Genetic Diversity in Nepalese Wheat Cultivars Based on Agro-Morphological Traits and Coefficients of Parentage

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ABSTRACT

Genetic diversity between parents is necessary to derive transgenic segregants from a cross. Coefficient of parentage (COP) and agromorphological traits (AMT) can be used to estimate diversity among cultivars. The pedigrees of 26 bread wheat cultivars were traced back to 77 ancestors and computed coefficient of parentage for all pair-wise combinations. All the cultivars used in the pedigree analysis were evaluated for six agromorphological traits in the National Wheat Research Programme (NWRP), Bhairahawa, Nepal in 1996. Six quantitative variables were used to compute dissimilarity distance matrix. Cluster and principal components analyses were performed on the matrix of COP and AMT values. COP matrix and the matrix based on agromorphological traits were compared. Mexico, India and Nepal were countries of the origin for 26 cultivars. A total of 77 ancestors originated from 22 different countries were used to develop these cultivars. Most of the ancestors were *aestivum* (80.52%) and spring growth habit (64.94%). Maximum dissimilarity was between RR 21 and Annapurna 3 and the most closely related pair was Rohini and BL 1022 based on the AMT. The mean of COP for all cultivars was 0.159 ± 0.256. The highest COP was between Annapurna 3 and Annapurna 2. Other more closely related pairs based on COP were Kalyansona and Annapurna 2, Pasang Lhamu and Annapurna 3, UP 262 and RR 21, Vaskar and Kalyansona, NL 297 and BL 1473, Pasang Lhamu and Annapurna 1. Completely unrelated pairs were L 52 and HD 1982, L 52 and Kalyansona, LR 64 and Kalyansona, Kalyansona and HD 1982, PI and Kalyansona, PI and L 52, RR 21 and HD 1982, RR 21 and Kalyansona, RR 21 and PI. Fifteen ancestors were present in at least about 65% of the cultivars. 17 ancestors had been used more frequently. Five and six clusters were formed based on AMT and COP, respectively. Correlation coefficient between COP and AMT was 0.18 (P = 0.0168). Cultivars surveyed represent a wide range of variation for different areas of origin and adaptation. This genetic variation may be useful for further improvement of wheat and it is necessary to conserve them.

Key words: Agromorphological traits, coefficient of parentage, genetic diversity, Nepalese wheat cultivars

INTRODUCTION

Wheat is the third most important crop after rice and maize in Nepal. During mid 1960s, the yield potential of dwarf high yielding varieties initiated scopes for raising wheat production in the country. Several exotic varieties were obtained through CIMMYT and USAID (NARC 1997). National Wheat Development Programme was established in 1972 to organize the research and the development works on wheat as a commodity. Since then, there have been a great achievement brought out by the consolidated efforts of wheat researchers, extension workers and farmers. So far, there are 35 improved wheat cultivars and 90% of the wheat area is covered by modern wheat cultivars in Nepal (Bhatta et al 2000).

Parental selection is the first step in any plant breeding progarmme. Genetic diversity between parents is necessary to derive transgenic segregants from a cross. One would like to detect genetic diversity among phenotypically superior breeding materials so that appropriate crosses could be produced. Both the potential for long term genetic gain and the reduction of genetic vulnerability may depend on the genetic diversity present in the genetic base. The genetic diversity depends on the number and the diversity of the original ancestors involved in the development of a germplasm pool. Coefficient of parentage (COP) and agromorphological traits (AMT) can estimate diversity among cultivars. COP has also been used to predict breeding behavior of the progeny of crosses (Cowen and Frey 1987), to summarize regional crop diversity (Souza et al 1994) and to identify parents that have contributed to yield improvements (Beer et al 1995). Diversity in wheat breeding programme based on morphological traits and pedigree information was measured by Autrique et al (1996) in durum wheat, Gerdes and Tracy (1994) in sweet corn, Schut et al (1997) in barley. Morphological markers often do not reliably portray genetic relationships because of environmental interactions, epistatic interactions and largely unknown genetic control of the traits (Smith and Smith 1989). The objective of this research was to study the level of diversity present in the Nepalese bread wheat cultivars. Diversity based on agromorphological traits and coefficient of parentage was measured and compared.

MATERIALS AND METHODS

Coefficient of parentage

We examined the pedigrees of 26 cultivars (Table 1) out of 35 released cultivars in Nepal. Due to unavailability of seeds of seven cultivars, these were excluded both in pedigree and agromorphological analyses. Altogether 35 cultivars had been released in Nepal from 1960 to 2001. Most of the cultivars were introduced either from CIMMYT, Mexico or India.

