Genetic Base of Wheat Cultivars Recommended in Nepal

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ABSTRACT

Plant breeding success is dependent, in part, upon the genetic diversity found within genetic resources. The genetic base of wheat (*Triticum aestivum* L.) cultivars recommended in Nepal is not well characterized. Therefore this study was carried out to quantify the genetic base of Nepalese wheat cultivars by coefficient of parentage (COP). Analysis of pedigree information was based on International Wheat Information System of the International Center for Maize and Wheat Improvement (CIMMYT), which consists of WCOP for calculation of COP and WPDEND for generating Mendelgram with contribution of ancestors to the cultivar if fully expanded. One hundred eighteen ancestors from 23 countries were identified in the pedigree of 24 recommended Nepalese cultivars. Of these, 32 ancestors contributed at least 1% each to the genetic base of Nepalese cultivars, with a total contribution of 79%. Ancestors originating from USA contributed 19.8% of the genes, India 11.2%, Japan 9.5%, Argentina 7.5%, Kenya 7.5% Australia 6.2%, Brazil 5.6%, Canada 5.5%, Italy 4.1% and remaining from other countries. At 30% similarity, 18 clusters were formed with largest cluster of five members. None of Nepalese landraces were traced in the pedigree of these cultivars. Relatively large amount of diversity in Nepalese cultivars exits based on their genetic background although small number of cultivars is recommended for cultivation.

Key words: Coefficient of parentage, diversity, *Triticum aestivum*, wheat breeding

INTRODUCTION

Genetic variation is required in a breeding program to achieve genetic gains. Breeders require information on the magnitude of variation in the genetic material. Originally developed by Wright (1922), the coefficient of parentage (COP) for two genotypes estimates the expected percentage of alleles identical by descent at loci which are polymorphic within a population, is commonly used measure to assess the genetic composition of cultivars developed through hybridization. The COP between two wheat genotypes is the inbreeding coefficient of their offspring. St. Martin (1982) adapted the COP analysis to inbred crops by assuming that each genotype is completely homozygous, that genotypes without common parentage are unrelated and that parents contribute equally to the offspring, despite inbreeding and selection. Highly selected, qualitative loci would not follow the assumption of random transmission of a large number of alleles. However, in a general sense, a COP is a measure of overall common ancestry of two genotypes and estimates latent genomic diversity that is not obvious until a crop is challenged by the appropriate biotic or abiotic stress. Breeders can use COP to increase genetic diversity by selecting lines for crossing with divergent parentage.

Using COP, one can quantify pattern of relatedness among cultivars, magnitude and importance of genetic drift, and the genetic base for crop breeding. COP has been used to estimate the genetic diversity among cultivars and parental germplasm (St. Martin 1982, Joshi et al 2004, Cowen and Frey 1987, van Beuningen and Busch 1997). 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), genetic base of cultivars and to identify parents contributing to increased yield (Beer et al 1995).

CIMMYT software, WCOP calculates the COPs among genotypes. A mainframe version was used to study wheats in the 17th to 27th International Spring Wheat Yield Nurseries (ISWYNs) (Fox et al 1994). Pedigree analysis identified genotypes with excellent industrial quality among germplasm that is genetically distant from major gene pools. Long-term trends in genetic diversity were compared using COPs for wheat in the Pakistani, Punjab and in the Yaqui Valley of Mexico (Souza et al 1994). There was no evidence of genetic erosion and patterns in varietal adoption were more important for diversity than varieties released per se. Researchers from India (Jain 1994), Canada (Thomas 1996), USA, Australia (Brennan and Fox 1995) and CIMMYT (Smale and McBride 1996) have used WPMS to examine the genetic base and gene flows in wheat. Landraces from certain regions do not appear in the genealogies of modern wheats. Generally, this seems to indicate that these materials have not been tried in breeding and thus represent novel sources of variation. Braun et al (1992) calculated the genetic variance of entries for grain yield in many environments in the first 19 ISWYNs. The relationship between these parameters and the average COPs for the entries (without distinguishing among sister lines) in individual ISWYNs was investigated (Fox and Skovmand 1996). The significant correlation suggests that both measures, one from yield data from international trials and the other from genealogical information, support each other and are useful measures of genetic diversity. In Nepal wheat cultivars are recommended for cultivation starting from 1960 (Morrin et al 1992). The major part of wheat breeding in Nepal is mostly screening of cultivars and lines from India and CIMMYT. Information on size of genetic diversity and genetic base in wheat in Nepal is limited. This study was carried out to assess the diversity on cultivars based on their pedigrees and contribution of ancestors to Nepalese cultivars.

