Geographical distribution and virulence phenotypes of *Puccinia striiformis* f. sp. *tritici* from wheat in Yunnan, China

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ABSTRACT: Wheat stripe rust, caused by *Puccinia striiformis* is a widespread and destructive disease of wheat, causing significant losses in yield and quality. Survey of wheat stripe rust samples and identification of physiological races using *Yr* single-gene differential lines are very important in describing virulence pattern variation and geographical distribution of rust pathotypes. In the present study, a total of 86 races characterized from 125 stripe rust isolates were collected from Yunnan and Sichuan provinces of China during the 2017/2018 wheat growing season. The races v1 and v2 were widely distributed with virulence frequency of 8.8 and 8%, respectively. The remaining races have a lower frequency ⩽ 3%. The 86 races clustered into two major virulence clusters: cluster-I comprised two races v29 and v30 and had relatively narrow virulence spectra, while cluster-II involved other 84 races and had broad virulence spectra. High virulence frequencies of *Pst* population (>73%) were detected for *Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr(17,29), Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25)*, and *Yr(10,Mor)* genes. Moderate virulence frequencies of *Pst* population (16–73%) were observed for *Yr3, Yr27, Yr(2,HVII)*, and *Yr(7,22,23)* genes. No isolate was detected to be virulent to *Yr5* and *Yr10* genes. The four genes *Yr5, Yr10, Yr15*, and *Yr24* were regarded as effective genes. Therefore, monitoring distribution and frequency changes of virulence toward the *Yr* genes is important for cultivar selection with adequate resistance for growing in specific geographic regions and for developing new cultivars with durable and a high-level resistance.

KEYWORDS: wheat, *Puccinia striiformis*, stripe rust, virulence, resistance gene

INTRODUCTION

Wheat stripe rust (yellow rust) caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) is the most destructive disease worldwide[1, 2]. China is the largest epidemic zone, where about 400 million hectares of the wheat crop is infected by the disease every year since the 1950s. Five significant booms and busts of stripe rust occurred in China[3]. The first outbreak of yellow rust disease occurred in 1950, breaking down resistance of *Yr1* gene in wheat variety Bima[4]. The second outbreak was in 1964, while the third was in 1987 due to the emergence of new race (CYR29) virulent to *Yr9* gene, located in chromosome 1BL. The fourth major epidemic broke out in 2002 due to the appearance of CYR32 race virulent to *Yr4* gene

present in wheat variety Fan-6[5]. The fifth change and current cycle of outbreaks occurred in 2008 due to break-down of resistance of *Yr24* and *Yr26* genes in wheat variety Guinong 22 by the stripe rust race V26[6].

Yunnan is located in Southwest China, neighboring the Himalayas, in which geography is complex, and altitude is quite different, which leads to a diverse climate and ecosystem. Therefore, wheat stripe rust occurs quickly; the pathogen constantly mutates, which results in complicated virulence and higher genetic diversity of pathogens[7]. The outbreak of wheat stripe rust in Yunnan causes not only economic yield losses, but also provide original incursion sources for other parts of China[8], which

plays a crucial role in large scale disease epidemics. Previous research indicated that the Himalayas and neighboring regions such as Pakistan, Nepal, as well as China, are the center of origin for wheat stripe rust pathogen[9]. Thus, Yunnan is a vital ring for the migration chain of wheat stripe rust pathogen in the world, or it may be one of the wheat stripe rust origins. Therefore, study on the population virulence of the pathogen and effectiveness of resistance genes will provide useful information for breeding and rational use of resistant genes; in the meantime, it will monitor new races and give evidence for the origin and migration of the pathogen.

Physiological races determined by infection type (IT) of isolates on a set of differentials, which include selective host genotype or monogenic lines. Due to differences among regions, the pathogen population structure, study level, as well as historical reasons, different countries, and areas use respective different nomenclature to characterize race and virulence in the world. International and European set combined as a set of differentials used in Europe, Australia, the Middle East, South Africa, and Nepal, of which binary system nomenclature is used. North American differentials employed in America and Canada use chronological terminology[10] and named up to V220 by 2016, including 18 single gene lines[11].