The pedigrees of 26 bread wheat cultivars were traced back to 77 ancestors (Figure 1, Table 2), that had no known relationship each other and computed coefficient of parentage for all pair wise combinations. The source of pedigrees and release dates for cultivars were Jain (1994), NARC (1997), Bland (2001), Skovmand et al (1997), Joshi and Mudwari (2003) and Skovmand et al (2000). The coefficient of parentage between two individuals is defined as the probability that a random allele at a locus in one individual is identical by descent to a random allele at the same locus in other individual. The following assumptions were made in computing coefficients of parentage: a) ancestors are unrelated, b) all cultivars, ancestors and parental lines are homozygous and homogenous, c) a cultivar derived from a cross obtains one-half of its genes from each parent, d) the COP between cultivar or ancestor and a direct selection from that cultivar or ancestor is 0.75, e) the COP between two selections from the same cultivar or ancestor is $(0.75)^2 = 0.56$ and f) the COP between a cultivar and itself is 1.0. Origin and growth habit of ancestors were also reported.

Agromorphological traits

All the cultivars used in pedigree analysis were evaluated for six agromorphological traits in National Wheat Research Programme (NWRP), Bhairahawa, Nepal in 1996. These traits were days to heading, days to maturity, plant height, 1000-grain weight, grain number per spike and grain yield (Table 3).

Data analysis

Six quantitative variables measured were used to compute dissimilarity distance matrix. The data was transferred with the STAND procedure from NTSYS-pc. The standardization procedure reduced the effect of different scales of measurement of different characters. In this transformation, the mean is subtracted from the original value and divided by the standard deviation. The standardized values were used in the SIMINT subroutine of NTSYS-pc to compute a matrix of dissimilarities among all pairs of cultivars with the average taxonomic distance. The computer programme, KIN was used to calculate the COP (Tinker and Mathur 1993).

Table 2. Ancestors of Nepalese wheat cultivars and their origin

SN	Name	Abb†	Origin		Growth habit	Species
			Name	Abb		
1.	21931	21931	ISREAL	ISL	-	AESTIVUM
2.	36896	36896	ARGENTINA	ARG	-	AESTIVUM
3.	8B	8B	INDIA	IND	-	-
4.	9D	9D	INDIA	IND	-	AESTIVUM
5.	AKAGOMUGHI	AGA	JAPAN	JPN	WINTER	AESTIVUM
6.	ALFREDO CHAVES 6.21	AC	BRAZIL	BRA	SPRING	AESTIVUM
7.	B4946.A.4.18.2.IY	B4946	-	-	-	-
8.	BONZA	BZA	COLOMBIA	COL	SPRING	AESTIVUM
9.	BREVOR	BVR	USA	USA	WINTER	AESTIVUM
10.	BUTTON	BUTTON	-	-	-	AESTIVUM
11.	C13	C13	INDIA	IND	SPRING	AESTIVUM
12.	C209	C209	INDIA	IND	SPRING	AESTIVUM
13.	CARIANCA422	CAR422	CHILE	CHL	WINTER	AESTIVUM
14.	CENTENARIO	CTR	BRAZIL	BRA	SPRING	AESTIVUM
15.	CHRIS	CHR	USA	USA	SPRING	AESTIVUM
16.	CLEMENT	CMT	NETHERLANDS	NLD	WINTER	AESTIVUM
17.	CPAN1687	CPAN1687	INDIA	IND	SPRING	AESTIVUM
18.	DAVIS6301	D6301	USA	USA	-	AESTIVUM
19.	EL GAUCHO	ELGAU	ARGENTINA	ARG	SPRING	AESTIVUM
20.	FEDERATION	FR	AUSTRALIA	AUS	SPRING	AESTIVUM
21.	FROCOR	FCR	BRAZIL	BRA	SPRING	AESTIVUM
22.	FUFAN17	FFN	CHINA	CHN	SPRING	AESTIVUM
23.	FURY	FURY	KENYA	KEN	SPRING	AESTIVUM
24.	GAZA	GAZA	EGYPT	EGY	SPRING	DURUM
25.	GABO-AUS	GB	AUSTRALIA	AUS	SPRING	AESTIVUM
26.	GENERAL URQUIZA	GU	ARGENTINA	ARG	SPRING	AESTIVUM
27.	HARD FEDERATION	HF	AUSTRALIA	AUS	SPRING	AESTIVUM
28.	HARDRED CALCATTA	HRC	INDIA	IND	SPRING	AESTIVUM
29.	HOPE	H44	USA	USA	-	AESTIVUM
30.	HYBRID DELHI845	HD845	INDIA	IND	SPRING	AESTIVUM
31.	IUMILLO	IU	USA	USA	SPRING	DURUM
32.	KANRED	KR	USA	USA	WINTER	AESTIVUM
33.	KAVKAZ	KVZ	RUSSIA	RSA	WINTER	AESTIVUM
34.	KENTANA48	KT48	MEXICO	MEX	SPRING	AESTIVUM
35.	KENYA GOVERNER	KGV	KENYA	KEN	SPRING	AESTIVUM
36.	KENYA STANDARD	KS	KENYA	KEN	SPRING	-
37.	KENYA117A	K117A	KENYA	KEN	SPRING	AESTIVUM
38.	KENYA256	K256	KENYA	KEN	SPRING	-
39.	KENYA324	K324	KENYA	KEN	SPRING	-
40.	KENYA350-A-D9-C-2	KAD	KENYA	KEN	SPRING	-
41.	KENYA58	K58	KENYA	KEN	SPRING	AESTIVUM
42.	KHAPLI	KHP	INDIA	IND	SPRING	DURUM
43.	KLEIN ATLAS	KLAT	ARGENTINA	ARG	SPRING	AESTIVUM
44.	KLEIN RENDIDOR	KLRE	ARGENTINA	ARG	SPRING	AESTIVUM
45.	LA ESTANZUELA2787C	LAEST	-	-	-	-
46.	LERMA ROJO	LR	MEXICO	MEX	SPRING	AESTIVUM
47.	MARNE DESPREZ	MD	FRANCE	FRA	WINTER	AESTIVUM
48.	MARROQUI	MRQ	MOROCCO	MAR	SPRING	AESTIVUM
49.	MCMURACHY	MCM	CANADA	CAN	SPRING	AESTIVUM
50.	MIDA-U	MIDA	USA	USA	SPRING	AESTIVUM
51.	MUNDIA	MUNDIA	INDIA	IND	-	-
52.	NAPO	NAPO	COLOMBIA	COL	SPRING	AESTIVUM
53.	NARINO59	NAR59	COLOMBIA	COL	SPRING	AESTIVUM
54.	NAINARI60	NAI60	MEXICO	MEX	-	AESTIVUM
55.	NORIN10	N10	JAPAN	JPN	WINTER	AESTIVUM
56.	NEW PUSA773	NP773	INDIA	IND	SPRING	AESTIVUM
57.	OLESEN'S DWARF	ON	ZIMBABWE	ZIM	SPRING	AESTIVUM
58.	P4160E	P4160E	MEXICO	MEX	SPRING	AESTIVUM
59.	POLYSSU	PSSU	BRAZIL	BRA	SPRING	AESTIVUM
60.	QUINTZEL	QTZ	-	-	-	-

