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Postulation of Stripe Rust Resistance Genes in 44 Chinese Wheat Cultivars

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ABSTRACT

Based on the gene-for-gene concept, genes can be postulated from the correlation of the responses of selected resistance sources with those of controls. Using 35 testers and 26 *Puccinia striiformis* f. sp. *tritici*, stripe rust resistance genes were postulated for 44 wheat cultivars commonly grown in Hebei, Henan and Shandong Provinces in China. 22 seedling *Yr* resistance genes (*Yr1*, *Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr17*, *Yr20*, *Yr21*, *Yr22*, *Yr23*, *Yr24*, *Yr27*, *Yr32*, *YrHV*, *YrSD*, *YrV23*, *YrRes*, *YrC591* & *Yrcle*in) were postulated in 18 of the 44 tested cultivars, either singly or in various combinations. The most commonly detected resistance gene was *Yr21*, which was present singly or in combination with other resistance genes in 13 cultivars (29.5%), followed by *Yr1* (27.3%) and *Yr6* (27.3%). No effective genes except *Yr24* against Chinese predominant PST races CYR32 and CYR33 were detected in the 44 tested cultivars. These results provided a better understanding of specific resistances in the 44 tested cultivars. The introduction and utilization of wheat germplasm with effective resistance genes such as *Yr5*, *Yr10*, *Yr15* and *Yr24/Yr26* are important in wheat breeding in Northern China. © 2011 Friends Science Publishers

Key Words: Gene postulation; *Puccinia striiformis*; Resistance gene; Wheat; Cluster analysis

INTRODUCTION

Wheat stripe rust, caused by *Puccinia striiformis* Westend. f. sp. *tritici* Eriks. (Pst), is the most important wheat disease worldwide. In China, stripe rust occurs in major wheat production regions and severely threatens the safety of our agricultural production. In recent years such as 2002, 2003 and 2009, it was the most evident and damaging rust in northwestern, southwestern, and northern China, as well as in the spring wheat areas in the northwest (Wan *et al*., 2004, 2007; Chen *et al*., 2009).

The use of resistant cultivars is the most effective, economical, and environmentally friendly means to control stripe rust and ensures wheat output increase. The genetic interaction between *P. striiformis* f. sp. *tritici* races and race-specific resistance genes in wheat is interpreted according to the gene-for-gene model (Flor, 1971). Gene postulation applies the gene-for-gene concept to determine the most probable resistance genes present in host lines and the presence of known rust resistance genes can be postulated using an array of rust cultures with known pathogenicity (multipathotype tests) (Sharma *et al.*, 1995; Singh *et al.*, 2001; Amin *et al*., 2006, 2007; Ochoa *et al.*, 2007; Feng *et al.*, 2009).

The objective of the current study was to postulate genes for seedling resistance to stripe rust in 44 wheat cultivars grown in Hebei, Henan and Shandong Provinces in China. It is meaningful to define the composition of stripe rust resistance genes in wheat cultivars, their genetic characteristics and resistance characteristics, to exploit new stripe rust resistance resources or resistance genes for avoiding large-scale planting a cultivar with single resistance gene, to last control of the disease epidemic, and to ensure the safety of wheat production.

MATERIALS AND METHODS

Wheat germplasm and *Pst* isolates: Forty four wheat cultivars from Hebei, Henan and Shandong Provinces in China, 35 tester lines with known *Yr* genes including susceptible check Mingxian 169, were provided by Plant Protection Institute, Chinese Academy of Agricultural Sciences (Table I & II). A total of 26 isolates were used in this study which originated from annual pathogenicity surveys of *P. striiformis* f. sp. *tritici* (*Pst*) conducted in China. Vacuum-dried urediniospores of these isolates were stored in liquid nitrogen in Plant Protection Institute, Chinese Academy of Agricultural Sciences. Before

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Table I: Tested cultivars and their pedigrees

