FPColl-198/99	N.S.	Menta Debir	2920
75	FPColl-199/99	N.S.	Hana Mariam	2960
76	FPColl-200/99	N.S.	Gragne	3140
77	FPColl-201/99	N.S.	Begochgat	3100
78	FPColl-202/99	N.S.	Nech Ager	2940
79	FPColl-203/99	N.S.	Debremismak mariam	2900
80	FPColl-204/99	N.S.	Seladingay	2880
81	FPColl-205/99	N.S.	Gudoberet	2860
82	FPColl-206/99	N.S.	Hausini amba	2840
83	FPColl-207/99	N.S.	Wusha wishi	2860
84	FPColl-208/99	N.S.	Debel	3000
85	FPColl-209/99	N.S.	Adgo Ager	3000
86	FPColl-210/99	N.S.	Kura mariam	3000
87	FPColl-211/99	N.S.	Ankober	2940
88	FPColl-212/99	N.S.	Welie Deneba	2940
89	FPColl-213/99	N.S.	Mehal Derie	2900
90	FPColl-214/99	N.S.	Aleyo	2840
91	FPColl-215/99	N.S.	Lemi	Market
92	FPColl-216/99	N.S.	–	–
93	FPColl-217/99	N.S.	–	–
94	FPColl-30/00	Arsi	Dosaha	2490
95	FPColl-31/00	Arsi	Aleltu shala	2590
96	FPColl-32/00	Arsi	Temensa gugesa	2520
97	FPColl-33/00	Arsi	Digelu Kidame	2600
98	FPColl-34/00	Arsi	Digelu bora	2680
99	FPColl-35/00	Arsi	Digelu bora	2660
100	FPColl-36/00	Arsi	Digelu bora	2680
101	FPColl-37/00	Arsi	Lemu Eddo	2800
102	FPColl-38/00	Arsi	Gobesa	2380
103	FPColl-39/00	Arsi	Gobesa	2380
104	FPColl-40/00	Arsi	Gobesa	2380
105	FPColl-41/00	Arsi	Biriti farachu	3000
106	FPColl-42/00	Arsi	Guji	2800
107	FPColl-43/00	Arsi	Guji	2800
108	FPColl-44/00	Arsi	Shashe	2900
109	FPColl-45/00	Arsi	Chofra Debora	2960
110	FPColl-46/00	Arsi	Gedeb asasa	2740
111	FPColl-47/00	Arsi	Gedeb asasa	2450
112	FPColl-48/00	Arsi	Shire bole	2730
113	FPColl-49/00	Arsi	Shire kombolcha	2820
114	FPColl-50/00	Arsi	Shire aragesa	2840
115	FPColl-51/00	Arsi	Fajimeti	2310

Table 1. Continued

SN[1]	Accession	Zone[2]	Locality	Altitude (m asl)
116	FPColl-52/00	Arsi	Munesa	2200
117	FPColl-53/00	Arsi	Tulujebi	1520
118	FPColl-54/00	Arsi	Tulubego	2700
119	FPColl-55/00	Arsi	Efa lode	2680
120	FPColl-56/00	Arsi	Jeyna barbuko	2380
121	FPColl-57/00	Arsi	Jeyna barbuko	2360
122	FPColl-58/00	Arsi	Gado gedemsa	2340
123	FPColl-59/00	Arsi	Sibe meraro	2390
124	FPColl-60/00	Arsi	Hiraro sibe	2400
125	FPColl-61/00	Arsi	Endeto	2420
126	FPColl-62/00	Arsi	Kako	2410
127	FPColl-63/99	Arsi	Endeto town	2400
128	FPColl-64/00	Arsi	Denbel Kilisa	2400
129	FPColl-65/00	Arsi	Sibe Meraro	2390
130	FPColl-66/00	Arsi	Jeyna	2330
131	FPColl-67/00	Arsi	Juyna	2330
132	FPColl-68/00	Arsi	Bulkobalkesa	2400
133	FPColl-69/00	Arsi	Marfogora gora	2400
134	FPColl-70/00	Arsi	Marfogora	2420
135	FPColl-71/00	Arsi	Malkicho	2420
136	FPColl-72/00	Arsi	Bamo genet	2440
137	FPColl-73/00	Arsi	Darole	2420
138	FPColl-74/00	Arsi	Bile	2400
139	FPColl-75/00	Arsi	Bile	2400
140	FPColl-76/00	Arsi	Askalo	2420
141	FPColl-77/00	Arsi	Jedda	2450
142	FPColl-78/00	Arsi	Jedda	2450
143	FPColl-79/00	Arsi	Jedda	2450
144	FPColl-80/00	Arsi	Jidda Jim	2440
145	FPColl-81/00	Arsi	Jida town	2460
146	FPColl-82/00	Arsi	Wadogomsa	2450
147	FPColl-83/00	Arsi	Wadogomsa	2500
148	FPColl-84/00	Arsi	Kurofta	2500