SN	Name	Abb†	Origin		Growth habit	Species
			Name	Abb		
61.	RED FIFE	RF	CANADA	CAN	SPRING	AESTIVUM
62.	RED MACE	RM	GREAT BRITAIN	GBR	WINTER	AESTIVUM
63.	REITI	REITI	-	-	-	-
64.	S339	S339	INDIA	IND	SPRING	AESTIVUM
65.	SANTA ELENA	SE	USA	USA	SPRING	AESTIVUM
66.	SINVALOCHO MA	SCHOMA	ARGENTINA	ARG	SPRING	AESTIVUM
67.	STEINWEDEL	SWD	AUSTRALIA	AUS	SPRING	AESTIVUM
68.	TEZANOS PINTOS PRECOZ	TZPP	ARGENTINA	ARG	SPRING	AESTIVUM
69.	THEW	THEW	AUSTRALIA	AUS	WINTER	AESTIVUM
70.	TIMESTEIN	T	AUSTRALIA	AUS	SPRING	AESTIVUM
71.	TYPE1	TYPE1	PAKISTAN	PAK	-	DURUM
72.	TYPE9	TYPE9	PAKISTAN	PAK	-	AESTIVUM
73.	VERNAL EMMER	VN	RUSSIA	RSA	SPRING	DURUM
74.	WEIQUE	WEIQUE	DUETSCHLAND	DEU	WINTER	AESTIVUM
75.	WILHELMINE	WHM	NETHERLANDS	NLD	WINTER	AESTIVUM
76.	WILLET ERONO	WTE	USA	USA	SPRING	AESTIVUM
77.	YAKTANA54	YT54	MEXICO	MEX	SPRING	AESTIVUM

† Abb, Abbreviation.

Table 3. Agromorphological traits of Nepalese bread wheat cultivars†

SN	Cultivar	DH	DM	Plant height, cm	TGW, g	G SPK^{-1}, N	Grain yield, t/ha
1.	Achyut	89	123	104	42.5	34.8	4.6
2.	Annapurna 1	86	121	97	42.2	61.5	7.6
3.	Annapurna 2	79	118	102	40	54	5.8
4.	Annapurna 3	87	123	98	38.3	64.2	6.2
5.	Annapurna 4	78	116	102	46.2	55.8	5
6.	Bhrikuti	86	123	92	46	50.4	4
7.	BL 1022	77	116	97	45.3	51.2	6.4
8.	BL 1135	72	116	101	43.7	49.4	6.2
9.	BL 1473	68	115	99	50	40	5.8
10.	HD 1982	77	119	91	43.9	41.5	4.6
11.	Kalyansona	86	123	96	36.5	35.9	5.8
12.	Kanti	88	122	122	52.7	59.2	6.2
13.	Lerma 52	88	120	135	41.3	50.8	3.4
14.	Lerma Rojo 64	86	122	108	38.3	46	3.4
15.	Lumbini	77	120	90	47.6	40.1	6.4
16.	Nepal Line 251	77	118	99	46.4	52.6	8
17.	Nepal Line 297	67	116	90	54.7	46.8	5
18.	Nepal Line 30	85	120	106	40.6	56.2	6.4
19.	Pasang Lhamu	81	118	111	38	42	3.5
20.	Pitic 62	90	125	102	43	48	4.5
21.	Rohini	75	115	104	46.9	51.6	6.6
22.	RR 21 (Sonalika)	68	115	91	56.1	37.8	4.4
23.	Siddhartha	74	120	86	44.4	45	7.6
24.	Triveni	79	116	101	47.1	59	4
25.	UP 262	81	119	99	49.9	36.5	5.2
26.	Vaskar	82	119	93	40	59.8	6.2
	Mean	80.11	119.15	100.61	44.67	48.85	5.49
	SD	6.80	2.97	10.35	5.12	8.51	1.30