Cultivar	Pedigree
Yumai18	Zhengzhou761/yanshi4hao
Ru0319(rumai0319)	Taiguhesterileline
Luohan2hao	78(111)ai/jinmai33
Zhengmai366	Yumai47/PH82-2-2
Yumai49	Wen2540mutant
Pingan6hao	Laizhou953/wen2540
Xiangmai969	Zhoumai9hao/yumai18//yumai18
Xin18	(C6/xinxiang3577)F3d1s//xinmai9hao
Xinmai208	Ji5418/yumai18
Luomai21	Luomai1hao/zhoumai13
Xinmai19	(C5/xinxiang3577)F3d1/xinmai9hao
Zhou20	Zhoumai12/xinmai9hao//wenmai6hao
04zhong36	Bainong64/zhoumai11
Taikong6hao	Yumai49hao
Tongzhoumai916	Yumai18/pumai8441//wenmai4hao
Zhengmai9023	Xinong881/shan213
Huapei5hao	Yumai18hao/(lumai1hao//yumai2hao/zhou13)
Zhongmai2hao	Luomai haoCo$^{60}\gamma$raymutation
Jinan17	Linfen5064/lumai13
Taishan22(taishan269)	Lumai18/lumai14
Yannong19	Yan1933/shan82-29
Jimai20	Lumai14/lu884187
Taishan21	(26744/taishan10hao//lumai7hao)/lumai18hao
Zimai12hao	917065/910292
Taishan23	876161/881414
Jimai21	865186/chuannongda84-1109//ji84-5418
Lumai23	Lumai8hao/gaolaiwheat"daliai"
Jimai19	Lumai13/5064
Jining13	Yan1934 82(4)046//liao83-1 2114
Lumai21	Baofeng7228/yanzhong144
Zimai7hao	856043/865017
Yanfu188	Yanzhong22/xingmai7721
Taimai1hao	Zinong003//841527/tai9010106
Shimai15	GSjimai38hao/92R137
Leting639	Fengkang12/yue1831
Jimai22	935024/935106
Shixin539	Shixin422/shixin612
Shixin733	Damuzhiai/shixin163
Guan35	Heng84guan749/heng87-263
Liangxing99	91102/lumai14hao//PH85-16
Shixin828	422/shixin63//612
Shiyou17	Ji935—352/lumai21
Liangxing66	Ji91102/ji935031
Shimai12	Shi92-5096/jimai23

inoculation, each isolate was purified, verified for the correct virulence phenotype on the differential genotypes and increased on 'Mingxian 169'.

Inoculation, disease assessment and gene postulation: Seedling tests were conducted under controlled greenhouse conditions with the day/night regime of 14 h light (22 klux) at 17^{o}C and 10 h of darkness at 12^{o}C, 70% relative humidity. Seeds of the cultivars (lines) were first soaked in 1% H_20_2 solution, and then 7-10 seeds per cultivar (line) were planted in a 35 cm ×24 cm plastic pot filled with a potting mixture of 2 surface soil from the field: 1 turfy or soddy soil. Seven to ten seedlings per cultivar (line) were tested with each isolate. Each line was tested in two replications. If there were significant differences between replications in reaction types, additional tests were conducted to obtain confirmed correct data.

When the first leaf was fully expanded, seedling inoculations were performed by brushing urediniospores of each isolate from a fully infected susceptible cultivar, Mingxian 169, onto the seedlings. After inoculation, seedlings were then transferred to growth chambers (15-18^{o}C day/10-14^{o}C night temperature cycle) with a 12-14 h photoperiod. Infection types (ITs) were scored 15-16 days after inoculation when rust was fully developed on the susceptible check Mingxian 169.

Based on the 0-4 scale (0, 0;, 1, 2, 3, 4) of infection type (IT), the disease assessment standard was further detailed with "+", "-" and divided into 0, 0;, 0;$^{+}$, 1, 1^{+}, 2^{-}, 2, 2^{+}, 3^{-}, 3, 3^{+}, 4, in which IT 0-2 was resistant, and IT 2^{+}-4 was susceptible. Based on the gene-for-gene hypothesis, resistance gene or genes in each cultivar (line) were postulated by comparing their resistance spectra with previously determined spectra on testers with known *Yr* resistance genes according to Dubin *et al.* (1989).

Statistical analysis: Based on the result of gene postulation, the resistance genes in the 44 wheat cultivars same as those in the tester lines were recorded as 1, none genes in the wheat cultivars same as those in the tester lines were recorded as 0. Similarity analyses were done with the NTSYS-pc ver. 2.11 software (Rohlf, 2000). Dendrogram chart was produced according to the un-weighted pair-group mean arithmetic method (UPGMA) using NTSYS-pc software (Sneath & Sokal, 1973).