MATERIALS AND METHODS

Twenty-four cultivars among all 35 cultivars recommended for cultivation in Nepal were used in the study (Table 1). The cultivars were not included in the study whose pedigree information was incomplete. Two international cultivars; Marquis and Pavon and three South Asian cultivars; Chirya 3, PBW 343 and Kanchan were also used for comparative analysis. All of the pedigree information and analysis were based on International Wheat Information System (IWIS TM, Version 4) (Payne et al 2001). IWIS consists of WCOP to retrieve parentage information from CIMMYT pedigree management system (Fox and Skovmand, 1996). Specific Cross Identification (CID) numbers and Selection Identification (SID) numbers were used for all unique cultivars. WCOP use the CID to retrieve from the Pedigree Management System, a pedigree history that traced back to at least grand parents but often to ancestral landraces. WCOP formats the pedigree history into a file and then calls the FORTRAN program RCL to calculate COP values between pair wise combinations. A total of 29 (24 cultivars and 5 additional reference cultivars) were included in the final similarity matrix. The COP matrix of Nepalese recommended cultivars and reference cultivars was used as a similarity matrix for cluster analysis in NTSYS (Rohlf 1990), with SHAN clustering option using UPGMA method.

The parental contribution of an ancestral genotype to a modern cultivar was determined in following way. Ancestors were defined as founding stocks with no known pedigree. Contribution of an ancestor was defined as the fraction of genes in modern cultivars that could be traced from the progeny of that ancestor through pedigree analysis. COP between ancestors (landraces, treated as unrelated) and Nepalese recommended cultivars were computed from pedigree information using WPDEND (Wheat PMS Dendogram V2.0 CIMMYT 1997). When a genotype is fully expanded (so that all ancestors were landraces ie lines with unknown parentage), Mendelgram were generated using the same software. The Mendelgram presents the theoretical percentage contribution of ancestors to a pedigree assuming equal contribution from both parents in a cross. The average contribution of ancestors to the 24 cultivars under study was determined as average of all coefficients between the ancestors (landraces) and the Nepalese cultivars.

Table 1. Wheat cultivars included in the study for analysis of diversity and genetic base