† DH, Days to heading. DM, Days to maturity. TGW, 1000-grain weight. G SPK^{-1}, Grain number per spike. SD, Standard deviation.

Cluster analysis was performed on the matrix of COP and AMT values using the computer programme NTSYS-pc (Rohlf 1994), which employed the unweighted pair group method of clustering. A dendrograph was drawn based on the cluster analysis. The hierarchical dendrogram of pedigree clusters was formed by successively joining groups with the highest coefficient of parentage. Principal component analysis was performed upon the matrix of relationships among cultivars for reduction of dimensions for analysis of cultivar relationship. This procedure permits the representation of the cultivars as points in Euclidean space.

COP matrix and the matrix based on agromorphological traits were compared by the MXCOMP routine of NTSYS-pc (Rohlf 1994) that uses the normalized Mentel Z statistics. The statistical consideration for these analyses were discussed by Beer et al (1993).

RESULTS AND DISCUSSION

Mexico, India and Nepal are countries of origin for 26 cultivars. In Nepal four cultivars had been originated and the maximum number of cultivars was originated from Mexico. Four cultivars were released in 1997, which is the year of releasing highest number of cultivars. These cultivars were Achyut, Kanti, Pasang Lhamu and Rohini. Lerma 52, first improved cereal variety to be released in the history of cereal breeding in Nepal (Bland 2001) was released in 1960. Shuttling of generation lines during the off-season help to develop wheat cultivars within a short period of time. Due to the varied agroecological diversity of the country, it is possible to plant the same cultivar in both winter and summer seasons.

Most of the recommended cultivars are adapted to plains but there is lack of climatic information in defining plains. Site-specific adapted cultivars are necessary because of diverse climate in Nepal. The trend of releasing many cultivars in the same year for the same domain is not strong strategy of breeding programme. Strategy is better to adopt a system of releasing a cultivar for some specific domain regularly. Cultivars performance may be affected by origin of ancestors, number of ancestors used and times of crossing considered for developing them. Nine parents with 7 times crosses were used for developing Sonalika, which has been a popular cultivar in the country. Therefore, study on origin of ancestors, number of ancestors and crossing frequency may be useful for crop improvement programme and gene conservation.

The level of genetic variation present in gene pools of most important crops has been analyzed by studying the pedigree relationship between cultivars. Kinship coefficients estimation of cultivars of oat (Souza and Sorrells 1989), soybean (Cox et al 1985a), winter wheat (Cox et al 1985b), rice (Dilday 1990) and barley (Martin et al 1991) has shown that a restricted number of ancestral genotypes account for a large proportion of the variation present in released cultivars. Relatively more number of ancestors has been used in developing Nepalese wheat cultivars. A total of 77 ancestors originated in 22 different countries were used to develop 26 cultivars. Highest number of ancestors was from India (Table 2). Ancestors of both *aestivum* and *durum* species having winter, spring and intermediate growth habit indicated the collection of wide gene pool. Most of the ancestors were *aestivum* (80.52%) and spring growth habit (64.94%). CIMMYT (1987) reported that crosses between winter and spring wheat gene pools are far more common and offer a new source of diversity. Landraces from Nepal were not used in developing these cultivars, though 150 landraces have been maintained by National Wheat Research Programme, Bhairahawa. Cultivated landraces of spring and winter type, wild landraces and diploid species of wheat are found in Nepal (Bland 2001) (Mudwari 1999). Gene pool from these landraces along with international gene pool could make to success in developing high yielding cultivars with wide adaptability.

We assumed here that ancestors are not related but some of genes may be similar. Therefore, ancestors' dissimilarity at molecular level, if we could add on COP analysis may be better way of diversity assessment of ancestors used in developing cultivar. If more number of ancestors is used, more genes are conserved in a single cultivar. The number of ancestors used to develop a cultivar ranged from 3 to 23. Diversity on ancestors with respect to growth habit and species was low, it indicates that these 26 cultivars may have also narrow diversity on these aspects. However, there are possibility of increasing diversity through mutation and transgressive segregation,. Similarly, the number of origin country may not be good indicator of diversity rather geographic differences among these countries may be better way to discuss about variation present in released cultivars.

