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The Suggested Strategies to Use Wheat Core Collection Based on Some Important Agronomic Traits Evaluation

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ABSTRACT

The importance of core collection is accepted worldwide. Wheat (*Triticum aestivum* L.) core collection has been established in China for years, but few attentions have been paid on systematically agronomic performances. Objective of this study was to suggest the reasonable strategies to effectively use them based on some important agronomic traits and on both stripe rust and powder mildew resistance evaluation. Field tests were conducted in two locations in different years. Resistance tests revealed that landraces had a better adaptability than modern varieties, and there were abundant variations existed in almost agronomic traits examined both among and within regions. Additionally, the differences between two locations in these traits were not significant at $P=0.05$ level, and some varieties, possessing excellent traits in the past, exhibited poor performances. The strategies are to choose some elite genotypes from Middle and lower reaches of Yangtze River (MY) and Yellow-Huai River region (YH) as main receipt or donor parents for yield improvement, and to use the more landrace than modern varieties by multi-cross and backcross for resistance breeding, and to improve the plant type using the germplasm from YH, MY, Southwest of China (SWC), and South of China (SC), have been proposed and discussed.

Keywords: Agronomic performance, Core collection, Disease resistance, Strategies, Wheat.

Introduction

Crop germplasm has evolved into various ecotypes as a consequence of both artificial and natural selection. The number of genotypes within a species is over several thousands, and this is becoming a hamper to effectively use them in crop breeding. To facilitate their applications, Frankel and Brown (1984) coined the term "Core Collection", which represents the maximum repetitiveness in genetic diversity of a crop species and its wild relatives within a minimum subset. Subsequently, core collections for different species have been established, including soybean (Wang et al., 2006), sorghum (*Sorghum bicolor* (L.) Moench) (Deu et al., 2006), barley (Casas et al., 2005), peanut (*Arachis hypogaea* L.) (Holbrook et al. 1993), pea (Mcphee 2005), and rice (*Oryza sativa* L.) (Xu et al., 2005). In China, the wheat core collection has been established based on analyses both of biochemical and DNA markers by cluster analysis (Zhang et al. 2002; Dong et al. 2003; Hao et al. 2006).

The development of core collections have been very effective in enhancing the germplasm research in many crops, such as screening the genotypes for root-knot nematode resistance in peanut (Holbrook et al. 2000), molecular analysis of wild bean (Tohme et al. 1996) and peanut (Kottapalli et al. 2007), acid soil

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tolerance research in alfalfa (Bouton 1996). These studies have accelerated the breeding process. In wheat, many studies have mainly focused on the diversity on genetic (Smale et al. 2002; Dreisigacker *et al.* 2005; Hao et al. 2006), biochemical (Zhang et al. 2002; Shu et al. 2008), and physiological indices (Shu et al. 2008) rather than the agronomical traits evaluation of the germplasm.

Actually, the agronomic traits would play the more important role for wheat improvement (Tayyar et al. 2008). Therefore, to characterize the available genetic resources constitute an essential task in wheat breeding programs. Disease resistance is also one of the most important traits for development of sustainable agriculture. Stripe rust, caused by *Puccinia striiformis* f.sp. *tritici* Westend., and powdery mildew, caused by *Erysiphe graminis* DC f.sp. *tritici* Marchal., were the most important wheat diseases worldwide. The most economical and safe-environmentally way to control these diseases is to use resistant cultivars. However, the majority of the wheat cultivars have become susceptible due to the high frequent variation of the pathogen population, especially in the recent years (Chen *et al.* 2005; Luo *et al.* 2005). Previous report shows that it is possible to screen resistance genotypes from wheat core collection to the both diseases (Dong *et al.* 2003). Therefore, to identify new resistance sources constitutes a key objective in wheat resistance breeding program.

Although there are numerous reports on agronomic traits and disease resistance of wheat, those studies did not shed on the whole wheat resources, especially on the core collection, but on a limited number of genotypes (Shah *et al.* 1999a, b; Campbell *et al.* 2003; Atienza *et al.* 2007; Tayyar *et al.* 2008). Furthermore, reports on the diversity in phenotypic characteristics, and the evaluation of diseases resistance of wheat core collection are few. This would severely impede to use the core collection in wheat improvement, effectively. The objectives of the present study were to (i) investigate and evaluate the most important agronomic traits of the core collection, and (ii) discuss its potential for wheat breeding and suggest reasonable strategies to apply them in the breeding programs.