Chinese differentials are a half-opened system, include 19 cultivars, use chronological nomenclature[12], and by now named up to CYR34. By 2014, 303 races had been identified in the whole of China (National Initiative of Wheat Rust Annual Report, 2015). For naming races, various systems have been used to designate races of the rust pathogens. The number system, which names races with numbers and usually in sequential order, is the oldest and still widely used. Races of *P. striiformis* f. sp. *tritici* in China, India, and the United States have been named using numbers[6, 13–15].

Except North American differentials, the other differentials are not a set of near-isogenic lines (NILs) and contain one gene, multi-genes or unknown genes[10]. The results of races by these differentials cannot reflect the information of resistant genes directly, although they provide some useful information for the wheat production. Also, with the mutation of stripe rust pathogen virulence in China, current Chinese differentials cannot characterize many isolates in recent years, especially for Yunnan isolates, which needs to be adjusted to adapt the situation. Wan[10] suggested to use a NILs set as differentials, this can monitor the

effectiveness of resistant genes directly, and provide direct information for wheat production. Wellings et al[16] developed NILs to monitor virulence in the *P. striiformis* f. sp. *tritici* populations throughout the world.

Genetic control of wheat stripe rust is achieved by over 50 formally named Yellow rust (*Yr*) resistance (R) genes identified by the continuous efforts of plant breeders and pathologists over the last 100 years[17]. Historically, pathologists have focused on the isolation of *Pst* from wheat fields and have determined the ability of these isolates to infect a defined set of wheat lines carrying different *Yr* R genes. The resulting infection phenotypes determine the virulence profiles and pathogen race nomenclature of the *Pst* isolates, enabling a comparison between spatially and temporally distinct collection events[18]. In the last 10 years, modern DNA-based tools have expanded our ability to study this fungus, and this has led to the cloning of the first *Yr* R genes, the identification of the full life cycle of *Pst*, it's center of genetic diversity and past global migration patterns, and the provision of draft *Pst* genomes.

Control via *Yr* R genes is the most economical and preferred containment strategy for wheat stripe rust. R genes in wheat are historically divided into two phenotypically, mechanistically, and genetically distinct categories. Seedling resistance genes are characterized by a strong to moderate immune response that fully curtails fungal infection and sporulation at all developmental stages. While, adult plant resistance is seen as more durable because, in the asexual stage of *Pst*, a single genetic variation appears insufficient to overcome this type of resistance[19]. Novel genetically diverse *Pst* incursions, however, can reduce the effectiveness of adult plant resistance[20]. *Yr* genes provide useful information for identifying races and race groups for monitoring virulence changes. In this study, we use 29-*Yr*-gene differential lines to study race and virulence of *Pst* population of Yunnan and Sichuan provinces in China, to provide information for wheat production.

MATERIALS AND METHODS

Disease surveys

Wheat fields and disease nurseries (rust trap nurseries) were surveyed during 2017/2018 growing season to monitor the occurrence, development, and distribution of stripe rust in 11 counties of Yunnan and another county of Sichuan in China including Chuxiong (CX), Dali (DL), Honghe (HH), Kunming (KM), Lincang (LC), Lijiang (LJ), Nujiang

(NJ), Qujing (QJ), Wenshan (WS), Yuxi (YX), Zhaotong (ZT), Sichuan (SC).

Sample collections

Stripe rust samples were collected from more than 100 wheat cultivars. From monitoring nurseries, each wheat cultivar considered as a sampling site, and from the field, each sampling site was at least 1000 m apart. Three to five naturally infected wheat leaves were collected from each place, and each leaf was wrapped in bibulous paper. Wheat samples were taken from different regions, different altitudes, and various cultivars to make them truly representative.