Agromorphological traits (AMT)

The AMT showed great variation among these cultivars (Table 3). Annapurna-1 was the highest grain yielder followed by Siddhartha and Lerma 52 and LR 64 were lower yielder. Siddhartha was also the most dwarf genotype. PI matured late and BL 1473, Rohini and RR 21 were early maturing cultivars. Developing cultivars possessing desired period of maturity, height and yield seemed possible using these gene pools. Relative genetic dissimilarities based on AMT are given in Table 4. These values were the standardized relative genetic dissimilarity coefficients. Maximum dissimilarity was observed between RR 21 and Lerma 52. Other more distantly related cultivars were RR 21 with Annapurna 2, Kanti and Siddhartha with L 52; NL 297 with Annapurna 3 and L 52, and L 52 with BL 1477. The most closely related pair was Rohini and BL 1022. Others closely related pairs were Triveni and Annapurna 4, Rohini and BL 1135 and BL 1135 and BL 1022. Clustering by AMT largely reflected the differences in days to maturity, plant height and grain yield. Souza and Sorrells (1991a) showed that relationships based on quantitative traits of oats revealed a distribution of genotypes based on days to heading. Five distinctive clusters were identified (Figure 1). Clusters 1 and 2 included all the cultivars except Kanti, L 52, RR 21, BL 1473 and NL 297. Cluster 1 included mostly late maturing and medium grain yielding cultivars. Tall were grouped in clusters 4 and 5.

Variation in days to heading and days to maturity was low in compared to other agromorphological traits. These six traits are agronomically important and we can relate these traits to other findings. Because of environment sensitive traits, addition of other single gene governed traits ie morphological markers in such study may be more appropriate and easy to interpret. Dissimilarity value ranged from 0.361 to 2.607 based on AMT. The highest value between RR 21 and L 52 was attributed due to variation in plant height, 1000-grain weight and grain number. Similarly, the least value between Rohini and BL 1022 was due to similarity in days to heading, maturity, 1000-grain weight, grain number and grain yield. Diversity values (Table 4) and cluster groups (Figure 2) may be useful for selecting parental materials from these cultivars and developing conservation strategy.

Coefficient of parentage (COP)

The COP for all cultivars is given in Table 5. The mean of COP for all cultivars was 0.159 ± 0.256 and ranged from 0.000 to 0.603. The highest COP was between Annapurna 3 and Annapurna 1 ie these are the most closely related. Other more closely related pairs based on COP were Kalyansona and Annapurna 2, NL 297 and BL 1473, Pasang Lhamu and Annapurna 1, Pasang Lhamu and Annapurna 3, UP 262 and RR 21, and Vaskar and Kalyansona. Completely unrelated pairs were Kalyansona and HD 1982, L 52 and HD 1982, Kalyansona and HD 1982, L 52 and Kalyansona, Lerma Rojo 64 and Kalynasona, PI and Kalyansona, PI and L 52, RR 21 and HD 1982, RR 21 and Kalyansoan, RR 21 and PI. Fifteen ancestors were present at least in about 65% of the cultivars. Most commonly used ancestors were N 10, BE, YT 54, T, MRQ, K 324, HRC, RF, GB, KVZ, TZPP, NAR 59, WTE, SE, PJ, PISSU and LR. The COP mean across these cultivars is similar to those reported for oat and barley (Souza and Sorrells 1989, Martin et al 1991), but lower that those reported by Dilday (1990) and Autrique et al (1996). In barley, only five ancestors contributed more than 50% of the genetic make up of released cultivars (Martin et al 1991).

Table 4. Relative genetic dissimilarities of 26 Nepalese bread wheat cultivars estimated from six agromorphological traits

SN	Cultivar	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1.	ACH†	0.000													
2.	ANNA1	1.644	0.000												
3.	ANNA2	1.366	0.928	0.000											
4.	ANNA3	1.556	0.620	1.000	0.000										
5.	ANNA4	1.575	1.255	0.626	1.392	0.000									
6.	BK	0.964	1.325	1.173	1.160	1.214	0.000								
7.	BL1022	1.582	1.099	0.600	1.410	0.536	1.349	0.000							
8.	BL1135	1.651	1.321	0.636	1.561	0.637	1.504	0.378	0.000						
9.	BL1473	1.842	1.902	1.305	2.176	1.059	1.765	0.883	0.744	0.000					
10.	HD1982	1.095	1.497	0.904	1.540	0.939	0.916	0.878	0.899	1.036	0.000				
11.	KAL	0.710	1.451	1.239	1.374	1.667	1.182	1.510	1.559	1.892	1.092	0.000			
12.	KANTI	1.675	1.381	1.522	1.513	1.447	1.539	1.607	1.738	2.024	1.887	2.003	0.000		
13.	L52	1.551	2.067	1.630	1.881	1.678	1.799	1.991	1.957	2.289	1.962	1.941	1.446	0.000	
14.	LR64	0.786	1.606	1.123	1.306	1.353	0.934	1.552	1.561	1.931	1.139	1.030	1.673	1.155	0.000
15.	LUM	1.241	1.329	1.077	1.587	1.140	1.136	0.833	0.937	0.980	0.654	1.172	1.764	2.232	1.542
16.	NL251	1.727	0.882	0.875	1.369	0.998	1.553	0.586	0.747	1.175	1.253	1.585	1.493	2.183	1.817
17.	NL297	2.064	1.999	1.539	2.237	1.142	1.684	1.110	1.096	0.676	1.162	2.171	2.093	2.543	2.107
18.	NL30	1.275	0.608	0.528	0.684	0.945	1.141	0.925	1.058	1.669	1.217	1.191	1.208	1.513	1.112
19.	PAL	1.069	1.787	1.007	1.646	1.148	1.309	1.338	1.252	1.562	1.019	1.236	1.851	1.182	0.666
20.	PI	0.699	1.326	1.290	1.076	1.508	0.619	1.607	1.727	2.065	1.256	0.979	1.405	1.528	0.742
21.	ROH	1.753	1.286	0.781	1.621	0.593	1.592	0.361	0.396	0.805	1.123	1.748	1.548	1.943	1.710
22.	RR21	2.062	2.327	1.798	2.551	1.403	1.844	1.382	1.354	0.733	1.254	2.246	2.302	2.607	2.191
23.	SID	1.620	1.176	1.090	1.509	1.306	1.447	0.869	0.951	1.198	0.999	1.321	1.972	2.510	1.819
24.	TRI	1.677	1.450	0.878	1.481	0.363	1.184	0.873	0.967	1.289	1.070	1.842	1.525	1.672	1.358
25.	UP262	0.980	1.596	1.187	1.774	1.079	1.072	1.003	1.092	0.987	0.691	1.257	1.582	1.862	1.327
26.	VKR	1.547	0.622	0.520	0.702	0.880	1.124	0.798	0.982	1.617	1.101	1.334	1.622	1.964	1.341