[1]SN = Serial number.[2]N.W = North Wello, S.W. = South Wello, N.G. = North Gonder and N.S. = North Shewa.

Clustering of accessions was performed by average linkage method of SAS software using eleven traits that were found to be significantly different among the accessions at least at one of the locations. The pseudo *F* statistic and the pseudo t^2 statistic were examined to decide the numbers of clusters. Genetic distances between clusters as standardized Mahalanobis's D^2 statistics were calculated as:

$$D^2_{ij} = (xi - xj)'\mathrm{cov}^{-1}(xi - xj)$$

where $D^2{}_{ij}$ is the distance between cases *i* and *j*; *xi* and *xj* is the vectors of the values of the variables for cases *i* and *j*; and cov^{-1} is the pooled within groups variance–covariance matrix. Principal components based on correlation matrix were calculated using the same software as in clustering. The D^2 values obtained for pairs of clusters were considered as the calculated values of Chi-square (χ^2) and were tested for significance both at 1% and 5% probability levels against the tabulated value of χ^2 for '*P*' degree of freedom, where *P* is the number of characters considered (Singh and Chaudhary 1985).

Results and discussion

Analysis of variance revealed highly significant differences ($P < 0.01$) among the accessions for all characters but number of seeds/pod at both locations. This indicates that there was adequate variability among the accessions for most of the traits at both locations. However, pooled differences among the accessions were mostly non-significant (Table 2).

The accessions were grouped into five diversity classes (Table 3 and Figure 2), different members within a cluster being assumed to be more closely related in terms of the traits under consideration with each other than those members in different clusters. Similarly, members in clusters with non-significant distance were assumed to have more close relationships with each other than they are with those in significantly distant clusters. Cluster C_1 was the largest with 93 accessions or constituting closer to 63% of the total population followed by cluster C_2 with 42 accessions or almost 28% of the total population. These clusters constituted intermediate accessions for yielding potential, the least for seed size and number of podding nodes/plant and relatively more susceptible to ascochyta blight. Clusters C_3 constituted 11 (7%) accessions while clusters C_4 and C_5 had one accession each. Clusters C_3 and C_5 constituted the best yielding accessions with medium to large seed sizes. Cluster C_4 constituted a single accession inferior for grain yield and number of pods/node and the shortest for plant height. In a practical sense, days to flowering and maturity and ascochyta blight scores of the clusters were fairly closer to the grand mean with only slight deviations (Table 4).

The pairwise generalized squared distances (D^2) among the five clusters is presented in Table 5. The maximum distance was found between clusters C_4 and C_5(D^2 = 333). The second most divergent clusters were cluster C_2 and cluster C_5(D^2 = 180).The genetic divergence between clusters C_3 and C_4(D^2 = 157), C_1 and C_5(D^2 = 103), C_1 and

Table 2. Mean square, significance and CV% of morpho-agronomic characters and disease score of field pea germplasm.