Urediniospores production

Leaf samples of wheat were incubated on water-soaked tissue paper in Petri dishes in the dark at 20 °C for 5–6 h to produce fresh urediniospores, which were used to inoculate seedlings of the highly susceptible wheat cultivar Mingxian 169 to increase the urediniospores. Seven days after sowing, seedlings with the first leaf expanded completely inoculated with urediniospores from infected leaf samples. Inoculated plants were incubated in a dew chamber at 10 °C for 24 h without light and then kept in a growth chamber with temperature 11 °C–17 °C with 16 h of light. Plants inoculated with urediniospores from individual samples were separated using a booth to avoid contamination. Fresh urediniospores produced on inoculated seedlings leaves were then collected till approximately 50 mg for each isolate and temporarily stored in desiccators kept at 4 °C.

Race Identification

A set of 29-*Yr* genes differential lines was used to determine races of *Pst* (Table 1). Five to seven seeds of each differential planted in a plastic box. Seedlings were inoculated at the two-leaf stage with urediniospores of each isolate after mixing with talcum powder at a ratio of approximately 1:20. 14 to 16 days after inoculation, infection types (IT) on differential lines were recorded using the 0–4 scale, i.e., 0 = no visible symptoms, 0; = necrotic flecks, 1 = necrotic and chlorotic areas with restricted sporulation, 2 = small to medium uredia with chlorosis and necrosis, 3 = medium-sized uredia with chlorosis, and 4 = abundant sporulation without chlorosis[21]. In the scale, 0–2 = resistant lines (avirulent) while 3–4 = susceptible lines (virulent)[22].

Table 1 Set of wheat differential lines and their *Yr* genes used for resistance to *P. striiformis* f. sp. *tritici*.

Differential line	R gene/*Yr* gene(s)
Avocet S*/*Yr1*	*Yr1*
Kalyansona	*Yr2*
Danish 1	*Yr3*
T. spelta album	*Yr5*
Avocet S*6/*Yr6*	*Yr6*
Avocet S*6/Lee	*Yr7*
Avocet S*6/Compair	*Yr8*
Avocet S*6/ *Yr9*	*Yr9*
Avocet S*6/*Yr10*	*Yr10*
Avocet S*3/Joss Cambier	*Yr11*
Avocet S*6/*T. dicoccoides*	*Yr15*
Pavon 76	*Yr(17,29)*
Avocet S*6/*Yr17*	*Yr17*
Avocet S*6/*Yr18*	*Yr18*
Avocet S*6/*Yr24*	*Yr24*
Hugenoot	*Yr25*
Avocet S*6/*Yr26*	*Yr26*
Avocet S*6/*Yr27*	*Yr27*
Parula	*Yr30*
Avocet S*6/*Yr32*	*Yr32*
Avocet R	*YrA*
Avocet S*3/Opata 85	*YrSK*
Avocet S*6/*YrSP*	*YrSP*
Suwon 92/Omar	*YrSu*
Compare	*Yr(8,19)*
Reichersberg 42	*Yr(7,25)*
Heiens VII	*Yr(2,HVII)*
Moro	*Yr(10,Mor)*
Lee	*Yr(7,22,23)*

Determination of virulence frequency percentage

The percentage of virulence frequency for each of designated races in the survey was calculated as the number of virulent isolates to the total number of tested isolates, according to this equation[23]:

$$\text{Virulence frequency}\,(\%) = \frac{\text{No. virulence}}{\text{No. isolates}} \times 100$$

Virulence frequencies were classified as high (>73%), moderate (16–73%), and low (<10%). The distributions of the detected races were summarized by locations.

Cluster analysis and coefficients of correlations

A similarity matrix of virulence phenotypes based on simple matching coefficient was used to construct a dendrogram using the unweighted pair group method with arithmetic means (UPGMA) clustering method in numerical taxonomy system (NTSYSpc

version 2.2)[24]. The corresponding φ coefficient of association between virulence to the 29-*Yr*-gene differentials (formula 17.5)[25] was calculated using the NTSYSpc package, version 2.2, and based on the virulence-avirulence patterns of the 125 isolates. For each of tested *Yr* genes, virulence coded as one and avirulence as 0[26, 27].