RESULTS AND DISCUSSION

Gene postulation: Multiple pathotype seedling tests were conducted to postulate stripe rust resistance genes in the greenhouse using 26 Chinese Pst isolates and 35 testers with known *Yr* genes (Table III). When reactions of a cultivar matched those of a tester with known resistance gene or genes, the resistance gene(s) in the tester were postulated to also present in the cultivar. The result of gene postulation was listed in Table III. Based on the multipathotype tests conducted, 22 seedling *Yr* resistance genes (*Yr1*, *Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr17*, *Yr20*, *Yr21*, *Yr22*, *Yr23*, *Yr24*, *Yr27*, *Yr32*, *YrHV* , *YrSD*, *YrV23*, *YrRes*, *YrC591* & *Yrcle*in) were postulated in 18 of the 44 tested cultivars, either singly or in various combinations. Of 44 tested cultivars, 13 cultivars carried *Yr21*, accounting for 29.5%, 12 cultivars carried *Yr1* (27.3%), 12 cultivars carried *Yr6* (27.3%), 11 cultivars carried *Yr7*, *Yr22*, and *Yr23* gene combination (25%) and 11 cultivars carried *Yr6 and Yr20* gene combination (25%). The remaining *Yr* genes were present in less than 10 cultivars, either singly or in various combinations, indicating that the distribution of *Yr* genes among wheat cultivars grown in major wheat production regions in Northern China is not reasonable. The simplification of *Yr* genes was not conducive to the prevention of the wheat stripe rust in China.

Table II: Reaction patterns of 35 testers with known *Yr* resistance genes to 26 isolates of *Puccinia striiformis*