SN	Cultivar	Pedigree	CID	SID	Origin	Area of adoption
1	Annapurna 1	KVZ/BUDHO//KAL/BB	7691	394	Mexico	Hills
2	Annapurna 2	NAPO/TOB//8156/3/KAL/BB	141626	-1	India	Hills
3	Annapurna 4	KVZ/3/CC/INIA//CNO/ELGAU/SN64	162497	-1	Mexico	Hills
4	Bhrikuti	CDO/COC/3/PLO//FURY/ANA	251774	0	Mexico	Plains
5	BL 1022	PVN/BUC	541	7	Nepal	Western Tarai
6	BL 1135	QTZ/TAN	558	1	Nepal	Plains
7	BL1473	NL352/Nepal 297	166468	0	Nepal	Plains and Hills
8	HD 1962	E5557/HD845	122538	0	India	Western Plains
9	Kalyansona	Pj"S"/Gabo 55	6831	1	Mexico	Plains
10	Kanti	LIRA/FFN//VEE#5	22966	105	Mexico	Hills
11	Lerma 52	Mentana/Kenya 324	3011	7	Mexico	Hills
12	Lerma Rojo 64	Y50/N10B//L52/3/2*LR	6846	0	Mexico	Hills
13	Lumbini	E4871/PJ62	3117	1	India	Plains
14	Nepal 251	WH147/HD2160//2*WH147	142563	0	India	Plains
15	Nepal 297	HD2137/HD2186//HD 2160	142566	0	India	Plains
16	Nepal 30	HD832-5-5-OY/BB	142562	0	India	Western Plains
17	Pasang Lahmu	PGO/SERI	9368	198	Mexico	Hills
18	Pitic 62	YT54/N10B 26.1C	6674	7	Mexico	Hills
19	R 21	Sonalika= I53.388/AN/3/YT54/N10B/3/LR/4/B4946. A.4.18.2.IY/Y53//3*Y50	6977	3	Mexico	Hills and Plains
20	Rohini	PRL/TONI//CHIL	111639	5	Nepal	Plains
21	Siddhartha	HD2092/HD 1962//E4870/3/K65	84638	-1	India	Plains
22	Triveni	KAL/JANAK	85879	0	India	Plains
23	UP 262	S308/BAJIO 66	5435	1	India	Plains
24	Vaskar	TZPP/PL//7C	7401	9	Mexico	Mid-western Plain
International cultivars						
25	Marquis	HRC/RF	794	1	Canada	-
26	Pavon	VCM//CNO 67/7C/3/KAL/BB	7624	0	-	-
South Asian popular cultivars						
27	Chirya 3	CS/TH.CV//GLEN/3/ALD/PVN/4/NINMMAI NO.4/OLESON//ALD/YANGMAI NO.4	54384	0	Mexico	-
28	PBW 343	ND/VG 9144//KAL/BB/3/YACO/4/VEE#5	8890	1549	India	-
29	Kanchan	UP 301/SUJATA	2565	3	Bangladesh	-

CID, Cross identifier. SID, Selection identifier. The pedigree of Triveni is widely denoted by HD1963/HD1931 in Nepalese literatures, but based on CIMMYT pedigree database it was KAL/JANAK.

Source: CIMMYT 1997, NARC 1997.

RESULTS AND DISCUSSION

The contribution revealed that genetic base of recommended cultivars included in the study was fully defined by 119 ancestors. These ancestors' contribution to the genetic base of wheat were unequal, ranged from 0.0001 to 7.5%. It seems that large numbers of ancestors appear in pedigree of Nepalese wheat cultivars although more than half of the genetic base of Nepalese recommended cultivars constituted by only 14 ancestors (Table 2). Pedigree tree of Sonalika has shown how the genes of interest were combined (Figure 1). It indicates that efforts have been made in selecting landraces and hybridization. Agriculture Botany Division, NARC has conserved 390 accessions of wheat (Upadhyay and Joshi 2003). However, these landraces were not traced out in breading history of these cultivars. Only 4 cultivars, which were not included in this study, were bred and developed using foreign landraces (Joshi and Mudwari 2003). Thirty-two ancestors contributed at least 1% each to the genetic base of Nepalese cultivars. The contributions of these 32, taken together, amount to 79% of the total genetic base of Nepalese wheat cultivars.

Table 2. Landraces (genotypes with unknown parents) with their contribution to Nepalese cultivars

SN	Landrace	Origin	Contribution, %	Cumulative, %	Number of cultivars with contribution
1	Akagomughi	Japan	7.5	7.5	24
2	Red Fife	Canada	4.6	12.1	-
3	Kenya 324	Kenya	4.5	16.6	24
4	Turkey Red	USA	4.0	20.6	23
5	Rieti	Italy	3.8	24.4	24
6	Steinwedel	Australia	3.7	28.1	20
7	Hd 845	India	3.1	31.2	2
8	Hard Red Calcutta	India	3.0	34.3	23
9	Oro	USA	3.0	37.3	23
10	Kanred	USA	2.8	40.1	23
11	Polyssu	Brazil	2.6	42.8	-
12	Red Egyptian	South Africa	2.6	45.4	17
13	Iumillo	Spain	2.5	47.9	23
14	Gaza	Egypt	2.5	50.3	20
15	Kenya Bf4-3b.10.V.1	Kenya	2.3	52.7	18
16	Egypt Na101	Argentina	2.3	55.0	19
17	Fultz	USA	2.2	57.2	23
18	Alfredo Chaves 6.21	Brazil	2.1	59.3	18
19	Daruma	Japan	2.0	61.3	23
20	Squarehead	USA	1.9	63.2	24
21	Improved Fife	USA	1.5	64.8	23
22	Ladoga	USSR	1.5	66.3	23
23	Fife	Poland	1.5	67.8	23
24	White Naples	Australia	1.5	69.2	23
25	Maria Escobar	Argentina	1.5	70.7	-
26	Jacinth	-	1.3	72.0	22
27	Turkey	USA	1.3	73.9	23
28	Americano 25e	Uruguay	1.2	74.5	18
29	Mediterranean	USA	1.1	75.6	23
30	Barleta	Argentina	1.1	76.7	18
31	Chino	Argentina	1.1	77.8	18
32	Purple Straw	Australia	1.0	78.8	23