SN	Cultivar	15	16	17	18	19	20	21	22	23	24	25	26
15.	LUM	0.000											
16.	NL251	0.905	0.000										
17.	NL297	1.129	1.398	0.000									
18.	NL30	1.239	0.935	1.876	0.000								
19.	PAL	1.494	1.722	1.873	1.225	0.000							
20.	PI	1.391	1.692	2.133	1.063	1.296	0.000						
21.	ROH	1.049	0.647	1.115	1.068	1.424	1.804	0.000					
22.	RR21	1.275	1.711	0.508	2.134	1.896	2.268	1.373	0.000				
23.	SID	0.564	0.738	1.357	1.257	1.774	1.662	1.103	1.620	0.000			
24.	TRI	1.375	1.325	1.230	1.148	1.208	1.540	0.936	1.474	1.582	0.000		
25.	UP262	0.638	1.231	1.181	1.317	1.221	1.280	1.115	1.149	1.174	1.243	0.000	
26.	VKR	1.177	0.927	1.7007	0.592	1.412	1.301	1.067	2.021	1.069	1.046	1.424	0.000

† Refer Table 1 for full description of cultivars.

The COP (0.603) between Annapurna 1 and Annapurna 3 was due to the same ancestors used in developing them (Table 5). Value of zero indicates the completely different ancestors were used for developing these cultivars. As the value increases, the ancestral similarity increases. Eight pairs of cultivars were developed using completely different ancestors.

Five and six clusters were formed based on AMT and COP, respectively (Figure 1). Kanti and L 52 formed a single individual cluster within AMT and Lumbini and Achyut formed the single individual cluster based on COP. The maximum number of cultivars in a cluster were 15 and 13 based on AMT and COP, respectively. Plot of two dimension based on the multivariate analysis could help to locate cultivars responded with PC1 and PC2 (Figure 2). Cultivars scattered apart were RR 21 and Annapurna 3, L 52 and Siddhartha based on AMT and RR 21 and Annapurna 3, NL 251 and BL 1473 based on COP. First two PC accounted 55% and 85% of variation based on AMT and COP, respectively.

Cultivar pair, which has highest COP value, was not most diverse with respect to AMT. Probably this happens due to quantitative traits. Relatively cluster and scatter diagram drawn based on COP may be more reliable to pick the most diverse genotypes. This is also supported much by accounting much more variations by first two PCs in COP analysis. Among the four cells in PC graph, there was not any cultivar in right top quarter and most of the cultivars has fallen within two cells. But equal distribution of cultivars in four cells was found in graph based on AMT.

Table 5. Coefficients of parentage for all pair wise combinations of 26 Nepalese bread wheat cultivars