Tester	*Yr* gene	Isolate of *P. striiformis* and infection type																									
		85079	78080	75078	76088	96036	CYR29	86106	CYR26	58893	61009	68009	74187	60105	80551	CYR32	CYR31	82061	CYR17	78028	85019	CYR33	76093	Su-1	59791	78070	CYR27
Chinese166	*Yr1*	0	4	3	2	3+	3+	2	4	0;	0;	3+	4	3-	3	3	0-0;	0;	3	0;+	0;	0;+	3	3	2	4	3
Josscambier	*Yr2*	0 +	2	3-	0;	0 +	2+	2	3-	0;	2+	3-	3-	1	0;	2+	2	3	1	0;	1	1+	0	1+	32	2	2
Heines Kolben	*Yr2.6*	0 +	0;+	0;+	2+	3	0 +	2	0	0;+	3-	2	4	3-	2+	3-	1+	3+	0-0;	1+	0;+	1+	3	0;+	2	2	0
Maries Huntsman	*Yr2.3.4*	0 +	0;+	1	2	0 +	1	3	3+	0;	3	3-	2	0;+	2	4	0	4	1+	3	0;+	0;+	2	0	3-	1	2
Heiness	*Yr2.H*	1	1+	3	1	2	2	3	3-	1	1+	4	1+	3	3	1	3	3	2	2	2	2+	3-	2+	3	2	1
Strubes Dicddopf	*YrSD*	1+	3-	2	3-	3-	2	3	3	1	3+	4	3+	4	4	3	0	4	3-	3	2	0;+	4	3-	3	4	3
Vilmorin23	*Yr3.V23*	0 +	2	0;+	2	0;+	1	3+	0;+	0;	3+	3+	3-	3	2	3-	0;+	3	4	1	0;+	0;+	2+	2+	2+	3	0
Cappelle Deprez	*Yr3.+*	1+	2	2	0;+	1	1	2	0;	1	3-	4	3-	0;+	0;+	3	1	3	1	2	1+	0;+	1+	1+	3	2	3-
Mega	*Yr3*	0 +	4	0;+	2	3-	1+	3	0;	0;	3-	3+	3+	2+	1	3	0	3+	1+	1+	0;	0 +	3	0	2+	1+	0
Hybrid46	*Yr4.+*	0 +	2	1	2+	3-	0 +	3-	0;	1+	3	0;+	3-	3	3+	2+	0;+	3	1	2	0;+	0 +	2	3	1	1+	0;
T.Spelta Album	*Yr5*	0 +	0	0;+	0;+	0;+	0	0;+	40	0;	0;+	0;	0;+	0;	1	0;	0;	0;+	0;	0-0;	0	0 +	0 +	0;+	0;+	4	0;+
Lee	*Yr7.22.23*	4	4	3	0;+	3+	4	3	4	4	0;	3+	0;	0;	1+	3	2+	0;+	3	0;	4	3	1	3	0;	4	4
Reichersberg42	*Yr7.+*	1	3	1+	0;+	1	3	3-	1+	2	0;	3	0;+	0;	3-	0;+	1	0;+	3	0;	1	2+	1+	3	0;+	2	2
Cement	*Yr9.cle*	0	0	0	0	0	0	0;+	0;	0;	0;	0;	0	0	0;	3	0;	0	3	0	0	0	0;+	0	0;	0	0
Lovrin13	*Yr9.+*	0	0	0-0;	0	0;	0;	0;+	0;	0;	0	0;	0-0;	0	0;	3	0;	0	0;	0;+	0	0	0;	0	0;	0	0
Moro	*Yr10.Mor*	0;	0	0;	0	0	0	0	0;	0;	0	4	0;	0;	0	0	0	0	0;	0;	0	0 +	0	0	0;	0	0
VPMI	*Yr17*	0;	4	1+	1	1	2	2	0;	0;	2+	4	3-	2	2	2+	0;	2	0-0;	1	0;+	0 +	0;	4	2	4	0
Fielcer	*Yr6.20*	3-	4	4	0 +	3+	3+	3	3	4	0;+	4	0;+	0;	0	4	3	3+	4	0;+	3	2+	0;	4	0;	4	3
Lemhi	*Yr21*	3	4	3	2	3+	4	2	3	4	4	3	4	0	0	3	2	3	4	0-0;	3	3	4	3	4	3	2+
K733	*Yr24*	0;+	0 +	2	0	0;	0	2	3	2	3-	3-	3-	3	1	0;+	0;+	3	3+	0;+	0;+	2+	3-	0	4	2	2
AvocetS* /Yr15	*Yr15*	0	0	0;+	0	0;	0	0;+	0	0	0-0;	0;	0	0	0	0	0;+	0	0	0	0	0	0	0	0	0	0
TP981	*Yr25*	0 +	0;+	1	0;	0;+	0;	0;	3	0;+	4	0;+	4	0	0;	2+	0;	0;	1	0	0	0	0;	0	4	2	0;
LineR55	*Yr26*	0 +	0;+	0;+	0	0;	0	0;+	1+	0;+	0;+	0;	0;	0;	0	0;+	1+	0;+	0;	0;	0;	0 +	0;	0;+	0;	0;+	0
Selkirk	*Yr27*	2+	3-	3-	1	3-	3	2	4	4	3-	1	3+	2	0;+	2	3	3	3	3	3	3-	4	3	3-	3	2
T.tauschiiw-219	*Yr28*	0;	0;+	2+	0;	0;	0;+	0;	0;	0;	0;	0;	0;	0	1	3-	0;+	4	0;+	0;	0;+	0;+	0-0;	1+	3	0;	0
Carstensv	*Yr32*	1	2	2+	3-	3-	2	3	2	3	3+	4	3	3	3+	2+	2+	3-	3-	2	0;+	1	2	2	3-	3	0;
Spaldingsprolific	*YrSpp*	0;+	0;+	3+	0	0;+	0	2+	2	0	0	4	0;	0	0;+	3	2+	3	0	0;+	0;+	0;	0;+	0;	0;	2	0;
Res	*YrRes*	0;	0	0	0	0;	0	0;	0	0;	3+	4	0	3	4	13	1+	2	0;	0	0	0;	3-	0	0	0	0
C591	*YrC591*	1	0	0;+	0 +	2	1	1	0 +	2	0;+	2	2+	2+	0;	1+	1	2	0;+	0;	0;+	2	1	0;	2	0;+	0;
AvocetS* /Yr6	*Yr6*	3	3+	3+	0 +	3+	3	3	4	3-	0;+	4	2	0;+	3	3-	3	2	3	0;+	3	1	4	4	0;+	3	4
AvocetS* /Yr7	*Yr7*	3-	2	3+	0 +	3-	2	3-	3-	3-	0;+	4	1	0;	3-	4	2	0;+	4	0;	3	3	2	3+	0;	3	4
AvocetS* /Yr8	*Yr8*	4	2	2+	0 +	3-	3-	2	4	4	0;+	0;	0;	1+	1+	4	3	0	3	0;+	3	3	3-	3-	0;	3	4
AvocetS*/Yr9	*Yr9*	0	0	0	0	0;	0;	0;+	0	0	0	0	0	0;	0	3-	0	0	0	0;	0	0;	2	0	0	0	0
AvocetS* /Yr10	*Yr10*	0	0	0	0	0;	0;	0;	0	0	0	0	0;	0	0	0	0;	0;	0;	0	0	0;	0;	0	0	0	0
Mingxian169	*No*	3+	4	4	3	4	4	3	4	4	4	4	4	4	3+	4	3	4	4	3	4	4	4	4	4	4	4

Several resistance genes *Yr5, Yr10, Yr15* and *Yr24/Yr26* are still effective against Chinese predominant Pst races CYR32 and CYR33 (Kang *et al.*, 2010). In the present study, none of the 44 tested cultivars carried *Yr10*, *Yr15* and *Yr26.* There was only one cultivar (Huapei5) carried *Yr24*. The introduction and utilization of wheat germplasm with *Yr5*, *Yr10*, *Yr15* and *Yr24/Yr26* are important in wheat breeding in Northern China.