Trait	Mean square (CV%)		
	Holetta	Kulumsa	Combined
Days to flowering	100.89**(2.60)	82.03**(5.04)	6.71$^{\text{NS}}$(4.04)
Days to maturity	71.43*(5.36)	19.89**(2.33)	27.21$^{\text{NS}}$(4.45)
Grain filling period	66.03**(4.67)	50.96**(3.38)	12.79$^{\text{NS}}$(6.30)
Plant height	316.56**(8.41)	344.20**(9.82)	252.45$^{\text{NS}}$(9.44)
Ascochyta Blight	0.75**(13.56)	0.40$^{\text{NS}}$(22.12)	0.49$^{\text{NS}}$(19.15)
Number of nodes/plant	4.76**(8.98)	313.09$^{\text{NS}}$(28.32)	150.93$^{\text{NS}}$(32.01)
No. of podding nodes/plant	1.06$^{\text{NS}}$(11.13)	34.21**(36.77)	16.58**(31.04)
No. of pods/podding nodes	0.32*(25.16)	0.23*(31.65)	0.22**(28.03)
No. of pods/Plant	3.38**(10.87)	49.73$^{\text{NS}}$(38.30)	29.39**(32.16)
No. of seeds/pod	0.28$^{\text{NS}}$(11.74)	0.65$^{\text{NS}}$(19.89)	0.40$^{\text{NS}}$(15.32)
1000 seed weight (g)	192.66**(5.72)	173.52**(9.62)	84.91$^{\text{NS}}$(7.62)
Grain yield/plot (g)	28477.23 $^{\text{NS}}$(29.37)	10942.74**(35.00)	24286.58**(35.32)

NS, *, ** indicates non-significant, significant and highly significant differences, respectively.

Table 3. Grouping of 148 field pea genotypes into different diversity classes.

Cluster	Number of accessions	Accessions included (SN)	Origin
C_1	93	[2,3,5,6,7,8,10,11,12,14,15,17,19]	North Wello
		[20,21,23]	South Wello
		[27,29,30,32,33,34,36,39,41,42,43,44,47,48,49,51,57]	North Gonder
		[58,59,60,61,62,64,66,67,68,69,70,71,72,76,77,79,80,81,82,83,88,89,90,91]	North Shewa
		[94,97,100,101,102,103,104,105,107,111,113,115,117,118, 119,120,121,122,123,124,125,126,128,129, 130,131,132,134, 137,138,140,141,144,145,146,147]	Arsi
C_2	42	[4,9,16,18]	North Wello
		[22,24,25,26]	South Wello
		[28,31,35,37,38,40,45,50,53,55,56]	North Gonder
		[65,73,74,75,78,85,86,87,92,93]	North Shewa
		[95,98,99,106,108,109,112,114,116,127,135,139,142]	Arsi
C_3	11	[1,13]	North Wello
		[46,52,54]	North Gonder
		[63,84]	North Shewa
		[96,110,143,148]	Arsi
C_4	1	[133]	Arsi
C_5	1	[136]	Arsi

SN = Serial number.

$C_4(D^2 = 86)$, C_2 and $C_4(D^2 = 50)$, C_2 and $C_3(D^2 = 48)$ and C_3 and $C_5(D^2 = 46)$ were also highly significant ($P < 0.01$). Maximum genetic recombination and variation in the subsequent generation is expected from crosses that involve parents from the clusters characterized by maximum distances. Crosses between accessions selected from these clusters are, therefore, expected to provide relatively better genetic recombination and segregation in their progenies. However, the selection of parents should also consider the special advantages of each cluster and each accession within a cluster depending on the specific objectives of hybridization as suggested by others (Singh 1990; Chahal and Gosal 2002). In addition to genetic diversity, parents should express the optimum level of all the desired component traits for accumulating yield, should be resistant to biotic and abiotic environmental stresses and they should fulfill quality parameters required in the target area (Wallace and Yan 1998). Inter-cluster distances were nonsignificant between clusters C_1 and $C_2(D^2 = 11)$ and C_1 and $C_3(D^2 = 13)$, suggesting close relationship among the accessions.