RESULTS

Race frequency and distribution

Eighty-six races were characterized from 125 isolates collected from Yunnan and Sichuan provinces in China based on their virulence/avirulence patterns to the 29 wheat differential genotypes. The frequencies of races ranged from 0.8% (only one isolate) to 8.8% (v1). Two dominant races were 8.8% (v1), and 8% (v2) while 4 races were 2.4% (v3, v4, v5, and v6); other 80 races had frequencies below 2%. Races v1 and v2 were the most widely distributed races and were detected in 5 counties while v3 and v6 were distributed in 3 counties; the remaining races were only distributed in less than three counties.

Different numbers of races were detected in different locations. The number of races ranged from 1 in the Nujiang to 16 and 15 in Lincang and Yuxi, respectively. The site of Lincang, Yuxi, Chuxiong, and Sichuan had relatively high numbers of races compared to other counties, with more than 10 races. The percentage of virulence races for each county was listed in Table 2.

Table 2 Virulence races of *Puccinia striiformis* in different locations.

County	No. of races	*Pst* race	Race %
Lincang	16	v1, v2, v6, v7, v11, v15, v16, v17, v21, v27, v28, v34, v35, v48, v72, v75	18.60
Yuxi	15	v1, v2, v9, v12, v13, v15, v26, v52, v53, v65, v66, v67, v69, v85, v86	17.44
Chuxiong	14	v6, v25, v29, v36, v38, v54, v56, v58, v59, v64, v68, v76, v77, v82	16.28
Sichuan	13	v3, v4, v5, v7, v14, v17, v22, v41, v47, v60, v61, v70, v74	15.12
Qujing	10	v1, v2, v4, v8, v18, v20, v23, v50, v51, v81	11.63
Wenshan	9	v1, v2, v18, v30, v39, v43, v55, v62, v71	10.46
Kunming	8	v1, v3, v6, v9, v10, v11, v42, v44	9.30
Dali	7	v19, v46, v73, v78, v79, v80, v84	8.14
Lijiang	7	v24, v31, v32, v33, v37, v40, v45	8.14
Honghe	4	v14, v49, v57, v63	4.65
Zhaotong	2	v3, v83	2.33
Nujiang	1	v2	1.16

Cluster analysis

A dendrogram constructed using the NTSYSpc 2.2 software divided the races into two clades. Cluster-I comprises two races v29 and v30. Cluster-II comprises 84 races (Fig. 1). The two races of Cluster-I had relatively narrow virulence spectra. The v29 was virulent to 6, and v30 was virulent to 7 of the 29-*Yr* gene differentials. Cluster-II had 84 races that had wide virulence spectra, ranging from 8 (v84) to 24 (v3, v7, v11, and v60) virulence. The Cluster-II separated into two sub-clusters. Sub-cluster-1 comprised only one race (v84) and had narrow virulence spectra with Cluster-I. Sub-cluster-2 had wide virulence spectra ranging from 12 (v37) to 24 (v3, v7, v11, and v60) virulence (Table S1).