Materials and Methods

Plant materials and experiment design

A total of 178 wheat genotypes from eight regions in China have been detected in the present experiment, which was kindly provided by Prof. Dr. J. Z. Jia, Institute of Crop Germplasm Resources, Chinese Academy of Agricultural Science, Beijing. There are 105 (about 59%) landraces among them, which indicates its high significance for wheat breeding and research. Seeds were planted in two locations, (i) Center of Wheat Breeding of Sichuan Agricultural University between 2004-2005, Qiong Lai, with altitude 465 m, and about 30.42°N and 103.47°E; and (ii) Agricultural Research Center of Sichuan Agricultural University between 2005-2006, Ya'an, with altitude 500 m, and about 30°N and 103°E. Both soil types were clay with high organic matter and humus content because the returning of straw to field soil after harvested for several years. Nutrients and water were supplied as required throughout the growing seasons.

The design for both tests was randomized complete block with three replications. Each plot was 1 m wide with 3 m long rows (the spacing between rows was 25 cm). The interplant spacing was 10 cm. Harvest began when the plants had senesced thoroughly during late May of 2005 and 2006, respectively, due to maturity differences among these genotypes, mature plants were harvested by hand on a plant basis.

Measurements of agronomic traits

Six agronomic traits including straw length, spike length, tillers, spikelets per spike, neck length of spike, and 1000-grain weight per genotype were investigated in two different locations described above. The length from the base of the plant at soil level to the top spikelet excluding the awn has been recorded as straw length. The length from the neck of spike to top spikelet except the awn has been recorded as spike length. All stems originated from one seed have been recorded as tillers. The length from the bottom of joint between the flag leaf and main stem to the bottom of spike has been recorded as neck length of spike. The number of spikelets of one spike has been recorded as spikelets per spike. Wheat seeds were dried at 110°C for 36 hours and then the 1000-grain weight has been determined.

Stripe rust and powdery mildew tests

To avoid the interaction between both pathogenic bacteria, stripe rust resistance evaluation was conducted in Qiong Lai, Center of Wheat Breeding of Sichuan Agricultural University in 2005; and powdery mildew resistance evaluation was tested in Ya'an, Agricultural Research Center of Sichuan Agricultural University in 2006. Both locations are characterized by moist and warm environments, and the anterior and the latter are favorable to stripe rust and powdery mildew occurrence, respectively (Table 1).

Table 1: The climatic data of the two locations (Qionglai and Ya'an) in the latest 30 years' during the wheat growing stage. (These data kindly supplied by Dr. Y.X. Yang, Department of Meteorology and Ecology, College of Resource and Environment, Sichuan Agricultural University)

Region	Oct	Nov	Dec	Jan	Feb	Mar	Apr.	May	Mean/Total
Temperature (Qionglai)(° C)	17.3	12.2	7.7	5.8	7.5	12.2	17.1	21.2	12.6
Temperature (Ya'an) (° C)	16.6	12.1	7.8	6.1	7.7	12.2	17	20.5	12.5
Rain (Qionglai) (mm)	69.1	26.4	9.5	11.1	19	30.5	60.2	87	312.8
Rain (Ya'an) (mm)	115.1	61.6	22	18.5	29.2	52.5	93	141.6	533.5
Sunshine (Qionglai) (hour)	59.6	58.2	61	69.6	60.6	87.4	107.2	110.2	613.4
Sunshine (Ya'an) (hour)	55.3	52.7	52	58.7	56	81.3	106.1	99.4	561.5

The stripe rust and powdery mildew resistance tests were developed at seedling stage according to the previously described methods (Luo *et al.* 2005; Chen *et al.* 2005). The infection type was recorded as 6 classes (0 to 4) according to the methods also described by Luo *et al.* (2005), respectively as follows: 0, no visible symptoms; 0₁, few necrotic flecks; 1, small sporulating uredia surrounded by necrotic tissue; 2, small to medium uredia with chlorosis and necrosis; 3, moderately sized sporulating uredia surrounded only by chlorotic tissue; and 4, abundantly sporulating uredia without chlorosis. Reactions were classified into two groups, with resistant (R) (IT=0-2) and susceptible (S) (IT=3 and 4) infection types, respectively.

