

Genetic Relationships Among Peanut Cultivars and Breeding Lines in Shandong Province, PRC

H.Q. Xue* and T.G. Isleib¹

ABSTRACT

Shandong province is the leading peanut-producing province in China which in turn is the leading peanut-producing country in the world. Shandong Peanut Research Institute (SPRI), an institute of the Shandong Academy of Agricultural Science, has had an ongoing breeding program for more than 40 yr and is the source of the peanut cultivars that dominate production in Shandong province and northern China. About 75 peanut cultivars and breeding lines have been released in Shandong by SPRI and other institutions. The genetic base of Shandong peanut cultivars has been described as narrow. The objective of this study was to (a) determine the genetic contribution of main ancestors to the genetic base of Shandong peanut cultivars and (b) study the genetic relationships among the peanut cultivars released in Shandong province during 1950-1999. Twenty-six ancestors were identified in the pedigrees of 69 improved lines, 24 ancestors of Chinese origin contributed 96.1% of the Shandong peanut genetic base, and two exotic introductions contributed only 3.6%. The four most important ancestors based on average coancestry with the 69 improved lines are Fu Hua Sheng (PI 436545), Shi Tou Qi (PI 430227 and PI 461435), Jianggezhuang Ban Man (PI 433351), and Shuyang Da

Zhan Yang from which 67, 28, 27 and 19 lines were derived, respectively. Among the 20 dominant cultivars of Shandong province, recently released cultivars Lu Hua 14 and Lu Hua 15 have the lowest average coancestry with the others which means those two new cultivars have the high genetic divergence. In contrast, the very popular cultivars Fu Hua Sheng, Baisha 1016, Xuzhou 68-4, Lu Hua 9, and the new cultivar 8130 were closely related to the other cultivars. The results suggest that the genetic base of Shandong peanut cultivars released before 1990 is narrow, but that cultivars released after 1990 have broadened the genetic base due to introduction and use of new germplasm in the pedigrees. This information will be used as a guide for peanut breeders in choosing parents and avoiding genetic vulnerability to pests. For new cross combinations, parents with low coefficients of coancestry should be chosen in order to keep enlarging the gene pool of the new cultivars.

Key Words: *Arachis hypogaea* L., coefficient of coancestry, genetic base, genetic vulnerability.

¹Res. Asst. and Prof., Dept. of Crop Science, North Carolina State Univ., Raleigh, NC 27695-7629.

*Corresponding author (email: hxue@croppserv1.cropsci.ncsu.edu).

Shandong is the leading peanut-producing province in China, which in turn is the leading peanut-producing country in the world. Shandong's annual area under peanut (*Arachis hypogaea* L.) is 23% of the total for China, and the

province's production is 31% of the national total (He, 1996). Shandong is the central province in the northern Chinese peanut-producing area which includes Shandong, Henan, Hebei, Liaoning, northern Jiangsu, and southern Shanxi provinces and lies between latitudes 32°N and 42°N and east of longitude 107°E. Peanut is grown in several different production systems in Shandong, either as a full-season sole crop or as a rotation crop with wheat (*Triticum aestivum* L.), watermelon (*Citrullis lanatus* L.), or vegetables. About 60% of the Chinese peanut crop is crushed for oil and the meal fed to animals, and the remaining 40% is used for direct human consumption or for export. Peanut stover is commonly dried as hay and used as winter feed for ruminant livestock.

Shandong Peanut Research Institute (SPRI), an institute of the Shandong Academy of Agricultural Science, has had an ongoing breeding program for more than 40 yr. SPRI is the source of the peanut cultivars that dominate production in Shandong province and the rest of the northern Chinese peanut production area. About 75 peanut cultivars and breeding lines have been released in Shandong by SPRI and other institutions. Among these, Fu Hua Sheng, Hua 17, Hua 28, Hua 37, Xuzhou 68-4, Baisha 1016, Hai Hua 1, and Lu Hua 9 are the most important in terms of the extent of their cumulative cultivated areas. Lu Hua 14 and 8130 are new cultivars that show promise of similar broad acceptance by Shandong's peanut growers.

Genetic vulnerability and its converse, genetic diversity of crop species, have become global issues. Lack of genetic diversity among the cultivars of a crop makes it vulnerable to epiphytotic and widespread depredation by insect pests. Genetic diversity in crop species is generally assessed using some measure of distance or similarity among cultivars based on one or more of three main types of data—phenotypic data, genetic markers, and pedigree-based measures of degree of relatedness. The first two methods require that all pertinent cultivars be assembled and data collected. In the case of phenotypic traits, testing must be sufficiently extensive to provide confidence in the results. In the case of marker data, there must be a large number of markers exhibiting polymorphism within the population. Either method is resource intensive. In contrast, pedigree data are widely accessible and generally accurate, and its use does not require that the cultivars themselves be in hand for analysis.

Following the southern corn leaf blight [*Bipolaris maydis* (Nisikado & Miyake) Shoemaker] epiphytotic of 1970 in the United States, the U.S. government sponsored studies on the level of genetic vulnerability of major U.S. crops. Most were found to have fairly narrow genetic bases, including peanut (Hammons, 1972, 1976). Knauff and Gorbet (1989) found that use of more diverse parentage in development of new runner- and virgina-type cultivars after 1976 had somewhat broadened the genetic base of peanuts in the U.S., but that the average coancestry among seven of eight runner-type cultivars released after 1976 was 0.32, between the values for half- and full-sibs. Similar studies have not been performed on most crops in China, soybean being an exception (Cui *et al.*, 2000a,b). Such studies provide breeders with useful information regarding the risks inherent in the release of new cultivars closely related to existing ones. They also provide some guidance with respect to choices of

parents to initiate new breeding populations to serve as sources of new cultivars (Manjarrez-Sandoval *et al.*, 1997).