Most cultivars with *Yr* genes postulated in the present study carried *Yr1*, e.g., Zhengmai366, Xinmai208 and Luomai21, probably due to excessive utilization of Chinese wheat landraces in breeding programs (Niu *et al*., 2000). The present study showed that Yumai18 only carried *YrSD*. Ximai208 and Huapei5 from Yumai18 (based on the pedigree information) also carried *YrSD*, indicating that *YrSD* might be passed to offsprings Ximai208 and Huapei5 through hybridization.

Tester Lemhi has narrow resistant spectrum, only show resistance to Pst races 76088, 86106, 60105, 80551, 78028 and CYR31 and cannot distinguish from resistant spectrum of other testers. In the present study, the frequency of *Yr21* was the biggest, because the resistant spectrum of Lemhi was covered by resistance spectra of other testers. Since tester Lee showed resistance to Pst races 76088, 61009, 74187, 60105, 80551, 82061, 78028, 76093 and 59791 and tester Fielcer showed resistance to Pst races 76088, 61009, 74187, 60105, 80551, 78028, 76093 and 59791. The resistance spectrum of tester Fielcer was covered by the

Table III: Reactions of 44 wheat cultivars (lines) to 26 isolates of *Puccinia striiformis* and postulated *Yr* genes

Cultivar	Greenhouse testing with selected races of *P. striiformis*																										Postulated *Yr* genes
	85079	**78080**	**75078**	**76088**	**96036**	**CYR2**	**86106**	**CYR2**	**58893**	**61009**	**68009**	**74187**	**60105**	**80551**	**CYR3**	**CYR3**	**82061**	**CYR1**	**78028**	**85019**	**CYR3**	**76093**	**Su-1**	**59791**	**78070**	**CYR2**	
Yumai18	0;	3	0	0	0;	2	3	0;	0	0;	4	0	3	3	2	0;	4	4	0;	0;	0	0	3	4	3	0	*YrSD*
Ru0319	3	2	0;	-	0	0	0	3	3-	3	-	3	3-	0;	3-	0	0	3	0;	4	3	0	3	0	0	3	-
Luohan2	3-	2	2	2	3	2	2	3-	2	4	4	4	4	0;	3-	0;	3+	4	0;	3	0;	3	3	4	4	2	-
Zhengmai366	0	2+	3+	0;	0;	2	2	0	0	0	4	0	4	3-	3	0;	-	0;	0	0	0	3-	0	3+	0	0	*Yr1,YrSD,Yr9.cle,Yr21,Yr6*
Yumai49	-	3+	4	3	3	0	3-	3	4	3	2	3+	3+	3-	3-	0;	-	3	3	-	3+	3+	3	3-	4	3	-
Pingan6	3-	3-	4	1+	1	3-	1	2	1+	3-	3-	4	3	1+	0	3	0	2	3	4	-	3-	-	2	4	3	-
Xiangmai969	0	3+	0;	0;	0;	4	3-	0	0	0;	4	0	3	3	3	0;	0	4	0;	0;	-	4	4	3-	3	3	-
Xin18	3+	0	4	2	3	4	3-	-	4	4	4	3	3	3	-	4	0	4	4	4	-	4	4	2	4	-	-
Xinmai208	0	0;	1	0	2	0	0	0	0	0	0	4	0	0	-	0;	0	0;	0	0;	-	0	0	0	4	0;	*Yr1,YrSD,Yr3.V23,Yr17,Yr21,Yr27,Yr32*
Luomai21	0	0	0;	0	0;	0	0	0	0	0;	0;	0	0;	0;	0	0;	0	0;	0	0;	-	0	4	0	0;	0;	*Yr1,Yr2.H ,YrSD, Yr3.V23,Yr4.+,Yr7.22.23, Yr7.+,Yr17,Yr6.20,Yr21,Yr27,Yr6,Yr7,Yr8*
Xinmai19	3-	2+	4	3	3	4	1+	3	4	3	0	3	3	2	0	4	0	4	2	3	-	4	3	4	4	-	-
Zhou20	2	2	3-	-	-	1	1+	-	4	-	-	0;	0	-	3	-	0	-	4	0;	-	0	2	3	-	0	-
04zhong36	0;	0;	0;	0;	0;	2	0	0	0	0	0;	0	0;	0;	0	0;	0	0;	0	0;	-	0	1+	0	0;	3	*Yr1,YrSD,Yr3.+ Yr7.22.23 Yr6.20 Yr21,Yr6,Yr7,Yr8*