Data collection and analysis

Evenly and randomly sampling 10 plants per genotype from 3 replications were used for agronomic traits evaluation. The average value of the 10 measurements represented the results for each genotype in one location, the means of both averages as the final data of this genotype. Taking the genotypes from the same ecological region as a group, the final data described above of each agronomic performance per genotype used for analysis. Before these analyses were performed, ANOVA were conducted to test that whether there exist the significant differences between two locations in the traits examined. Mean, variances, and standard errors (SE) per trait were calculated for each region; and the test of homogeneity of variances has been conducted before ANOVA and Multiple comparison analysis (using *LSD* for equal variances and *Tamhane's T2* for not equal variances) of the agronomic traits among the eight regions of origin of the accessions was performed. All the analysis was done using SPSS 15.0 for Windows (SPSS Inc., Chicago, USA).

Results and discussion

Agronomic performances of core collection

The mean value of the 6 traits examined (mean \pm standard error of mean) for the wheat core collection was showed in Fig.1. The significant differences in the agronomic traits are not examined between two locations at $P=0.05$ level (Table 2). The test of homogeneity of variances and the ANOVA results are listed in Table 3 and the multiple comparison analysis was showed in Table 4.

Regarding the 1000-grain weight of core collection, the highest values corresponded to genotypes from YH, MY, SWC, and SC's (Fig. 1), and the significant differences were detected between 5 region-pairs at 0.05 level and 9 pairs at 0.01 level in this trait (Table 4), and these four regions also showed the highest variation among other agronomic traits examined (Table 3). Spike length showed low data (Fig. 1), compared with the wheat cultivars used in production, at present (Zhuang 2003), which may result in the low 1000-grain weight; and the abundant variation among and within regions were examined in spike length (Table 3; Table 4). The genotypes from SC showed the higher values for neck length of spike (23.64 cm) while genotypes from NWC have the shortest (12.67cm). ANOVA analysis showed significant differences among regions in this trait. However, multiple comparison analysis revealed that only 3 region-pairs, NC-SC, MY-NWC, SC-NWC have significant differences at 0.01 level (Table 4).

Regarding to the number of tillers, the number was around 10 in almost all regions, and there were 6 region-pairs where there exist significant differences (NC-SC, NC-YH, NC-QT, NC-SWC, MY-YH, and MY-QT). The range of the wheat core collection in the straw length was too large. The shortest and longest data were 117.32 cm of NC and 136.76 cm of NEC, respectively. The high straw length suggests poor lodging resistance. The genotypes from NC and YH show the shortest straw length compared with those from other regions. There were many genotypes over 120 cm in straw length. The variation for this trait was the lowest among the traits examined except the spikelets of spike (Table3, 4, 5), only two region-pairs, NC-MY and MY-YH showed significant differences. The number of spikelets per spike founded in the present experiment was also lower than that of cultivars used in production, nowadays (Zhuang 2003), and the ANOVA revealed that there not exist significant differences among eight regions. Therefore, no further analyses were performed on it.

Table 2: ANOVA showed that there not exist significant differences in the traits examined between two locations.