Populations from areas far separated geographically and having complex environment are

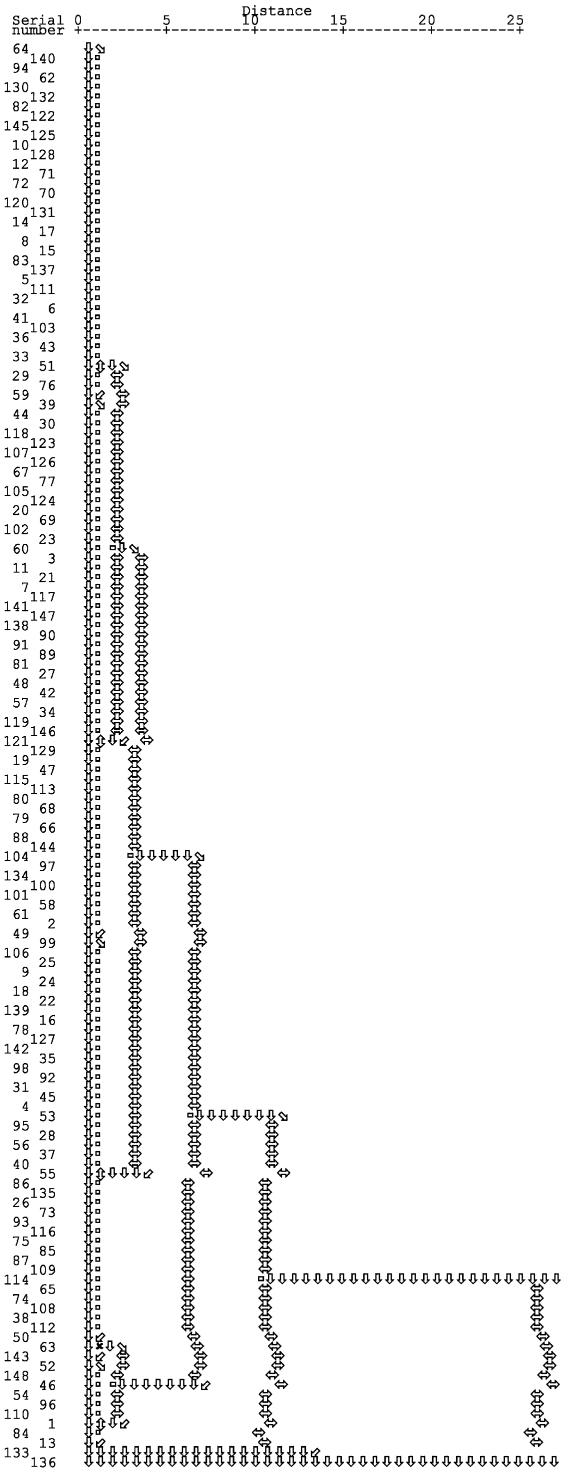

Figure 2. Dendrogram of 148 field pea accessions collected from different agro-ecologies based on average linkage hierarchical cluster analysis between groups.

Table 4. Cluster means for eleven characters in field pea accessions.

Character	Cluster					
	C_1	C_2	C_3	C_4	C_5	Grand mean
Days to flowering	66.8	68.8**	68.5	63.0	60.0*	65.42
Days to maturity	126.6	127.3	128.1**	124.0*	125.0	126.20
Grain filling period	60.0	58.6	59.6*	60.7	64.7**	60.72
Plant height	156.2	157.3	164.5**	124.0*	155.0	151.40
Ascochyta Blight	3.78**	3.75	3.58	3.17	3.67	3.59
No. of nodes/plant	41.5	41.4	43.9	48.9**	38.7*	42.88
No. of podding nodes/plant	10.78	9.93*	11.14	13.70**	13.50	11.81
No. of pods/node	1.39	1.40	1.52**	1.00*	1.25	1.31
No. of pods/plant	14.52	13.16	15.04	16.40	17.20**	15.26
1000 seed weight	117.8	111.9*	119.7	121.0	123.0**	118.68
Grain yield/plot	373.8	286.6	465.2	191.0*	638.0**	390.92

*Lowest value.