Virulence frequencies for *Yr* genes and their distributions

The virulence frequencies for *Yr1*, *Yr2*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr11*, *Yr17*, *Yr18*, *Yr25*, *Yr26*, *Yr30*, *Yr32*, *YrA*, *YrSK*, *YrSP*, *YrSu*, *Yr(8,19)*, *Yr(7,25)*, *Yr(10,Mor)* and *Yr(17,29)* genes were high, ranging from 73.6–98.4%, and this virulence was detected in all counties of Yunnan and Sichuan provinces (Table 3). No isolates virulent to *Yr5* and *Yr10* were detected, indicating that these two genes were still effective against all races identified so far in Yunnan and Sichuan provinces of China. Moderate frequency (16.8–47.2%) of virulence was detected for *Yr3*, *Yr27*, *Yr(2,HVII)*, and *Yr(7,22,23)* genes. The virulence frequencies to *Yr15* and *Yr24* were low (0.8% and 1.6%, respectively). Virulence to *Yr15* was detected only in the Sichuan province. Similarly, virulence to *Yr24* was identified only in Chuxiong county of Yunnan province (Table 3). All races were virulent to *Yr2* except v83 and v84, and to *Yr(17,29)* except v30 and v77.

φ Coefficient of correlation

The coefficient of correlation between virulence to the 29-*Yr*-gene differentials was calculated based on the virulence-avirulence patterns of the 125 isolates. A highly positive correlation (>0.50) was identified between virulence to *YrSP* and *Yr(8,19)* or *Yr17*; *Yr(10,Mor)* and *Yr17*, *Yr(8,19)* or *YrSP* (Fig. 2), indicated with yellow color. Negative correlation (<0) was found between virulence to *Yr1* or *Yr2* and *Yr3*, *Yr(17,29)*, *Yr17*, *Yr18* or *Yr25*; *Yr1* and *Yr2*, *Yr7*, *Yr11*, *Yr32*, *YrA*, *YrSK*, *Yr(7,25)* or *Yr(7,22,23)*; *Yr3* and *Yr6*, *Yr15*, *Yr24* or *Yr(2,HVII)*; *Yr6* or *Yr7* and *YrSP*, *Yr(8,19)*, *Yr(2,HVII)*, *Yr(10,Mor)* or *Yr(7,22,23)*; *Yr7* and *Yr8*, *Yr25*, *YrSP*, *Yr(8,19)*,
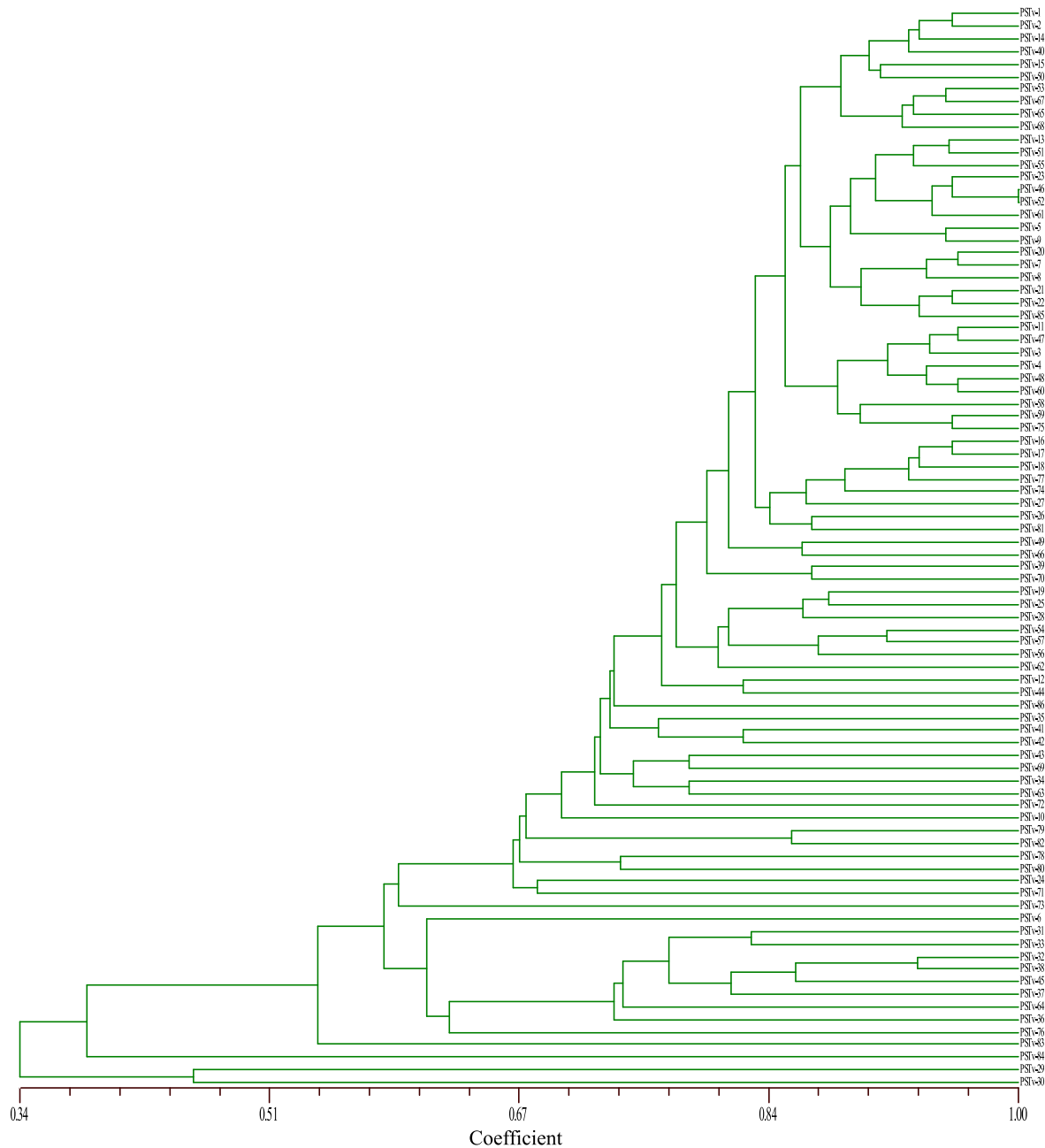
Fig. 1 Dendrogram showing the relationships among 86 *Pst* races identified based on their IT on the 29-*Yr*-gene differentials.