Trait	ANOVA of Eight Regions ^a									
	MY					NC				
		Sum of Squares	df	F	Sig.	Sum of Squares	df	F	Sig.	
1000-grain weight	Between Groups	30.147	1	1.2	0.3	16.182	1	0.4	0.5	
	Within Groups	1390.1	54			2577.95	58			
Neck Length of Spike	Between Groups	7.676	1	0.3	0.6	112.226	1	2.734	0.1	
	Within Groups	1367.3	54			2380.58	58			
spike length	Between Groups	3.874	1	0.9	0.3	8.152	1	2.9	0	
	Within Groups	232.01	54			161.83	58			
spikelets per spike	Between Groups	0.915	1	0.3	0.6	7.884	1	1.8	0.2	
	Within Groups	169	54			248.366	58			
Straw length	Between Groups	248.5	1	0.7	0.4	495.171	1	1.7	0.2	
	Within Groups	18045	54			17398.7	58			
Tillers	Between Groups	2.472	1	0.9	0.4	3.951	1	0.4	0.5	
	Within Groups	153.93	54			608.627	58			
		SC				SWC				
1000-grain weight	Between Groups	2.265	1	0	0.9	25.295	1	0.6	0.5	
	Within Groups	967.32	14			1667.8	38			
Neck Length of Spike	Between Groups	1.521	1	0	0.8	0.731	1	0	0.9	
	Within Groups	331.16	14			953.3	38			
spike length	Between Groups	0.758	1	0.3	0.6	4.932	1	1.5	0.2	
	Within Groups	39.747	14			122.447	38			
spikelets per spike	Between Groups	3.18	1	1.2	0.3	6.751	1	3.4	0	
	Within Groups	36.284	14			75.568	38			
Straw length	Between Groups	653.87	1	1.1	0.3	1.436	1	0	1	
	Within Groups	8207.6	14			21042.2	38			
Tillers	Between Groups	0.124	1	0	0.9	0.015	1	0	1	
	Within Groups	54.179	14			413.684	38			
		NEC				NWC				
1000-grain weight	Between Groups	183.74	1	3.5	0	61.587	1	0.6	0.5	
	Within Groups	951.73	18			2334.67	22			
Neck Length of Spike	Between Groups	27.986	1	1	0.3	29.561	1	0.7	0.4	
	Within Groups	501.06	18			962.498	22			
spike length	Between Groups	3.472	1	1.3	0.3	0.378	1	0.2	0.7	
	Within Groups	48.963	18			49.207	22			
spikelets per spike	Between Groups	0.735	1	0	0.8	3.458	1	1	0.3	
	Within Groups	210.49	18			76.509	22			
Straw length	Between Groups	499.33	1	1.6	0.2	299.761	1	0.9	0.3	
	Within Groups	5699	18			6985.35	22			
Tillers	Between Groups	4.263	1	0.8	0.4	2.119	1	0.2	0.7	
	Within Groups	93.706	18			233.494	22			
		YH				QT				
1000-grain weight	Between Groups	0.863	1	0	0.9	26.532	1	0.6	0.4	
	Within Groups	8324.9	116			877.983	20			
Neck Length of Spike	Between Groups	51.369	1	1	0.3	53.217	1	1.1	0.3	
	Within Groups	5937.7	116			952.405	20			
spike length	Between Groups	0.771	1	0.2	0.6	0.08	1	0	0.9	
	Within Groups	369.84	116			48.543	20			
spikelets per spike	Between Groups	4.497	1	0.3	0.6	0.134	1	0	0.8	
	Within Groups	1784.9	116			60.019	20			
Straw length	Between Groups	11.997	1	0	0.9	995.861	1	2.9	0.1	
	Within Groups	87401	116			6934.89	20			
Tillers	Between Groups	0.796	1	0.2	0.7	2.122	1	0.8	0.4	
	Within Groups	456.87	116			52.89	20			

^a NC, North of China MY, Middle and lower reaches of Yangtze River NEC, Northeast of China SC, South of China; YH, Yellow-Huai Rivers region; QT, Qinhai-Tibet region NWC, Northwest of China SWC, Southwest of China.

Resistance responses to both stripe rust and powdery mildew

The different resistance level to stripe rust and powdery mildew among wheat core collection was listed in Table 5. The results show that only 20% (36) genotypes, with 70% landraces, of the core collection have the resistance to stripe rust, and that 33.7% genotypes, also with 70% landraces, of the core collection have the resistance to powdery mildew.

The landraces from YH possess the larger resistance potential to stripe rust (43%) and powdery mildew (60%), and in NC, the percentages were 47% and 6%, and in MY, the numbers were 37% and 5%, and in SWC, the percentages were 50% and 12.5%, respectively. Oppositely, the modern varieties showed the poor resistance for the both diseases, in YH region, the percents of resistance varieties in the whole modern genotypes were 17% (for stripe rust) and 10% (for powdery mildew), and in MY, the numbers even both to 0%. However, the contrast result in SWC was investigated. In this region, the percentages of modern varieties higher than that of landraces both in stripe rust and powdery mildew tests.

Table 3: The test of homogeneity of variances and analysis of variance evaluating the difference on the six agronomic traits examined of core collection. For ecological abbreviations see Table 2.