Taikong6	3+	3-	4	2	3	3+	0	3	4	2+	3	3	3	2	3	3	0	4	3	4	-	3-	4	3-	4	3	-
Tongzhoumai916	3	3-	3	0	0;	3	0	3	3-	3+	3	3	3-	0	0	0;	0	2	2	4	-	1+	0	0	3	0	-
Zhengmai9023	3	3	4	2	3+	3	0	3	4	4	4	3	4	0	0	3	0	4	2	4	-	4	4	4	4	3	-
Huapei5hao	0;	0;	0;	0	0	0	0	0	0	0	0;	0	3	0;	-	0	0	0;	0	0;	-	0;	0	0	0	0	*Yr1,Yr2.6,Yr2.H ,YrSD,Yr3.V23,Yr3,Yr4.+,Yr24,Yr32,YrC591,Yr6*
Zhongmai2	0;	4	0;	0	0	3+	1+	0	0;	0	4	0	3	2	3+	0;	0	3+	0;	0;	-	0;	3	3	3-	4	-
Jinan17	1+	2	2	0	0	1+	2	0;	4	2	3+	3	3	0;	0	0	0	1	0;	0	-	3	1	4	2	0	-
Taishan22	3	3+	4	2	3	3	3-	3	4	0;	3	3-	3	0	0	0;	0	4	3	3	-	-	0	3	4	3	-
Yannong19	3-	3+	4	2	4	3	3	3	4	4	3	4	3	3-	3-	3	0	4	3	4	-	4	3	3	4	3	-
Jimai20	4	2+	4	2	3	3	3	3	3+	3+	4	3-	3	2	3	3	0	3	3	3	-	4	3	3+	4	4	-
Taishan21	0;	3-	0;	3	0;	3+	1+	0;	0;	3+	4	3	0	0;	4	0	0	4	3	0;	-	0	4	3	2	0	-
Zimai12	0	0;	0;	0	0;	0	0;	0	0;	0	0	0	0	0;	0	0	0	0;	0;	0	-	0	4	0	0;	0	*Yr1,Yr2.H ,YrSD,Yr3.V23,Yr4.+,Yr7.22.23,Yr7.+,Yr17,Yr6.20,Yr21,Yr27,Yr6,Yr7,Yr8*
Taishan23	3	2+	3	2	3+	3	3	3	4	3	4	3	3	2	3-	3	4	3	3	3	-	3	3	3	4	0	-
Jimai21	3	2	4	2	3+	3+	2+	3	3+	3	4	3	3	3-	3	3	3	4	3	4	-	3+	4	3-	4	4	-
Lumai23	2+	4	3	3-	3	3	2	2	4	4	3	3	1	0;	3	0;	0	4	3	3	-	4	3	3	3-	0;	-
Jimai19	2	3+	4	1	0;	3	0;	2	3-	2	4	0;	1	2	3-	1+	0	2	0;	2	-	3-	3	3	3-	0;	*Yr21*
Jining13	3-	-	0	2	3	0	0;	3	4	0	3	3	0	2+	4	2	_	0;	3	0;	-	0	0	0	-	3	-
Lumai21	2+	2	3-	1+	2	4	3	2	1	3-	3+	3	3	3-	2	3	0	3	2	2	-	3	3	-	3-	0;	-
Zimai7	3-	0;	2	0;	2	3	2	2	3-	2	0	2	2	1	1+	1+	-	-	0;	0	-	0;	3	3-	3	0	*Yr21 Yr27*
Yanfu188	3-	3-	3	0	2+	2	3+	3	3-	0;	4	0;	0	0	3+	3+	0	3	0;	4	-	0	3-	0	3	3	*Yr7.22.23 Yr6.20 Yr6*
Taimai1	-	4	-	0	-	3	0;	-	0;	0;	1	-	0;	0;	-	0	-	-	0	0	0;	0	4	0	0	-	*Yr1, Yr7.22.23 Yr7.+ Yr6.20 Yr21 Yr27 Yr6*
Shimai15	0	3-	0	0	0	3	3	0;	0	0	4	0	0	0;	3	0;	0	4	0;	0;	0;	0	3	0	0;	4	*Yr7.22.23 Yr6.20 Yr6*
Leting639	2	3+	2+	0	3	3	2	1+	3+	3+	4	3	3	2	2	0;	-	3	3	2	0;	0;	3	4	3	3	-
Jimai22	0;	3	0	0	0	3-	2	0	0	0	4	0	0;	0	0	0;	0	3	0;	0;	0;	0;	3	0	0;	0;	*Yr1, Yr7.22.23 Yr7.+ Yr6.20 Yr21 Yr6*
Shixin539	0	4	0;	0	0	3-	3-	0	0	0	4	0	3-	2	0	0;	0	3+	0;	0;	0;	0;	3	2	0;	0;	-
Shixin733	0;	3+	0;	0	0	3	3	0	0;	0	4	0	3-	3	0	0;	0	0;	0;	0;	0;	3	3	3-	0;	0	-
Guan35	0;	0;	0	0	0	0	0;	0	3-	0	0	0	0	0	0	0	0	0;	0;	0	0;	0;	0	0	0;	0	*Yr7.22.23 Yr6.20 Yr21 Yr27 Yr32 Yr6 Yr7 Yr8*
Liangxing99	0;	3-	0	0	0;	2	2	0	0	0	4	0	0;	0;	0	0;	0	3	0;	0;	0;	0;	4	0	0;	2	*Yr1,YrSD Yr7.22.23 Yr7.+ Yr6.20 Yr21 Yr6*
Shixin828	0;	3	0;	0	0;	4	2	0	0;	0;	4	0;	3	3	0;	0;	0	4	0;	0;	0;	0;	3	2	0;	0;	*Yr1*
Shiyou17	3-	3-	3	1	3	2	2	3	3	3-	3	3-	3	1+	3	2	0	3	3	3	0;	3-	2	3	2	2	-
Liangxing66	0;	3-	0	0	0	3	0;	0	0	0	4	0	0;	0;	0	0;	0	3	0;	0;	0;	0;	2	0	0;	0;	*Yr1,Yr7.22.23 Yr7.+ Yr6.20 Yr21 Yr6*
Shimai12	0;	3-	0	0;	0;	2+	2	0	0	0;	3	0	0;	0;	0;	0;	0	3-	0;	-	0;	0;	0	0	0;	0;	*Yr1,Yr7.22.23 Yr7.+ Yr6.20 Yr21 Yr6*