Yr(2,HVII), *Yr(10,Mor)* or *Yr(7,22,23)*; *Yr8* and *YrSK* or *Yr(17,29)*; *Yr15* or *Yr(17,29)* and *YrSK* or *Yr(7,22,23)*; *Yr(17,29)* or *Yr18* and *Yr25*, *YrSu*, or *Yr(8,19)*; *Yr18* and *Yr24*, *Yr27*, *YrSK*, *Yr15*; *Yr24* and *Yr(2,HVII)*, or *Yr(7,22,23)*; *Yr25* and *Yr8*, *Yr26*, *Yr30*, *YrSK*, *Yr(7,25)*; *Yr(2,HVII)* or *Yr(7,22,23)*; *Yr(7,25)* and *Yr32*, *YrSu*, *YrSP*, *Yr(8,19)*, *Yr(2,HVII)*, *Yr(10,Mor)*; *YrSK* and *Yr9*, *Yr17*, *YrSP*, *YrSu*, *Yr(8,19)*; and *Yr(7,22,23)* and *Yr11*, *Yr26* or *Yr30*, indicated with blue color in Fig. 2. None of the isolates was virulent to *Yr5* and *Yr10*, and avirulence to these two genes was highly associated (1.00). The remaining pairwise associations were positive but not high (ranged from 0.01–0.49), indicated with green color in Fig. 2.

Table 3 Virulence frequencies of *Puccinia striiformis* population on *Yr* genes and their distribution.