Trait	Test of homogeneity of variances			ANOVA				
	Levene Statistic	Sig.	Sources	SS	df	MS	F	Sig.
1000-grain weight	0.938	0.48	Between Groups	2216	7	317	5.6	0
			Within Groups	9540.6	170	56.1		
			Total	11757	177			
Neck Length of Spike	2.837	0	Between Groups	1083.3	7	155	3.8	0
			Within Groups	6943.6	170	40.8		
			Total	8026.9	177			
spike length	0.297	0.95	Between Groups	92.905	7	13.3	4.3	0
			Within Groups	521.58	170	3.07		
			Total	614.49	177			
spikelets 1.035	0.41		Between Groups	55.667	7	7.95	1.2	0.3
			Within Groups	1105.7	170	6.5		
			Total	1161.4	177			
Straw length	2.746	0	Between Groups	10013	7	1430	2.8	0
			Within Groups	86217	170	507		
			Total	96230	177			
Tillers 1.693	0.11		Between Groups	133.03	7	19	3.3	0
			Within Groups	971.55	170	5.72		
			Total	1104.6	177			

Table 4: The multiple comparisons analyze evaluating the mean difference on six agronomic traits examined from eight regions in China. For ecological abbreviations see Table 2.

Trait	Region	Region						
		MY	NEC	SC	YH	QT	NWC	SWC
1000-grain weight	NC	-5.8962**	0.6491	-9.3974**	-7.7705**	-0.55	-0.03	-2.66
	MY		6.5453*	-3.501	-1.874	5.3469*	5.8672*	3.239
	NEC			-10.0465**	-8.4196**	-1.2	-0.678	-3.31
	SC				1.6269	8.8481*	9.3684**	6.7397*
	YH					7.2212**	7.7415**	5.1128**
	QT						0.5203	-2.11
	NWC							-2.63
	SWC							
Spike length	NC	-0.195	-1.8683**	-0.415	0.98468*	0.474	-0.313	-0.1
	MY		-1.6732*	-0.22	1.1797**	0.669	-0.118	0.136
	NEC			1.4538	2.8530**	2.3425**	1.5549*	1.8095**
	SC				1.3992*	0.889	0.1012	0.356
	YH					-0.51	-1.2980*	-1.0434*
	QT						-0.788	-0.53
	NWC							0.255
	SWC							
Tillers	NC	0.4894	1.5628	1.9186*	2.0835**	2.7674**	1.1771	1.4886*
	MY		1.0734	1.4293	1.5941**	2.2781**	0.6878	0.999
	NEC			0.3558	0.5207	1.205	-0.386	-0.1
	SC				0.1649	0.849	-0.742	-0.43
	YH					0.684	-0.906	-0.59
	QT						-1.59	-1.28
	NWC							0.312
	SWC							
Neck Length of Spike	NC	-5.013	-4.2731	-7.5522**	-3.004	-0.49	3.4174	-2.94
	MY		0.7396	-2.54	2.0082	4.52	8.4301**	2.076
	NEC			-3.279	1.2686	3.781	7.6905	1.336
	SC				4.5478	7.06	10.9696**	4.615
	YH					2.512	6.4219	0.07
	QT						3.9098	-2.44
	NWC							-6.35
	SWC							
Straw length	NC	-19.4464**	-19.03	-15.84	-1.499	-12.7	-6.212	-7.56
	MY		0.4193	3.6043	17.9477**	6.717	13.235	11.89
	NEC			3.185	17.529	6.298	12.816	11.47
	SC				14.344	3.113	9.6308	8.281
	YH					-11.2	-4.713	-6.06
	QT						6.5179	5.168
	NWC							-1.35
	SWC							

* The mean difference is significant at the 0.05 level.

** The mean difference is significant at the 0.01 level.

Table 5: The description of core collection and the resistance responses to powdery mildew and stripe rust. For ecological abbreviations see Table 2.

Region	M/L	Resistance to PM ^a (M/L)	Resistance to SR ^b (M ^c /L ^d)
NC	15/15	39447	39635
MY	39709	39447	39453
NEC	39602	39447	39447
SC	39511	39478	39447
YH	29/30	39524	39580
QT	39486	39447	39448
NWC	39574	1/0	39509
SWC	39553	39508	39485
Total	73/105	39776	18/42

^a PM: Powdery Mildew.

^b SR: Stripe Rust;

^c M: Modern varieties;

^d L: Landrace;

In all, the results indicate that the core collection possesses greater resistance potential to powdery mildew (60/178=33.7%) than that to stripe rust (36/178=20%), generally.