The objectives of this study were to (a) determine the genetic contribution of main ancestors to the genetic base of Shandong peanut cultivars and (b) study the genetic relationships among peanut cultivars and breeding lines in Shandong province. This information will be used as a guide for peanut breeders in choosing parents and avoiding genetic vulnerability to diseases and pests.

Materials and Methods

The 75 peanut cultivars and breeding lines in the analysis (Table 1) included officially released cultivars, lines not officially released but distributed to and widely grown by farmers, breeding lines heavily used as parents in cultivar development, and breeding lines released as germplasm. Of the 75, 47 were developed at SPRI; 16 were developed at other institutes of Shandong province; and two, Xuzhou 68-4 and Baisha 1016, were developed in Jiangsu and Guangdong provinces and introduced to Shandong where they eventually became very important cultivars.

The 75 lines include three Chinese plant types—virginia-type (alternate-branching forms typical of subsp. *hypogaea* vars. *hypogaea* and *hirsuta* Köhler); spanish-type (typical of subsp. *fastigiata* Waldron var. *vulgaris* Harz); and middle-type, a type intermediate to virginia and spanish based on growth habit and pod characteristics. Among the 75 lines, one was a landrace (Fu Hua Sheng), four were selected from unidentified landraces (Qun Xuan 5, Xie Kang Qing, Zhong Xuan 48, and Zhong Xuan 65), and one was a line for which there was no further pedigree information (Chang Da 6). The remaining 69 were improved lines including seven selected as naturally occurring variants within landraces (Xi Xuan 7, Zhong Xuan 62) or cultivars (Shuang Ji 2, Lu Hua 10, Lu Hua 6, Peng Xuan 2, and Qi Xuan 2); three were selected following mutagenesis (Chang Hua 4, Lu Hua 7, and Lu Hua 12); and 59 were selected following hybridization.

Details of pedigree information for most cultivars have been published (SPRI, 1983; Gu and Xue, 1997). Some pedigree and related data information are from crop registration information and personal communications. Ancestry was traced back until no further information was available. Each line was assigned to a "breeding level" depending on how many cycles of crossing and selection the line was removed from the ancestral lines. In this system, ancestral lines were assigned to Level 0, lines selected from Level 0 ancestors, or from crosses between Level 0 lines were assigned to Level 1, and so on. Each line was assigned to the level one above that of the higher of its parents. The genetic contribution of an ancestor to a modern cultivar or line was determined as the fraction of genes in the modern cultivar that could be traced to an ancestor through pedigree analysis (Gizlice *et al.*, 1996). Coefficient of parentage (θ) was used to make this determination and is defined as the probability that a random allele at any locus in one cultivar is identical by descent to a random allele at the same locus in the second cultivar (Malécot, 1948; Kempthorne, 1969). Techniques for the calculation of θ are widely known. If the parents of lines X are A and B, and the parents of line Y are C and D, then the coancestry between X and Y, θ_{XY} , can be calculated as

Table 1. Cultivars, breeding lines, and hybrids figuring in the pedigrees of 75 Chinese peanut cultivars and breeding lines, their parentage, USDA plant introduction numbers, and assigned breeding level.