Note: “-”means no postulated *Yr* gene

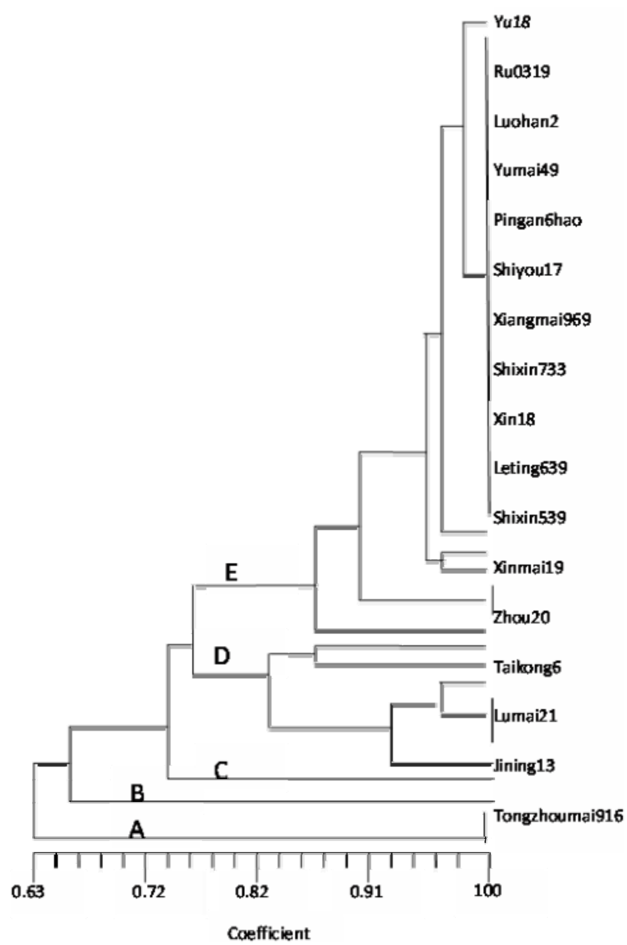
resistance spectrum of tester Lee. As a result, cultivars with *Yr7*, *Yr22* and *Yr23* gene combination also carried *Yr6* and *Yr20* (Table III). Actually, the resistance spectra of testers Lee and Fielcer were also narrow, which explained why 25% cultivars carried *Yr7*, *Yr22* and *Yr23* gene combination and *Yr6* and *Yr20* gene combination. Luomai21 and Zimai12 were postulated to carry over 10 *Yr* genes. The low infection types from Luomai21 and Zimai12 might be due to inadequate inoculation.