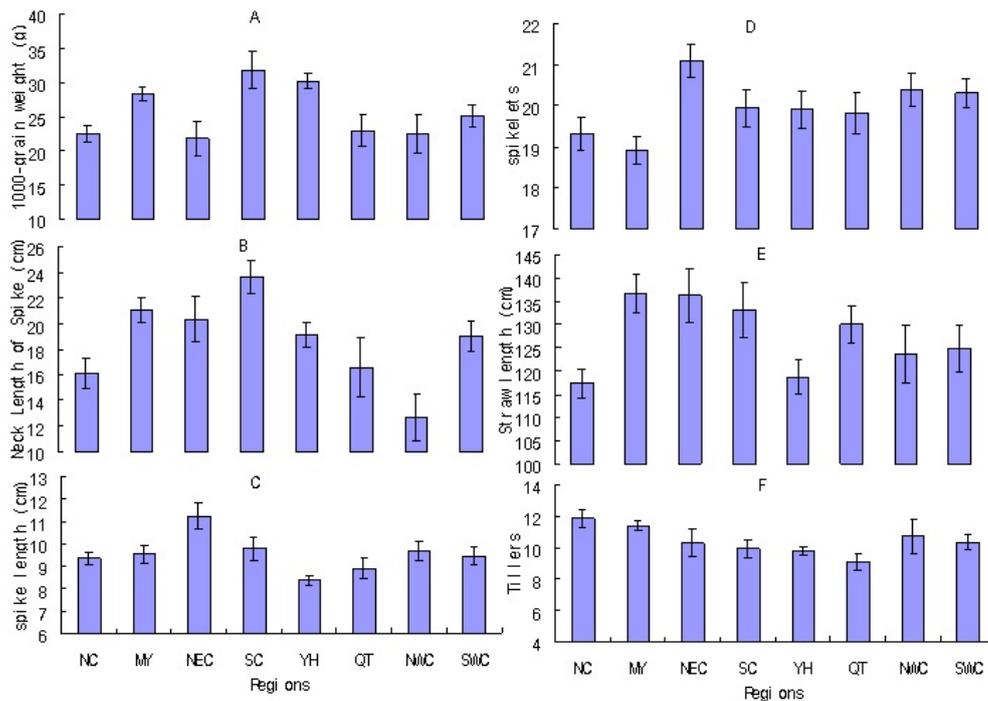


Fig. 1: Mean value of the 6 traits examined (mean ± standard error of mean) for wheat core collection from eight ecological regions. Where A: 1000-grain weight; B: Neck length of spike; C: spike length; D: spikelets; E: straw length; F: tillers. For ecological abbreviations see Table 2.

The strategies to use core collection based on agronomic traits evaluation

The necessity of core collections is accepted worldwide since they constitute a reservoir of genes for crop breeding and basic research. Agronomic traits are probably the most important characteristics in wheat production and variety certification because they directly express and influence the yield (Fagam *et al.* 2006). The existence of variability is the key for breeding progress; therefore no variability means no progress. In this study, the results showed that the variations of the traits examined both among and within regions are different, generally the order from high to low is 1000-grain weight>spike length>neck length of spike>tillers> straw length>spikelets (Table 3).

As one of the most important yield components, the 1000 grain weight made maximum contribution to phenotypic stability of the genotypes, especially to wheat yield (Verma *et al.* 1998). In the present study, the 1000-grain weight and spike length have the largest variation both among and within the regions, the order from high to low of 1000-grain weight generally is SC>YH>MY>SWC, and the order of spike length is NEC>SC>MY>NC>YH. Generally, the high variation founded for the spike length is concordant with the variation of the 1000-grain weight. However, YH's genotypes possess the high 1000-grain weight with the

lowest spike length data, and NEC's genotypes possess the low 1000-grain weight with the highest spike length data, this may be explained by different grain densities in the spike among genotypes. In this experiment, we found that some genotypes showed low grain density on the spike with loosely and small-volume grains such as NEC's genotypes, and contrast, some showed the higher density with large grains tightly such as YH's genotypes.

The neck length of spike and tillers showed the abundant variation both among and within the ecotype regions secondly by the 1000-grain weight and spike length. The order were SC>MY>NEC>YH for neck length of spike and NC>MY>NWC for tillers, generally. These two traits influence the yield component directly (Fagam *et al.* 2006). The straw length and spikelets per spike showed the low level variation in this experiment. Many genotypes are over 120cm in straw length, generally; accordingly they had poor lodging resistance ability in the field trial. As a consequence we had to use string and sticks to fix the plants. Regarding to spikelets, there not exist significant differences among eight regions. Therefore, no further analyses were performed on it.