Level*	Identity	Parentage	PI or NPGS no.	Level*	Identity	Parentage	PI or NPGS no.
0	534-11	—	—	2	Hua 103*	Baisha 1016/Jianggezhuang Ban Man	—
0	Beijing Da Hua Sheng	—	—	2	Huang Hua 1*	Jianggezhuang Ban Man/Baisha 1016	—
0	Chang Da 6*	—	—	2	Hun Jiu 5	Nanchong Hun Xuan 1/Jiu Guo	—
0	Cheng Shi 3	—	—	2	Kai Nong 8	Da Fu 3/Dong De 8476840	—
0	Da Hua Sheng	—	—	2	Lu Hua 2*	Za Xuan 4/Baisha 1016	—
0	Da Ma Ke	436542	—	2	Lu Hua 5*	Hua 27/Baisha 1016	—
0	Deyang Ji Wo	—	—	2	Lu Hua 7*	Selection from Lin Hua 1	—
0	Dongcun Zhan Yang	—	—	2	mA143	Selection from Baisha 1016	—
0	Florunner	—	—	2	Qun Yu 157*	Za Xuan 4/Baisha 1016	—
0	Fu Hua Sheng*	436545	—	2	Shuang Ji 2*	Selection from Lin Hua 1	—
0	Jianggezhuang Ban Man	433351	—	2	Xuzhou 68-4**	Xuzhou 402/Fu Hua Sheng	—
0	Jiu Guo	—	—	2	Y0351	Y082/Baisha 1016	—
0	Laiyang Ban Man	—	—	2	Y0359	Baisha 1016/Mei 2	—
0	Luojiang Ji wo	461458	—	2	Za Xuan 2*	Wendeng Da Li Dun/Hybrid X	—
0	Mei 2	—	—	—	—	—	—
0	Qun Xuan 5*	—	—	3	78104	Kai Nong 8/Hun Jiu 5	—
0	RH-77-4-2	—	—	3	78105	Kai Nong 8/You Ma 1-1	—
0	Sheyang You Guo	—	—	3	78961	mA143/RH-77-4-2	—
0	Shi Tou Qi	430227, 461435	—	3	Hai Hua 1**	Lin Hua 1/Baisha 171	476825
0	Shuyang Da Zhan Yang	—	—	3	Hua 19*	Lin Hua 1/Xuzhou 68-4	—
0	Tengxian Xiao Ma Ye	—	—	3	Hua 31*	Lin Hua 1/Baisha 171	—
0	Wendeng Da Li Dun	—	—	3	Hua 32*	Lin Hua 1/Baisha 171	—
0	Wulian Cheng Po Tun	—	—	3	Hua 34*	Lin Hua 1/Xuzhou 68-4	—
0	Xie Kang Qing*	—	—	3	Hua 54*	Jianggezhuang Ban Man/Za Xuan 2	—
0	Y082	—	—	3	Hua 67*	Jianggezhuang Ban Man/Za Xuan 2	—
0	Zhaoyuan Ban Man	—	—	3	Hua 71*	Jianggezhuang Ban Man/Za Xuan 2	—
0	Zhong Xuan 48*	—	—	3	Hua 80*	Shi Tou Qi/Za Xuan 2	—
0	Zhong Xuan 65*	—	—	3	Hua 93*	Jianggezhuang Ban Man/Za Xuan 2	—
—	—	—	—	3	Hua 244*	Jianggezhuang Ban Man/Za Xuan 2	—
—	—	—	—	3	Hybrid 3 (F1) ^b	mA143/Chang Da 6	—
1	8123	Shi Tou Qi/Fu Hua Sheng	—	3	Kang Qing 10*	Xuzhou 68-4/Xie Kang Qing	—
1	Baisha 1016**	Shi Tou Qi/Fu Hua Sheng	462321, 476821	3	Kang Qing 11*	Xuzhou 68-4/Xie Kang Qing	—
1	Chang Hua 4*	Selection from Fu Hua Sheng	442570	3	Lai Nong 11*	Xuzhou 68-4/Qun Xuan 5	—
1	Da Fu 3	Beijing Da Hua Sheng/Fu Hua Sheng	—	3	Lu Hua 1*	Xuzhou 68-4/Baisha 171	—
1	Dong De 8	Dongcun Zhan Yang/Deyang Ji Wo	—	3	Lu Hua 3**	Xuzhou 68-4/Xie Kang Qing	—
1	Hua 27*	Fu Hua Sheng/Da Hua Sheng	—	3	Lu Hua 6*	Selection from mA143	—
1	Hua 63*	Laiyang Ban Man/Fu Hua Sheng	—	3	Lu Hua 10**	Selection from Hua 17	—
1	Hua 64*	Tengxian Xiao Ma Ye/Fu Hua Sheng	—	3	Peng Xuan 2*	Selection from Hua 17	—
1	Hybrid X ^b	Fu Hua Sheng/Jianggezhuang Ban Man	—	3	Yue You 22	Fu Shi/Fu Hua Sheng	476842
1	Jiunan 1*	Tengxian Xiao Ma Ye/Fu Hua Sheng	—	3	—	—	—
1	Lai Nong 10*	Zhong Xuan 48/Fu Hua Sheng	—	4	78102*	Lu Hua 3/Kai Nong 8	—
1	Lin Hua 1*	Fu Hua Sheng/Wulian Cheng Po Tun	—	4	79266**	Lu Hua 1/Hun Jiu 5	—
1	Lin Hua 2*	Fu Hua Sheng/Wulian Cheng Po Tun	—	4	Hua 28**	Hua 71/Xuzhou 68-4	462322
1	Lu Hua 8**	Fu Hua Sheng/Zhaoyuan Ban Man	—	4	Hua 29*	Hua 71/Xuzhou 68-4	—
1	Nanchong Hun Xuan 1	Selection from Luojiang Ji wo	—	4	Hua 37**	Xuzhou 68-4/Hua 80	478774
1	r25KR	Selection from Florunner	—	4	Hybrid 2 ^b	Fu Hua Sheng/Lu Hua 1	—
1	rP1	Selection from Fu Hua Sheng	—	4	Hybrid 4 (F2) ^b	78961/Florunner	—
1	Shi Xuan 64	Selection from Shi Tou Qi	476843	4	Lu Hua 4*	Hua 17/Hua 93	—
1	Xi Xuan 7*	Selection from Zhaoyuan Ban Man	—	4	Lu Hua 9**	Hua 19/Hua 17	GRIF 13912
1	Xuzhou 402	Selection from Shuyang Da Zhan Yang	—	4	Lu Hua 14**	78105/78104	—
1	You Ma 1-1	Sheyang You Guo/Da Ma Ke	476828	4	P12*	Hybrid 3 (F1)/Baisha 1016	—
1	Yue You 431	Fu Hua Sheng/Shi Tou Qi	—	4	Qun Yu 172*	Hua 67/Lin Hua 1	—
1	Za Xuan 4*	Fu Hua Sheng/Jianggezhuang Ban Man	—	4	Yue You 551	Yue You 22/Yue You 431	436549, 50688
1	Zhong Xuan 62*	Selection from Tengxian Xiao Ma Ye	—	5	8223	P12/Baisha 171	—
2	93*	Hua 27/Baisha 1016	—	5	Hua Yu 17**	Lu Hua 9/79266	—
2	383*	Hua 27/Baisha 1016	—	5	Hybrid 1 ^b	Lu Hua 4/rP1	—
2	Baisha 171	Cheng Shi 3/8123	—	5	Lu Hua 11**	Hua 28/534-11	—
2	Chang Hua 5*	Hua 27/Baisha 1016	442571	5	Lu Hua 12**	Selection from Hybrid 2	—
2	Chang Hua 6*	Fu Hua Sheng/Baisha 1016	442572	5	Lu Hua 13**	Lu Hua 6/P12	—
2	Chang Hua 8*	Hua 27/Baisha 1016	—	5	Lu Hua 15**	Hybrid 4 (F2)/r25KR	—
2	Fu Shi	Selection from Shi Xuan 64	—	5	Pingdu 204*	Hua 28/Yue You 551	—
2	Hua 11**	Baisha 1016/Zhong Xuan 65	433348	5	Qi Xuan 2*	Selection from Hua 28	—
2	Hua 17**	Za Xuan 4/Jianggezhuang Ban Man	433349	—	—	—	—
2	Hua 98*	Za Xuan 4/Jianggezhuang Ban Man	—	6	8130**	rP1/Hybrid 1	—
2	Hua 101*	Baisha 1016/Zhong Xuan 65	—	6	Hua Yu 16**	8223/Lai Nong 10	—

*Breeding level defined as the maximum number of breeding cycles (mutation/hybridization/selection or mass selection) from ancestral lines.