Joshi et al (2004) have reported 77 ancestors originated from 22 countries used for 26 Nepalese cultivars. Introduced genotypes along with landraces and wild relatives have made Nepal a wheat genes rich country (Mudwari 1999, Bhatta et al 2000, Joshi and Mudwari 2003). This diversity should be characterized systematically and utilized effectively for long-term food security in the country.

Most of the cultivars released in Nepal are from CIMMYT source, directly or indirectly. COP was estimated with 8 CIMMYT most popular lines/crosses because COP was used by many national programs worldwide (Bayerlee and Moya 1993). The COP values show moderate to high relation with newly released and some old cultivars and it ranges from 0 to 1 (Table 3). Joshi et al (2004) showed that the most closely related cultivars were Annapurna 3 and 2 and some of the highest dissimilarity was between Kalyansona and HD 1982, and L52 and HD 1982 based on the COP.

Figure 1. The pedigree tree for Sonalika (RR21) expanded to reasonable label. Fully expanded to level of all landraces include the contribution of 39 landraces.

The origin of most of the ancestors for Nepalese cultivars were from USA (13%), India (13%), France (12%), Argentina (6%), and Italy (6%) (Table 4). None of the ancestors were of Nepalese origin. On the basis of contribution, ancestors from USA (19.8%), India (11.2%), Japan (9.5%), Argentina (7.5%), Australia (6.2%), Brazil (5.6%), Canada (5.5%) and Italy (4.1%) constitute approximately 70% of the total contribution. Only two of Japanese ancestors, Akagomughi (7.5%) and Daruma (2.0%) contributed almost ten percent.

Table 3. Coefficient of parentage between recommended Nepalese wheat cultivars with six internationally popular wheat lines/crosses developed by CIMMYT

SN	Cultivar	Blue Bird	II8156	Pavon	Bobwhite	Bluejay	Ciano	Buckbuck	Veery
1	Annapurna 1	0.446	0.264	0.297	0.231	0.177	0.172	0.192	1
2	Annapurna 2	0.494	0.353	0.437	0.276	0.252	0.182	0.229	0.32
3	Annapurna 4	0.190	0.074	0.165	0.164	0.096	0.32	0.152	0.18
4	Bhrikuti	0.237	0.118	0.159	0.117	0.106	0.165	0.132	0.14
5	BL 1022	0.383	0.252	0.425	0.228	0.212	0.251	0.622	0.25
6	Bl 1135	0.309	0.168	0.293	0.180	0.168	0.252	0.195	0.19
7	BL1473	0.219	0.159	0.215	0.156	0.146	0.201	0.193	0.15
8	HD 1962	0.046	0.044	0.062	0.051	0.057	0.063	0.057	0.05
9	Kalyansona	-	-	-	-	1	-	-	0.38
10	Kanti	0.289	0.162	0.206	0.167	0.132	0.144	0.141	0.35
11	Lerma 52	0.056	0.036	0.095	0.098	0.12	0.092	0.089	0.08
12	Lerma Rojo 64	0.054	0.044	0.12	0.094	0.106	0.079	0.076	0.1
13	Lumbini	0.196	0.297	0.200	0.146	0.196	0.139	0.207	0.17
14	Nepal 251	0.11	0.164	0.111	0.084	0.111	0.074	0.093	0.09
15	Nepal 297	0.105	0.079	0.108	0.102	0.105	0.16	0.115	0.06
16	Nepal 30	0.547	0.216	0.267	0.175	0.137	0.185	0.243	0.26
17	Pasang Lahmu	0.414	0.258	0.361	0.230	0.195	0.211	0.407	0.42
18	Pitic 62	0.185	0.156	0.183	0.152	0.151	0.347	0.242	0.14
19	Rohini	0.484	0.269	0.467	0.289	0.198	0.379	0.276	0.3
20	Siddhartha	0	0	0	0	0	0	0	0.09
21	Sonalika	0.088	0.070	0.101	0.091	0.10	0.145	0.11	0.07
22	Triveni	0.181	0.282	0.241	0.158	0.175	0.108	0.138	0.21
23	UP 262	0.135	0.088	0.133	0.124	0.14	0.214	0.141	0.25
24	Vaskar	-	1	-	-	-	-	-	0.18