Generally, the genotypes from South region of China (included SC, SWC, YH) and middle regions (MY) showed the highest yield potential. A possible explanation for the facts is that where are the cross regions from North to South of China. So, the genotypes developed within there have to endure the selection pressure from both regions. Consequently these accessions show the greatest adaptation ability to the present area. In contrast, the genotypes from QT had the lowest 1000-grain weight and fewer tillers than the genotypes from other regions. Since the climatic conditions of QT is different sharply, and the genotype from this region can't endure the climatic conditions of experiments region, so breeders should choose the materials from QT, carefully and cautiously. Consequently, the wheat breeders in SWC should consider the genotypes from these areas as parent lines to accelerate breeding, to improve wheat yield or/and morphologic indices. These conclusions are supported by our previous report (Shu *et al.* 2008) from biochemical and physiological indices.

The strategies to use core collection based on resistance test

The occurrence of stripe rust and powdery mildew is highly influenced by environmental factors. The environmental conditions of Southwest China were optimal for the both diseases (Luo *et al.* 2005; Ma *et al.* 2007). Therefore, to identify new resistance genotypes in this region is an essential task especially in core collection.

In the resist subsets, among resistant genotypes to stripe rust, 70% were landraces, with the similar percentage for powdery mildew resistance (Table 5). The landraces constitutes an excellent material pool for wheat resistance breeding. Many studies revealed that the landraces and wheat relative species may possess great abilities to stripe rust and powdery mildew (Schneider *et al.* 2008; Xie *et al.* 2008); it is maybe that they contained multi-resistance genes as a reservoir gene pool. The authors have reported the new gene(s) for resistance to powdery mildew, PmE and PmYU25 (Ma *et al.* 2007) from relative species and to stripe rust, YrCN19 from a wheat landrace (Luo *et al.* 2005), and the expression and segregation of YrCN19 in different genetic background were evaluated (Luo *et al.* 2006). We found that many modern varieties possess single resistance gene, become soon ineffective to the new pathogenic races (Luo *et al.* 2005). So, breeders ought to focus on the genetic resources available, including both landraces and wild species, to transfer the resistance genes to wheat genetic background by traditional crossing or by using modern genetic engineering methods.

The landraces from some regions such as YH, MY, SWC and SC possess the highest resistant ability to both diseases. Besides the genotypes have the highest 1000-grain weight values and excellent agronomic performance. Therefore they should be excellent parents for wheat breeding. A suggested order for choose the genotypes as main parents based on the evaluation of agronomic traits and resistance tests is YH, SWC, MY, NC. However, the contrast result in SWC was investigated. In this region, the modern varieties showed the stronger potential than that of landraces both in stripe rust and powdery mildew tests. The possible explanation for this fact is that the demands for wheat breeding, the both diseases are the most important standards for variety certification.

In this core collection, the modern varieties showed lower resistance level and agronomic performance than those of the landraces. These modern varieties possess the low 1000-grain weight (25.63g), and the longest neck length of spike (18.57cm), averagely, and in average, the spike length, spikelets per spike, straw length and tillers was 9.54cm, 19.97, 127.61cm, 10.43, respectively. They showed undesirable traits for production. Furthermore, many elite cultivars in the past such as *Yanzhan No. 1*, *Bima No. 1 and 4*, *et al.*, have lost their resistance against stripe rust and powdery mildew. There are two possible explanations for this fact, (i) most of genotypes released in other regions can not endure the ecological conditions of the experiment area, which underlines the high significant differences from Southwest China in both climate and ecological conditions; and (ii) the declining of variation intensifies this phenomenon. In order to stay the varieties' excellent performances and great diseases resistance and great yield for a long time, it is suggested that wheat breeders ought to pay more attention on landrace and relative species to introduce the alien gene to improve wheat, and to use more parent genotypes, and to focus on many agronomic traits by multi-cross and backcross.

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Abbreviations

MY, Middle and lower reaches of Yangtze River; **NC**, North of China; **NEC**, Northeast of China **NWC**, Northwest of China; **QT**, Qinhai-Tibeat region; **SC**, South of China; **SWC**, Southwest of China; **YH**, Yellow-Huai River region.

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