^bHybrid names arbitrarily assigned to hybrids not identified by name or number in published records.

*,**Denotes members of the set of 75 Chinese cultivars and breeding lines and the set of 20 important cultivars and breeding lines, respectively.

$$\theta_{XY} = (\theta_{AY} + \theta_{BY})/2 = (\theta_{XC} + \theta_{XD})/2 = (\theta_{AC} + \theta_{AD} + \theta_{BC} + \theta_{BD})/4 \quad [\text{Eq.1}]$$

Additional rules are required to calculate coancestry between inbred relatives derived by self-fertilization (Cockerham, 1983).

The assumptions used to calculate θ in this study were (a) all ancestors, cultivars and parental breeding lines were homozygous and homogeneous; (b) a cultivar derived from a cross obtained 50% of its genes from each parent; (c) the θ value between a naturally occurring variant or a selection from induced mutation with its antecedent is 0.99. Some lines were derived from the same cross. Because no information was available on the selection path for different lines derived from a given cross, they were assumed to derive from different F_2 plant selections within the populations.

Twenty cultivars were identified as important in the history of Shandong peanut production on the basis of their popularity with growers. Exact production figures are not presented, but each of these 20 cultivars was commonly grown in Shandong province. To analyze the change of genetic base of the 20 important peanut cultivars in Shandong province, the cultivars were separated in two groups by release date, those released before 1990, and those released after 1990. Because current Chinese production is divided into small-seeded cultivars having less than 71 g per 100 seeds (more than 40 seeds oz⁻¹) and large-seeded cultivars having more than 74 g per 100 seeds (fewer than 38 seeds oz⁻¹), this distinction was made among the cultivars released after 1990.

Results and Discussion

Genetic Base of the 69 Improved Shandong Peanut Cultivars. Twenty-six ancestors were identified in the pedigrees of 69 improved cultivars and breeding lines (Table 2; Fig. 1). Those ancestors accounted for 99.7% of the genetic base of the Chinese peanut cultivars. The remaining 0.3% represented genetic variation of unknown origin in lines derived by selection within others. Among the 26 ancestors, 24 are of Chinese origin including 17 landraces, three cultivars selected by mass selection from unknown landraces (Zhong Xuan 48, Zhong Xuan 65, and Qun Xuan 5), and four breeding lines with unknown pedigree (Cheng Shi 3, Chang Da 6, 534-11, and RH-77-4-2). Two ancestors were exotic introductions (Xie Kang Qing and Florunner).

Coefficient of parentage analysis revealed that 24 ancestors of Chinese origin contributed 96.1% of the Shandong peanut genetic base. The two exotic introductions accounted for 3.6% of the genetic base and appeared in the pedigrees only five cultivars. Most ancestors belonged to var. *hypogaea* and var. *vulgaris*. There were two ancestors from var. *hirsuta*, Da Ma Ke and Luojiang Ji Wo, but they account for only 0.9% of the genetic base of Shandong peanuts. Most cultivars or breeding lines were derived directly or indirectly from hybridization between var. *hypogaea* and var. *vulgaris*; some from hybridization within var. *vulgaris*; and only a few from hybridization of var. *hirsuta* with var. *hypogaea* or var. *vulgaris*.

The relative genetic contributions of individual ancestors to the 69 cultivars ranged from 0.2 to 36.2% (Table 2). Seven ancestors (534-11, Da Ma Ke, Florunner, Laiyang Ban Man, Qun Xuan 5, RH-77-4-2, and Sheyang You Guo) had only

Table 2. Importance of 26 ancestors in the pedigrees of 69 improved cultivars and breeding lines in Shandong.

Ancestor	No. of descendants	Mean θ among 69	Cumulative θ	Mean θ	
				among nonzero values	Maximum θ
Fu Hua Sheng	67	.3621	.3621	.3729	.9900
Shi Tou Qi	28	.0966	.4587	.2381	.5000
Jianggezhuang Ban Man	27	.1671	.6258	.4270	.7500
Shuyang Da Zhan Yang	19	.0591	.6850	.2147	.4950
Wendeng Da Li Dun	16	.0421	.7271	.1816	.5000
Wulian Cheng Po Tun	12	.0533	.7804	.3065	.5000
Cheng Shi 3	8	.0208	.8012	.1795	.2500
Da Hua Sheng	6	.0254	.8265	.2917	.5000
Xie Kang Qing	4	.0254	.8519	.4375	.5000
Chang Da 6	3	.0063	.8582	.1458	.2500
Jiu Guo	3	.0072	.8655	.1667	.2500
Luojiang Ji wo	3	.0072	.8727	.1650	.2475
Tengxian Xiao Ma Ye	3	.0288	.9015	.6633	.9900
Beijing Da Hua Sheng	2	.0036	.9051	.1250	.1250
Deyang Ji Wo	2	.0036	.9087	.1250	.1250
Dongcun Zhan Yang	2	.0036	.9124	.1250	.1250
Zhaoyuan Ban Man	2	.0216	.9340	.7450	.9900
Zhong Xuan 48	2	.0109	.9448	.3750	.5000
Zhong Xuan 65	2	.0145	.9593	.5000	.5000
534-11	1	.0072	.9666	.5000	.5000
Da Ma Ke	1	.0018	.9684	.1250	.1250
Florunner	1	.0108	.9792	.7450	.7450
Laiyang Ban Man	1	.0072	.9864	.5000	.5000
Qun Xuan 5	1	.0072	.9937	.5000	.5000
RH-77-4-2	1	.0018	.9955	.1250	.1250
Sheyang You Guo	1	.0018	.9973	.1250	.1250