** Highest value.

Table 5. Pair wise generalized squared distances (D^2) among one-hundred forty eight field pea accessions in seven clusters.

Cluster	C_1	C_2	C_3	C_4	C_5
C_1	0	11	13	86**	103**
C_2		0	48**	50**	180**
C_3			0	157**	46**
C_4				0	333**
C_5					0

**Indicates highly significant difference ($p < 0.01$)

normally expected to accumulate enormous genetic diversity (Chandel and Joshi 1983). However, the distribution of strains in different clusters did not follow definite pattern with regard to geographical origins in the present case. Some accessions from different regions were found to be closely related regardless of their geographic origin (source) and the rugged nature of the terrain which could have favored isolation among the accessions and, hence, distinct lines of evolution in each region. This could be realized from the overlapping in clustering pattern among accessions from different parts of the country. In most of the cases, accessions from different places of origin fell into the same clusters. For instance, clusters C_1 and C_2 constituted accessions from all regions and cluster C_3 accessions from all regions except those from South Wello. However, most of accessions from the northern half of the country (North Wello, South Wello, North Gonder and North Shewa) showed a tendency to fall into clusters C_1 and C_2 which were non-significantly distant (Tables 3 and 6). This agrees with the report by Singh and Tripathi (1985) who studied genetic diversity in 100 field pea accessions collected mostly from India and noted that there was no clear interrelationship between geographic origin and genetic diversity despite the presence of high intra- and inter-regional diversity among the accessions.

Several possible reasons could be given for the genetic similarity among accessions from different regions. Most of the materials might have originally been introduced from the same source. There could also be a tendency, particularly among resource-poor farmers in marginal areas, of selecting for the same traits of interest like yield stability, resistance to diseases, insects and abiotic calamities and low dependence on the external inputs (de Boef et al. 1996). Although the original sources might vary, the crop might have also been forced to evolve in the same direction by this kind of local breeding for the same targets which may emanate from similar economic, social, cultural and ecological reasons in the area.

Table 6. Clustering pattern of field pea accessions from different origins over seven clusters.

Origin	Number of accessions	No. of accessions in each cluster				
		C_1	C_2	C_3	C_4	C_5
North Wello	19	13	4	2	–	–
South Wello	7	3	4	–	–	–
North Gonder	31	17	11	3	–	–
North Shewa	36	24	10	2	–	–
Arsi	55	36	13	4	1	1

Some accessions from the same origin were also found to scatter over different clusters while others were limited to two or three clusters, indicating that genetic diversity in field pea is not uniformly distributed over the regions. Accessions from Arsi were distributed allover the clusters but in an irregular pattern. The distances between accessions from Arsi origin in clusters C_4 and C_5, C_2 and C_5, and C_1 and C_5 were highly significant that crosses between parents extracted out of them are expected to result in good level of genetic recombination and generate desirable segregants with broad genetic base. This indicates that, unlike in the northern parts of the country, there might be more intra-regional diversity in Arsi as compared to other parts of the country and accessions from the same origin might have different genetic background. This finding dose not concur with the early estimate that more genetic diversity in field pea might rather be located in the northern half of the country (Gojam, Gonder, Shewa and Wello) (Hailu et al. 1991).