Cluster analysis: The dendrogram of UPGMA demonstrated 5 arbitrary groups A, B, C, D and E by clustering infection types of the 35 tester lines and 44 cultivars with more than 82% similarity (Fig. 1). Group A only included cultivars Zimai12 and Luomai21, on which only the race Su-1 was virulent. Group B has one cultivar Huapei5. Comparing with the results of gene postulation, if we put this result in comparison with the above mentioned gene postulation; we would find that cultivar Huapei5 was resistant to 25 isolates used in the present study and only susceptible to race 60105. Group C also had only one cultivar Xinmai208, which was susceptible to races 74187 and 78070. In the present study, Xinmai208 and Huapei5 were all highly resistant to stripe rust. Anyway, based on pedigree information, both Xinmai208 and Huapei5 shared a common parent Yumai18 modest resistant to stripe rust (Xu *et al*., 1992). The reason may be either to pyramid multiple resistant genes during breeding, or just because mixed races under naturally infected conditions were more virulent than single race inoculated one by one in the present study (Zhou *et al*., 2003). Seven cultivars Liangxing99, Liangxing66, Shimai12, Jimai22, Taimai1, Guan35, 04Zhong36 fell in group D, which were determined by carrying known genes *Yr1*, *Yr21* or *Yr26* or combination of known genes *Yr7+Yr22+Yr23* or *Yr6+Yr20*. Except 04Zhong36, all the remaining six cultivars Liangxing99, Liangxing66, Shimai12, Jimai22, Taimai1, Guan35 are major wheat cultivars in Shandong Provinces, China. Hence, most currently cultivated wheat cultivars in Shandong Provinces have a narrow genetic basis for resistance to stripe rust. Wheat breeders and local government need pay more attention to this situation.

Among the 5 groups, group E was the biggest one, including 7 cultivars (Zhengmai366, Shimai15, Shimai15, Yanmai188, Zimai7, Jimai19, Shixin828 & Yu18) with postulated known *Yr* genes and 26 cultivars with un-known genes (Fig. 1). The reason may be that the cluster analysis was based on resistance genes in the cultivars. 26 cultivars had not been postulated known genes in the present study and definitely were grouped in the same group. Anyway, we can conclude that the 26 cultivars shared the same similarity with the 7 cultivars Zhengmai366, Shimai15, Shimai15, Yanmai188, Zimai7, Jimai19, Shixin828 and Yu18.

To certain extent, postulation might provide false positive results and can be only applied for preliminary genetic information. More isolates with different virulence formulae on these *Yr* genes and/or near-isogenic lines

Fig. 1: Dendrogram of the 44 cultivars using UPGMA cluster analysis method



(NILs) with other resistance genes would be used to obtain more accurate gene postulation. So far, Wellings *et al.* (2004) reported that 13 single gene NILs including *Yr1*, *Yr5*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr10*, *Yr15*, *Yr17*, *Yr18*, *Yr24*, *Yr26* and *Yr32* were obtained in his research group based on an Australian spring wheat 'Avocet Susceptible' (AVS) selection, and Xu *et al.* (2004) successfully obtained 7 single gene NILs including *Yr1*, *Yr2*, *Yr5*, *Yr7*, *Yr10*, *YrSpP*, and *YrKy2* based on Taichung 29. All these NILs can be used to differentiate races of *P. striiformis* f. sp. *Tritici* in the future and to more accurately conduct gene postulation. Feng *et al.* (2009) used cluster analysis to support the gene postulation results and make up the deficiency of using gene postulation.

In the present study, cluster analysis was used to assess the characteristics of 44 wheat cultivars, which can classify the resistance of some cultivars with unknown gene(s) or gene combinations and attain more information for deployment and arrangement of unknown genes and production to control wheat yellow rust.

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