one descendant each, and made a cumulative contribution of only 4.1% of the Shandong peanut genetic base. The four most important ancestors based on number of descendants among the 69 improved lines and average coancestry with all 69 improved lines were Fu Hua Sheng (67 descendants, mean θ = 0.36), Shi Tou Qi (28 descendants, mean θ = 0.10), Jianggezhuang Ban Man (27 descendants, mean θ = 0.17), and Shuyang Da Zhan Yang (19 descendants, mean θ = 0.06). These four ancestors accounted for 68.5% of the genetic base of Shandong peanut.

The 20 most important peanut cultivars released during 1950-1999 traced to 22 ancestors (Table 3) which accounted for 99.7% of the genetic base of the 20 cultivars. There were 12 ancestors related only to one cultivar each, and the four most common ancestors of the 20 cultivars were same as the four most common ancestors of all 69 improved lines. These four most frequent ancestral lines together contributed 67.7% of genetic base of the 20 cultivars. No other line contributed more than 4.0% of the genetic base. The average θ of an ancestor with the 20 important cultivars and its average θ with all 69 improved lines were strongly correlated ($r = 0.997$, $P < 0.01$). The high frequency of the four most common lines in pedigrees not only suggested their importance in peanut cultivar development in Shandong, but also the narrow genetic base of peanut cultivars of the province.

Fu Hua Sheng was ancestral to 67 of the 69 improved lines (exceptions were the two lines selected directly from other landraces) and all 20 important cultivars of Shandong

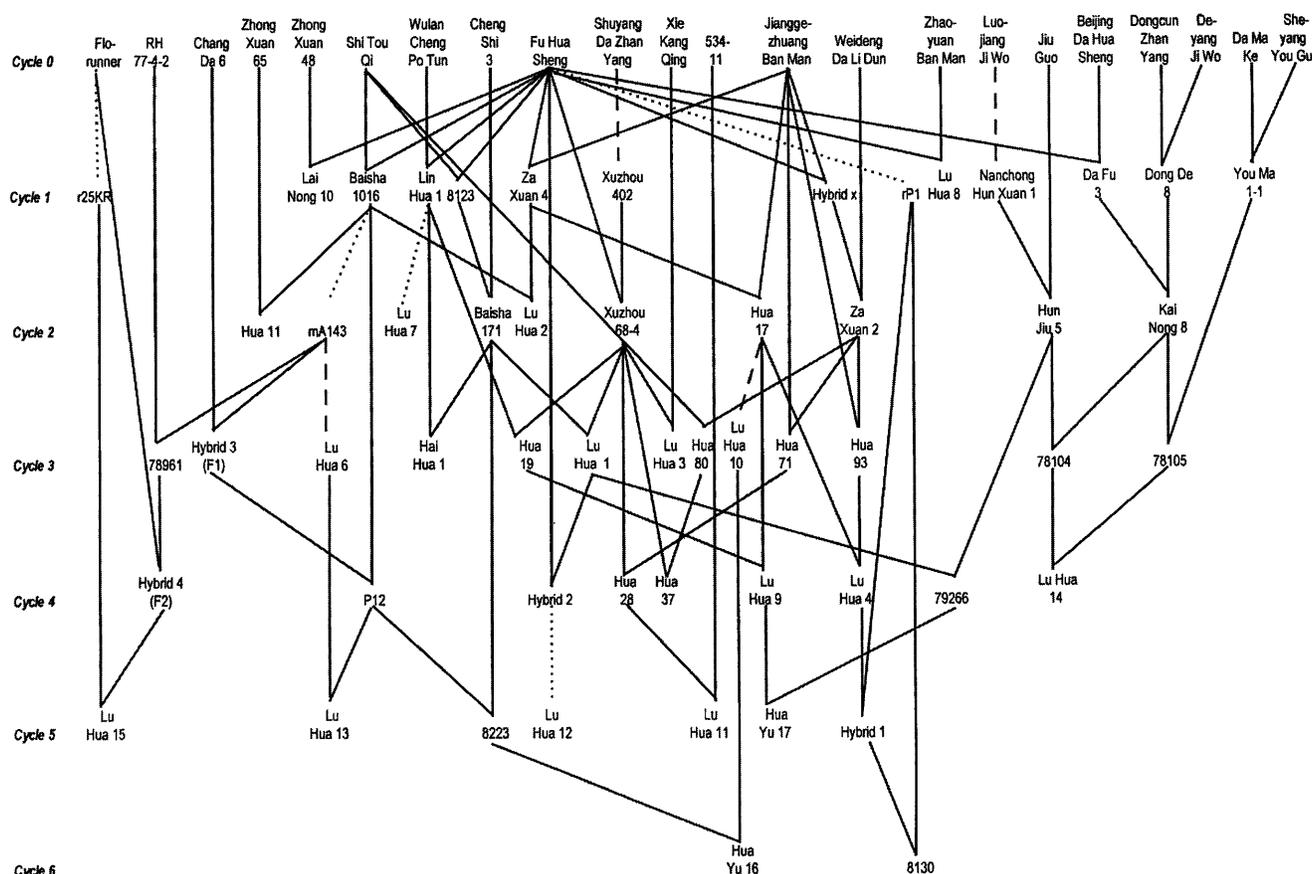


Fig. 1. Ancestry of peanut cultivars and breeding lines from Shandong province, PRC; (.....) selections following mutation; (----) mass selections, and () hybrid lines.