Table 4. Origin of ancestors and their contribution to Nepalese cultivars

SN	Country	Number of ancestors contributing	Cumulative contribution of ancestors
1	USA	15	19.8
2	India	14	11.2
3	Japan	2	9.5
4	Argentina	7	7.5
5	Kenya	5	7.5
6	Australia	5	6.2
7	Brazil	5	5.6
8	Canada	5	5.5
9	Italy	7	4.1
10	Zaire	1	2.6
11	Egypt	2	2.5
12	Spain	1	2.5
13	Uruguay	3	2.4
14	USSR	3	2.2
15	Poland	1	1.5
16	Mexico	4	1.2
17	Germany	3	0.9
18	Chile	1	0.5
19	China	4	0.3
20	France	13	0.3
21	Zimbabwe	1	0.02
22	Sweden	1	0.1
23	United Kingdom	1	0.001
24	Unknown origin	13	4.1

Cluster analysis was done to group cultivars with similar genealogies (Figure 2). At 30% similarity level 18 clusters were formed. Cluster 7 was the largest which include Annapurna-2, Kalyansona, Rohini, BL 1022, Pasang Lahmu and Pavon. Some cultivars that are closely related were Nepal 297 and BL 1473 (COP = 0.55), Sonalika and UP 262 (COP = 0.55), Triveni and HD 1962 (COP = 0.52), Annapurna 2 and Kalyansona (COP = 0.47), Lerma 52 and Lerma Rojo 64 (COP = 0.45), Pasang Lahmu and BL 1022 (COP = 0.43) and Annapurna 1 and Kanti (COP = 0.35). Among reference cultivars, three South Asian cultivars PBW 343, Kanchan, Chirya 3 and International cultivar Marquis had low COP values with the studied genotypes. PBW 343 was related with Annapurna 1 (COP = 0.38). The assumption of the COP calculation may also bias the conclusions for sets of the cultivars within the study. A specific example is the assumption of lack of genetic similarity between cultivars without demonstrable ancestry (St. Martin 1982).