SN	Cultivar	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	ACH†	1.000													
2	ANNA1	0.029	1.000												
3	ANNA2	0.027	0.394	1.000											
4	ANNA3	0.029	0.603	0.394	1.000										
5	ANNA4	0.067	0.157	0.086	0.157	1.000									
6	BK	0.040	0.122	0.113	0.122	0.126	1.000								
7	BL1022	0.031	0.221	0.230	0.221	0.134	0.095	1.000							
8	BL1135	0.020	0.170	0.173	0.170	0.087	0.072	0.199	1.000						
9	BL1473	0.051	0.141	0.148	0.141	0.126	0.078	0.129	0.084	1.000					
10	HD1982	0.007	0.016	0.012	0.016	0.041	0.018	0.030	0.016	0.038	1.000				
11	KAL	0.019	0.355	0.440	0.355	0.014	0.071	0.223	0.148	0.145	0.000	1.000			
12	KANTI	0.027	0.349	0.227	0.349	0.130	0.110	0.137	0.105	0.090	0.013	0.192	1.000		
13	L52	0.046	0.020	0.012	0.020	0.058	0.037	0.021	0.015	0.029	0.000	0.000	0.022	1.000	
14	LR64	0.100	0.069	0.006	0.069	0.058	0.150	0.042	0.023	0.066	0.016	0.000	0.092	0.125	1.000
15	LUM	0.023	0.014	0.013	0.014	0.049	0.020	0.018	0.013	0.043	0.016	0.004	0.013	0.063	0.021
16	NL251	0.026	0.084	0.106	0.084	0.022	0.025	0.056	0.038	0.078	0.010	0.215	0.048	0.034	0.017
17	NL297	0.067	0.046	0.047	0.046	0.120	0.060	0.052	0.034	0.527	0.046	0.023	0.041	0.040	0.120
18	NL30	0.027	0.248	0.235	0.248	0.105	0.113	0.148	0.135	0.109	0.078	0.128	0.152	0.012	0.022
19	PAL	0.033	0.434	0.339	0.434	0.146	0.117	0.287	0.192	0.145	0.027	0.320	0.355	0.021	0.056
20	PI	0.014	0.044	0.031	0.044	0.089	0.043	0.095	0.049	0.093	0.250	0.000	0.032	0.000	0.031
21	ROH	0.029	0.209	0.188	0.209	0.105	0.119	0.169	0.115	0.109	0.019	0.179	0.162	0.023	0.072
22	RR21	0.047	0.035	0.021	0.035	0.108	0.064	0.037	0.026	0.136	0.000	0.000	0.039	0.000	0.215
23	SID	0.089	0.044	0.044	0.044	0.078	0.051	0.041	0.028	0.070	0.009	0.042	0.038	0.094	0.136
24	TRI	0.049	0.052	0.046	0.052	0.154	0.074	0.059	0.041	0.072	0.023	0.017	0.049	0.039	0.158
25	UP262	0.098	0.055	0.053	0.055	0.201	0.094	0.077	0.047	0.133	0.016	0.006	0.053	0.023	0.118
26	VKR	0.028	0.189	0.255	0.189	0.045	0.055	0.130	0.085	0.097	0.004	0.501	0.109	0.010	0.034

SN	Cultivar	15	16	17	18	19	20	21	22	23	24	25	26
15	LUM	1.000											
16	NL251	0.033	1.000										
17	NL297	0.067	0.088	1.000									
18	NL30	0.027	0.040	0.062	1.000								
19	PAL	0.017	0.079	0.052	0.225	1.000							
20	PI	0.031	0.019	0.092	0.172	0.083	1.000						
21	ROH	0.019	0.048	0.050	0.140	0.251	0.057	1.000					
22	RR21	0.062	0.011	0.239	0.021	0.036	0.000	0.050	1.000				
23	SID	0.055	0.056	0.094	0.049	0.048	0.018	0.041	0.063	1.000			
24	TRI	0.032	0.017	0.086	0.052	0.057	0.047	0.054	0.108	0.062	1.000		
25	UP262	0.050	0.016	0.175	0.052	0.069	0.031	0.066	0.541	0.109	0.124	1.000	
26	VKR	0.007	0.114	0.044	0.075	0.178	0.009	0.104	0.017	0.042	0.046	0.063	1.000

† Refer Table 1 for full description of cultivars.