Table 3. Importance of 26 ancestors in the pedigrees of 20 important cultivars and breeding lines in Shandong.

Ancestor	No. of descendants	Mean θ among 20	Cumulative θ	Mean θ among nonzero values	
				among nonzero values	Maximum θ
Fu Hua Sheng	20	.3496	.3496	.3496	.7894
Shi Tou Qi	10	.0965	.4461	.1930	.5000
Shuyang Da Zhan Yang	9	.0928	.5389	.2061	.4950
Jianggezhuang Ban Man	8	.1379	.6768	.3448	.7500
Cheng Shi 3	5	.0343	.7111	.1373	.2500
Wendeng Da Li Dun	4	.0172	.7283	.0859	.1250
Jiu Guo	3	.0250	.7533	.1667	.2500
Luojiang Ji wo	3	.0248	.7780	.1650	.2475
Wulian Cheng Po Tun	3	.0219	.7999	.1458	.2500
Chang Da 6	2	.0094	.8093	.0938	.1250
534-11	1	.0250	.8343	.5000	.5000
Beijing Da Hua Sheng	1	.0063	.8405	.1250	.1250
Da Ma Ke	1	.0063	.8468	.1250	.1250
Deyang Ji Wo	1	.0063	.8530	.1250	.1250
Dongcun Zhan Yang	1	.0063	.8593	.1250	.1250
Florunner	1	.0373	.8965	.7450	.7450
RH-77-4-2	1	.0063	.9028	.1250	.1250
Sheyang You Guo	1	.0063	.9090	.1250	.1250
Xie Kang Qing	1	.0250	.9340	.5000	.5000
Zhaoyuan Ban Man	1	.0250	.9590	.5000	.5000
Zhong Xuan 48	1	.0125	.9715	.2500	.2500
Zhong Xuan 65	1	.0250	.9965	.5000	.5000
Da Hua Sheng	0	.0000	.9965	--	.0000
Laiyang Ban Man	0	.0000	.9965	--	.0000
Qun Xuan 5	0	.0000	.9965	--	.0000
Tengxian Xiao Ma Ye	0	.0000	.9965	--	.0000

province. Its average coancestries with the 69 improved lines and 20 important cultivars were 36.2 and 35.0%, respectively. Fu Hua Sheng is a var. *vulgaris* cultivar selected from landraces of Shandong province in the 1950s. It has early maturity, high and stable yield, broad adaptation, and drought tolerance. It was the most popular cultivar in China in the 1950s and 1960s. By 1995, the cumulative area under Fu Hua Sheng was 7,866,000 ha, making it first among Chinese peanut cultivars. Fu Hua Sheng is still grown by a few farmers.

Shi Tou Qi is in the pedigree of 28 of the 69 improved lines and 10 of the 20 important cultivars. It is a var. *vulgaris* landrace from Guangdong province in southern China. Baisha 1016, a var. *vulgaris* cultivar derived from the cross of Shi Tou Chi with Fu Hua Sheng, was another important cultivar in China's peanut production history. It figured prominently in the pedigrees of more recent cultivars and lines, passing along the genetic contribution of Fu Hua Sheng and Shi Tou Qi. Its cumulative area was 5,685,000 ha, ranking third; and it was widely used as a parent in the Shandong breeding program. Fu Hua Sheng and Shi Tou Qi two together have contributed 45.9% of the genetic base of the 69 improved lines and 44.6% of the 20 important cultivars.

The next two most important ancestors were var. *hypogaea* cultivars, Jianggezhuang Ban Man and Shuyong Da Zhan Yang. Jianggezhuang Ban Man is a landrace of Shandong province. Za Xuan 2 and Za Xuan 4 are the two important

breeding materials derived from Jianggezhuang Ban Man in combination with Fu Hua Sheng and Weideng Da Li Dun. Twenty-seven of the 69 improved lines and eight of the 20 important cultivars are descended from Jianggezhuang Ban Man. Shuyong Da Zhan Yang was an ancestor of 19 of the 69 improved lines and nine of the 20 important cultivars. The most important cultivar and parental material derived from it was Xuzhou 68-4, a high yielding middle-type variety released by Xuzhou Agricultural Institute. Xuzhou 68-4 was introduced and became successful in Shandong, Hebei, and elsewhere in the northern peanut production area.

Extensive use of a few local cultivars and breeding lines as parents in the Shandong breeding program resulted in the narrow genetic base of Shandong peanut cultivars. More recently, utilization of var. *hirsuta*-type germplasm and exotic material has enhanced genetic variability among these cultivars. Two var. *hirsuta* ancestors, Luojiang Ji Wo and Da Ma Ke, accounted for 0.9% of the genetic base of the 69 improved lines and 3.1% of the 20 important cultivars. These lines are ancestral to the recently released high yielding and disease-resistant cultivars 79266 (resistant to early leaf spot (*Cercospora arachidicola* Hori), and late leaf spot [*Cercosporidium personatum* (Berk. & M.A. Curtis)

Deighton]), Lu Hua 14 [resistant to web blotch (*Phoma arachidicola* Marasas *et al.*), early and late leaf spots, and peanut stripe virus], and Hua Yu 17 (resistant to early and late leaf spots). The introduced lines important in the ancestry of Shandong peanuts were Xie Kang Qing, a cultivar selected from material from India, and Florunner from the USA. Xie Kang Qing is resistant to bacterial wilt [*Pseudomonas solanacearum* (Smith) Smith] and was an ancestor of the wilt-resistant cultivar Lu Hua 3. Florunner was an ancestor of Lu Hua 15, a newly released cultivar with high yield and improved ratio of oleic to linoleic fatty acids in the oil.