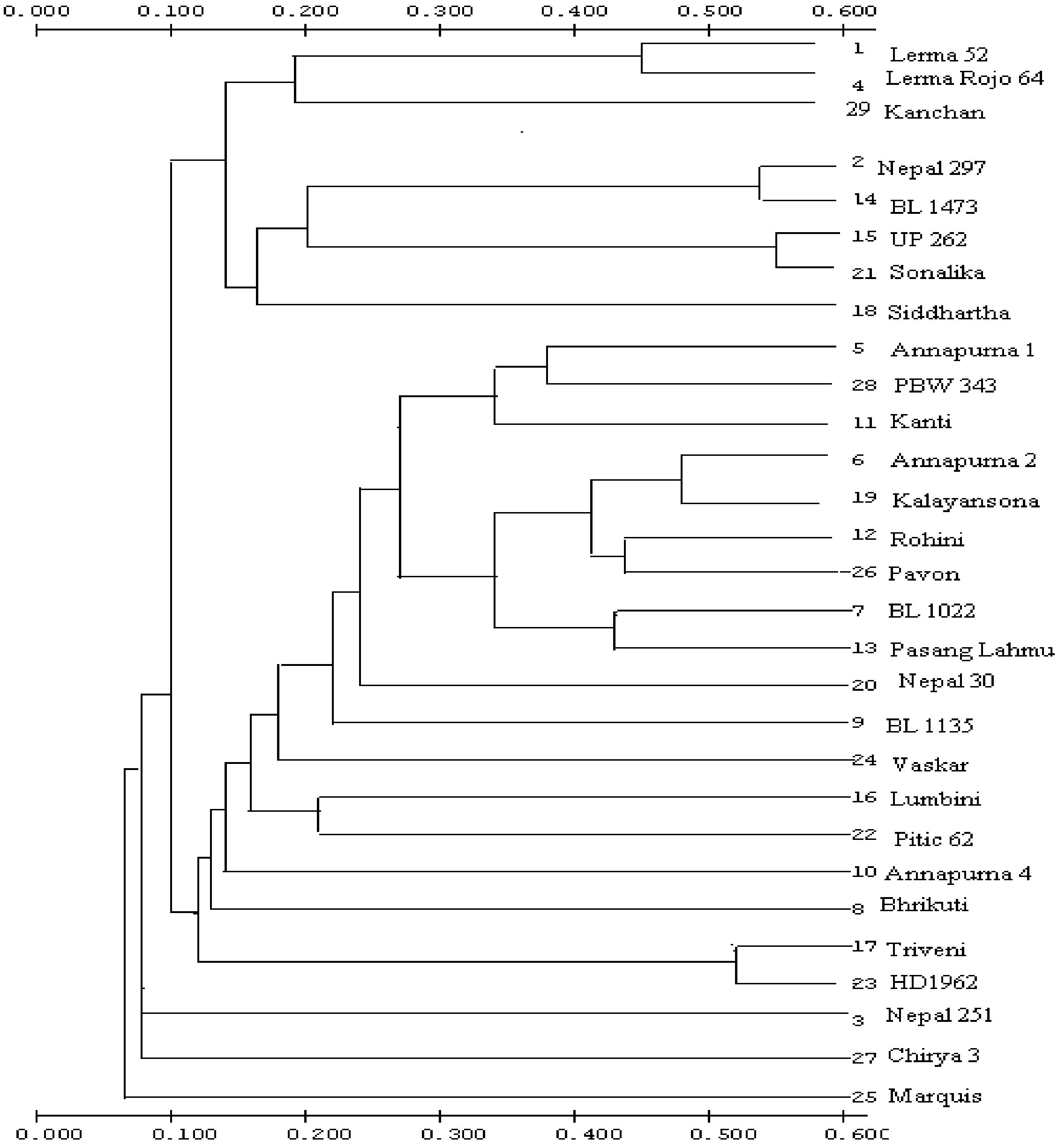

Figure 2. Cluster analysis of wheat cultivars released for cultivation along with national and international checks based on coefficient of parentage.

Results of cluster analysis show weak relatedness among the cultivars forming a large number of clusters of genotypes, often single member cluster at low level of similarity. This shows considerable diversity exists in the recommended cultivars. So, crossing programs aimed to cross two recommended cultivars may be less restricted in selection of parents. The gain may be further widened if the COP values were considered in account. Breeders making cross should consider COP values and selection of parents should be done from distantly related genotypes. For example, Bhrikuti has unique genetic base than other genotypes.

This study show that there is large amount of diversity in Nepalese cultivars based on their genetic background even though relatively smaller number of cultivars is recommended in Nepal. The origin of the diversity is not native one rather due to introduction from time to time. Thus, cultivars recommended in Nepal are internally diverse. That’s why, these are adopted to diverse environments of Nepal. Improved wheat cultivars cover more than 93% of total wheat area (Bhatta et al 2000). Recently, a participatory approach is taken to increase adoption rate (Mudwari et al 2005). This helps to develop site-specific variety faster (Mudwari et al 2004) and management of existing diversity should be continued

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