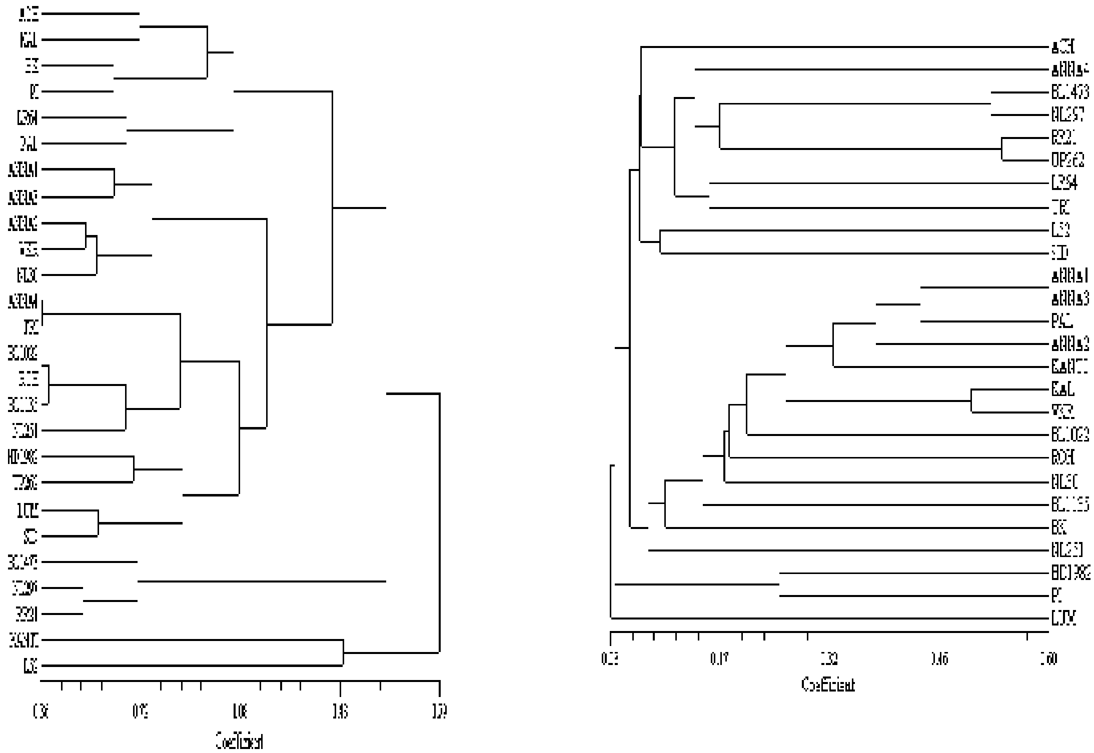

Figure 2. Dendrograph based on agromorphological traits (A) and coefficients of parentage (B) among 26 Nepalese bread wheat cultivars (Refer Table 1 for full description of cultivars).

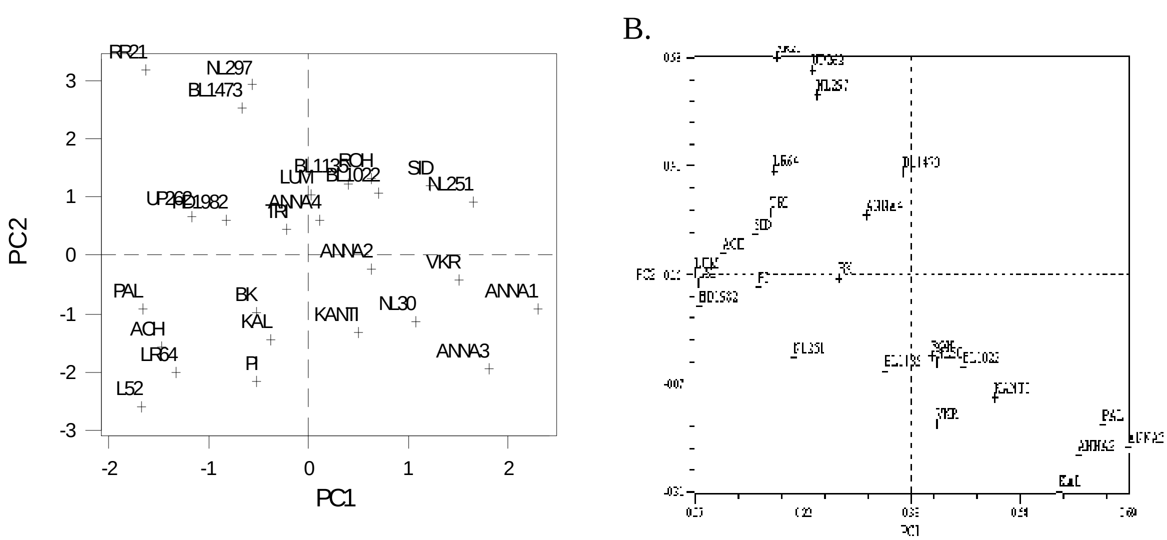

Figure 3. Plot of the first (PC1) and second (PC2) principal components from principal components analysis of agromorphological traits (A) and coefficients of parentage (B) among 26 Nepalese bread wheat cultivars (Refer Table 1 for full description of cultivars).

Comparison of different measures of similarity

The degree of relationship between the distance estimation based on COP and AMT was measured with the normalized Mantel Z statistics. Correlation coefficient between COP and AMT was 0.18 (P = 0.0168). The correlation coefficient was lower than the reported in durum wheat (Autrique et al 1996). Cox et al (1985a) found close agreement between modern soybean cultivars based on pedigree data and estimates based on biochemical and morphological markers.

In this study, cultivars surveyed represent a wide range of variation for different areas of origin and adaptation. This genetic diversity may be useful for further improvement of wheat. The results of this study may help in the selection of the most diverse cultivars and greatly expand genetic variation for wheat improvement. Measures of genetic diversity can be used to maximize the level of variation in segregating populations by intermating cultivars with greater genetic distance. Contributions of different measures might be useful in the prediction of progeny performance, diversity or both. Prediction of progeny performance in winter wheat namely F_2

heterosis with morphological distance estimation was better predictors than COP (Cox and Murphy 1990). But COP was reported to be a better predictor than morphological traits of F_4 family performance in oats and a combined measure was a better estimator of specific combining ability in F_1 (Souza and Sorrells 1991b). If we can add the inheritance pattern of important traits in pedigree trees, it will be very useful in breeding programme.

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