The Genetic Relationship Among Peanut Cultivars.

To analyze the change of genetic base of the important peanut cultivars in Shandong province, the cultivars were separated in two groups by release date. Important cultivars released before 1990 (Table 4) were all in breeding Levels 0 to 4; those released after 1990 were in Levels 4 to 6. The average degree of relationship among pre-1990 releases was somewhat higher (mean $\theta = 0.25$, range 0.06 to 0.99) than that among post-1990 releases (mean $\theta = 0.16$, range 0.01 to 0.56). The 11 pre-1990 releases were closely related to Fu Hua Sheng ($0.25 \leq \theta \leq 0.50$, mean $\theta = 0.35$). The average

Table 4. Coefficients of coancestry among Fu Hua Sheng and 20 important improved cultivars and breeding lines in Shandong.

Line no.	Level	Cultivar name	Line number																				
			000	001	002	003	004	005	006	007	008	009	010	011	012	013	014	015	016	017	018	019	020
Lines released before 1990																							
000	0	Fu Hua Sheng	---	.50	.50	.25	.25	.50	.38	.25	.25	.31	.31	.38	.19	.13	.28	.16	.79	.41	.68	.43	.06
001	1	Baisha 1016	.50	---	.25	.50	.13	.25	.25	.13	.12	.16	.28	.19	.13	.06	.16	.08	.39	.37	.37	.86	.12
002	1	Lu Hua 8	.50	.25	---	.13	.13	.25	.19	.13	.12	.16	.16	.19	.09	.06	.14	.08	.39	.20	.34	.22	.03
003	2	Hua 11	.25	.50	.13	---	.06	.13	.13	.06	.06	.08	.14	.09	.06	.03	.08	.04	.20	.19	.19	.43	.06
004	2	Hua 17	.25	.13	.13	.06	---	.13	.09	.06	.99	.31	.13	.56	.05	.03	.30	.16	.37	.10	.17	.11	.02
005	2	Xuzhou 68-4	.50	.25	.25	.13	.13	---	.19	.50	.12	.53	.53	.38	.28	.06	.33	.27	.39	.20	.53	.22	.03
006	3	Hai Hua 1	.38	.25	.19	.13	.09	.19	---	.09	.09	.12	.15	.23	.19	.05	.21	.06	.30	.28	.37	.22	.03
007	3	Lu Hua 3	.25	.13	.13	.06	.06	.50	.09	---	.06	.27	.27	.19	.14	.03	.16	.13	.20	.10	.26	.11	.02
008	3	Lu Hua 10	.25	.12	.12	.06	.99	.12	.09	.06	---	.31	.12	.56	.05	.03	.30	.15	.37	.10	.17	.11	.02
009	4	Hua 28	.31	.16	.16	.08	.31	.53	.12	.27	.31	---	.36	.33	.15	.04	.24	.50	.31	.13	.31	.13	.02
010	4	Hua 37	.31	.28	.16	.14	.13	.53	.15	.27	.12	.36	---	.23	.17	.04	.20	.18	.27	.17	.32	.24	.03
011	4	Lu Hua 9	.38	.19	.19	.09	.56	.38	.23	.19	.56	.33	.23	---	.12	.05	.56	.16	.38	.15	.30	.16	.02
Large-seeded lines released after 1990																							
012	4	79266	.19	.13	.09	.06	.05	.28	.19	.14	.05	.15	.17	.12	---	.15	.56	.08	.15	.14	.34	.11	.02
013	4	Lu Hua 14	.13	.06	.06	.03	.03	.06	.05	.03	.03	.04	.04	.05	.15	---	.10	.02	.10	.05	.09	.05	.01
014	5	Hua Yu 17	.28	.16	.14	.08	.30	.33	.21	.16	.30	.24	.20	.56	.56	.10	---	.12	.27	.15	.32	.13	.02
015	5	Lu Hua 11	.16	.08	.08	.04	.16	.27	.06	.13	.15	.50	.18	.16	.08	.02	.12	---	.16	.06	.15	.07	.01
016	6	8130	.79	.39	.39	.20	.37	.39	.30	.20	.37	.31	.27	.38	.15	.10	.27	.16	---	.32	.54	.34	.05
017	6	Hua Yu 16	.41	.37	.20	.19	.10	.20	.28	.10	.10	.13	.17	.15	.14	.05	.15	.06	.32	---	.34	.38	.05
Small-seeded lines released after 1990																							
018	5	Lu Hua 12	.68	.37	.34	.19	.17	.53	.37	.26	.17	.31	.32	.30	.34	.09	.32	.15	.54	.34	---	.32	.05
019	5	Lu Hua 13	.43	.86	.22	.43	.11	.22	.22	.11	.11	.13	.24	.16	.11	.05	.13	.07	.34	.38	.32	---	.11
020	5	Lu Hua 15	.06	.12	.03	.06	.02	.03	.03	.02	.02	.02	.03	.02	.02	.01	.02	.01	.05	.05	.05	.11	---
Mean θ			.35	.26	.19	.14	.21	.29	.18	.16	.21	.24	.22	.26	.16	.06	.23	.13	.31	.19	.31	.24	.04
SD of θ			.18	.19	.12	.12	.23	.16	.10	.11	.23	.14	.12	.16	.12	.04	.14	.11	.16	.12	.15	.19	.03
Minimum θ			.06	.06	.03	.03	.02	.03	.03	.02	.02	.02	.03	.02	.02	.01	.02	.01	.05	.05	.05	.05	.01
Maximum θ			.79	.86	.50	.50	.99	.53	.38	.50	.99	.53	.53	.56	.56	.15	.56	.50	.79	.41	.68	.86	.12
θ w/ pre-1990			.35	.25	.20	.15	.26	.32	.17	.18	.26	.27	.24	.30	.13	.05	.25	.16	.36	.20	.33	.27	.04
θ w/ post-1990, large			.32	.20	.16	.10	.17	.26	.18	.13	.17	.23	.17	.24	.21	.08	.24	.09	.20	.14	.30	.18	.02
θ w/ post-1990, small			.39	.45	.20	.23	.10	.26	.21	.13	.10	.15	.20	.16	.15	.05	.16	.08	.31	.26	.18	.21	.08