It is hardly possible to give precise reasoning for the higher genetic diversity in populations collected from Arsi as opposed to the ones from the northern parts of the country. The materials from Arsi might have originally been introduced from different sources. The crop also might have been forced to evolve in different direction through local breeding for different targets in the same region. Farmers could play important roles in the dynamics of genetic diversity by providing opportunities for hybridization by bringing together geographically and ecologically isolated landraces and selection for desirable agronomic traits (Teshome et al. 1997). Higher genetic diversity in collections from Arsi as compared to those from Welo and Gojam was also reported in barley (Demissie and Bjørnstad 1997).

The results showed that there was high genetic diversity in Ethiopian field pea landraces. Genetic architecture of a population is generally believed to be the result of breeding system, gene flow within and between populations, isolation mechanisms and prolonged selection by various natural and artificial forces (Chandel and Joshi 1983). Ecological environment is believed to be the major force in crop evolution (Spagnoletti Zeuli and Qualset 1987). Therefore, this diversity in Ethiopian field pea could mainly be attributed to diverse agro-climatic conditions in the country as suggested by Harlan (1969). However, there was no definite relationship between geographic diversity and genetic diversity. The concept that geographic diversity could be used as an index of genetic diversity (Joshi and Dhawan 1966) was also not supported by a number of workers in different crops. It is suggested that selection of parents for hybridization need not necessarily be based on geographic diversity but genetic diversity must form the base for parental selection. Not only interregional diversity but also intra-regional diversity should be considered as a useful component in field pea hybridization programs in Ethiopia.

Principal component analysis (PCA) showed that the first five principal components accounted for 80% of the total variation, of which 55% was contributed by the first two principal components (PRIN1 and PRIN2) (Table 7). PRIN1 contributed nearly 38% while PRIN2 contributed about 16% of the total variation. It is normally assumed that characters with larger absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero (Chahal and Gosal 2002). Accordingly, most of the characters individually contributed small effects (± 0.048–0.458) to the total variation and, therefore, the differentiation of the accessions into different clusters was rather dictated by the cumulative effects of a number of characters. However, characters with relatively greater weight in PRIN1 had higher relative contribution to the total diversity and they were the ones that most differentiated the populations.

Conclusions

There is high genetic diversity in the Ethiopian field pea landraces even though it was not uniformly distributed across the regions. Accessions from different regions of origin might be closely related regardless of their geographic origin and accessions from the same regions of origin also might have different genetic background. There was no definite correspondence between geographic origin and genetic diversity. Parental selection should, therefore, not be based on geographic difference but it should rather be made

Table 7. Percentage and cumulative variances and Eigenvectors on the first five principal components for eleven characters in 148 field pea accessions.

Parameter	PRIN1	PRIN2	PRIN3	PRIN4	PRIN5
Eigen value	4.160	1.541	1.154	0.873	0.750
% Variance	38.04	15.50	11.09	8.50	7.21
Cumulative	38.04	53.54	64.64	73.14	80.35
Character	Eigen vectors				
Days to flowering	−0.458	0.121	−0.077	−0.077	0.009
Days to maturity	−0.309	0.018	0.049	0.387	0.509
Grain filling period	0.386	−0.148	0.098	0.323	0.147
Plant height	−0.178	0.328	0.460	−0.273	−0.243
Ascochyta Blight	0.357	−0.208	0.076	−0.165	−0.103
No. of nodes/plant	−0.048	0.475	−0.412	−0.445	0.358
No. of podding nodes/plant	0.402	0.277	−0.234	−0.050	−0.019
No. of pods/plant	−0.250	0.276	−0.180	0.468	−0.607
No. of pods/node	0.343	0.377	−0.309	0.212	−0.151
1000 seed weight	0.177	0.316	0.559	−0.152	−0.077
Grain yield/plot	0.104	0.438	0.316	0.387	0.351

based on systematic assessment of genetic distance in a specific population.

Future collection and conservation missions and breeding programs should focus on effective and efficient exploitation of not only inter-regional diversity but also on intra-regional diversity in the species. Inter-cluster gene recombination of sample accessions drawn from the significantly distant clusters followed by selection should prove to generate agronomically desirable progenies as expected.

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