coancestry of Fu Hua Sheng to the post-1990 releases was similar (0.32 for large-seeded and 0.39 for small-seeded releases), but the range of values was larger (0.13 to 0.79 for large-seeded and 0.06 to 0.68 for small-seeded releases). It has been fairly common practice in the Shandong peanut breeding project to backcross a line to one of its parents, to intermate half-sibs, and to select within existing cultivars with or without mutagenesis, leading to high degrees of relationship between ancestors and descendants.

The average coancestry of individual pre-1990 releases with other releases in that group was at least 0.15. Hua 11, Hai Hua 1, and Lu Hua 3 had the lowest average degree of relationship with the others. One of the parents of Hua 11, Zhong Xuan 65, is of unknown ancestry, so we have assumed that Zhong Xuan 65 has no relationship with the other ancestors. One of the parents of Hai Hua 1 was var. *vulgaris* cultivar Cheng Shi 3 from Guangdong province. It is another ancestor of unknown origin and like Zhong Xuan 65 was assumed to have no relationship with the other ancestors, but it may be related to Shi Tou Qi based on its phenotype and geographic origin. Lu Hua 3 was developed for use in an area with a bacterial wilt problem. It was descended from Xie Kang Qing, a resistant exotic introduction from India.

Fu Hua Sheng, Baisha 1016, Xuzhou 68-4, Hai Hua 1, and Lu Hua 9 were the most popular cultivars during the past several decades. All are highly related (mean $\theta = 0.32$, intermediate between half- and full-sibs, with a range of 0.19 to 0.50) and trace to only six ancestors.

The coancestries among the large-seeded post-1990 releases were variable. Lu Hua 14 and Lu Hua 11 had the lowest average coancestries with the other cultivars in this group (mean $\theta = 0.08$ and 0.09 , respectively). Lu Hua 14 had eight ancestors, six of which were ancestral only to Lu Hua 14. Lu Hua 11 also had a unique ancestor, 534-11.

The most important large-seeded type cultivars released since 1990 are Lu Hua 11, Lu Hua 14, 8130, Hua Yu 16, and Hua Yu 17. These new releases trace to 15 ancestors. The coancestries among these releases average 0.13 and range from 0.02 to 0.27. Hua Yu 16 and 8130 are highly related to Fu Hua Sheng. The coancestry of 8130 with Fu Hua Sheng was 0.79 due to backcrossing to rP1, a line selected from irradiated Fu Hua Sheng.

Although Lu Hua 9 and Lu Hua 10 are still in commercial production, the genetic base of large-seeded Shandong peanuts has expanded dramatically since 1990. The change has occurred because contributions of var. *vulgaris* ancestors Fu Hua Sheng and Shi Tou Qi have decreased through the incorporation of more diverse ancestry in new cultivars. The new releases have more var. *hypogaea* and var. *hirsuta* ancestry in their pedigrees, expanding the genetic base.

Small-seeded peanut cultivars are grown on fewer hectares than large-seeded cultivars in Shandong province, and the breeding programs for the two types have been separate within SPRI. The new small-seeded cultivars Lu Hua 12 and Lu Hua 13 are still closely related to Fu Hua Sheng and Baisha 1016 because they trace to lines derived from Fu Hua Sheng by mutation breeding. The recently released Lu Hua 15 derives 75% of its ancestry from the introduced cultivar Florunner and therefore is probably more closely related to U.S. runner cultivars than it is to other Shandong cultivars.

The average coancestry of Lu Hua 15 with the other 19 improved lines was less than 0.06 except with Baisha 1016 ($\theta = 0.12$). Wide use of Lu Hua 15 in Shandong has reduced the domination of Fu Hua Sheng and Shi Tou Qi as the main sources of ancestry of small-seeded cultivars grown in the province.

The analysis above shows that recently developed cultivars exhibit larger numbers of ancestors in the pedigree than do cultivars released before 1990. A diverse ancestral background within individual cultivar may prevent the genetic vulnerability associated with a narrow genetic base. Scientists at SPRI have made great effort to enhance the genetic base of peanut cultivars during the past 20 yr. As a result, the genetic diversity of peanut cultivars in Shandong province had expanded dramatically. This level of genetic diversity can be maintained if the SPRI breeding program continues to make judicious use of introduced germplasm and avoids crossing related parents to create new breeding populations.

Although these results are primarily of use to peanut breeders in China, there also may be some application in breeding programs in the U.S. The only genetic relationship between Chinese and U.S. germplasm is due to the use of Florunner as an ancestor of Lu Hua 15. Because most U.S. cultivars are related to some extent to Florunner (Knauff and Gorbet, 1989), Lu Hua 15 is related also to that U.S. germplasm. Otherwise, the Chinese germplasm is completely unrelated to U.S. cultivars and breeding lines. Therefore, Chinese germplasm may be useful to U.S. breeders in developing breeding populations of diverse genetic background.

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