Yr Gene	No. of isolates	Virulence freq. (%)	Distribution of isolates[*]
Yr5	0	0	None
Yr10	0	0	None
Yr24	1	0.8	CX(1)
Yr15	2	1.6	SC(2)
Yr3	21	16.8	CX(1), DL(1), KM(2), LC(3), LJ(1), QJ(4), SC(3), YX(4), ZT(2)
Yr27	30	24.0	CX(4), KM(2), LC(6), LJ(1), QJ(5), SC(7), WS(2), YX(1), ZT(2)
Yr(7,22,23)	30	24.0	CX(6), DL(3), HH(2), KM(4), LC(6), SC(4), WS(1), YX(3), ZT(1)
Yr(2,HVII)	59	47.2	CX(7), DL(5), HH(3), KM(2), LC(11), LJ(5), NJ(2), QJ(6), SC(8), WS(4), YX(5), ZT(1)
YrSK	92	73.6	CX(13), DL(2), HH(4), KM(5), LC(19), LJ(6), NJ(2), QJ(11), SC(9), WS(8), YX(11), ZT(2)
Yr7	96	76.8	CX(12), DL(3), HH(4), KM(7), LC(13), LJ(7), NJ(2), QJ(14), SC(9), WS(8), YX(16), ZT(1)
Yr11	100	80.0	CX(10), DL(1), HH(3), KM(6), LC(16), LJ(3), NJ(2), QJ(16), SC(15), WS(9), YX(18), ZT(1)
Yr(8,19)	102	81.6	CX(8), DL(6), HH(2), KM(7), LC(18), LJ(1), NJ(2), QJ(15), SC(15), WS(10), YX(16), ZT(2)
Yr9	103	82.4	CX(12), DL(5), HH(4), KM(6), LC(16), LJ(2), NJ(2), QJ(16), SC(13), WS(8), YX(18), ZT(1)
Yr8	105	84.0	CX(10), DL(7), HH(3), KM(7), LC(17), LJ(5), NJ(2), QJ(16), SC(15), WS(8), YX(14), ZT(2)
Yr25	105	84.0	CX(11), DL(6), HH(2), KM(7), LC(16), LJ(2), NJ(2), QJ(16), SC(14), WS(11), YX(16), ZT(2)
Yr30	105	84.0	CX(11), DL(2), HH(3), KM(7), LC(18), LJ(7), NJ(2), QJ(16), SC(14), WS(7), YX(17), ZT(1)
Yr(10,Mor)	106	84.8	CX(11), DL(6), HH(3), KM(6), LC(18), LJ(2), NJ(2), QJ(16), SC(15), WS(9), YX(16), ZT(2)
YrSu	106	84.8	CX(10), DL(5), HH(2), KM(7), LC(16), LJ(4), NJ(2), QJ(16), SC(15), WS(10), YX(17), ZT(2)
Yr32	107	85.6	CX(10), DL(4), HH(4), KM(6), LC(18), LJ(6), NJ(2), QJ(16), SC(15), WS(9), YX(15), ZT(2)
Yr17	108	86.4	CX(11), DL(5), HH(4), KM(7), LC(19), LJ(1), NJ(2), QJ(16), SC(14), WS(9), YX(18), ZT(2)
YrSP	113	90.4	CX(11), DL(7), HH(4), KM(7), LC(18), LJ(2), NJ(2), QJ(16), SC(15), WS(11), YX(18), ZT(2)
Yr6	116	92.8	CX(15), DL(5), HH(4), KM(8), LC(18), LJ(7), NJ(2), QJ(15), SC(15), WS(11), YX(17), ZT(1)
Yr18	117	93.6	CX(12), DL(7), HH(4), KM(7), LC(17), LJ(7), NJ(2), QJ(16), SC(15), WS(10), YX(18), ZT(2)
YrA	118	94.4	CX(13), DL(6), HH(4), KM(7), LC(19), LJ(7), NJ(2), QJ(16), SC(15), WS(10), YX(18), ZT(1)
Yr(7,25)	119	95.2	CX(16), DL(6), HH(4), KM(8), LC(18), LJ(7), NJ(2), QJ(16), SC(13), WS(10), YX(18), ZT(1)
Yr26	119	95.2	CX(15), DL(5), HH(4), KM(8), LC(18), LJ(7), NJ(2), QJ(16), SC(15), WS(10), YX(17), ZT(2)
Yr1	120	96.0	CX(15), DL(7), HH(4), KM(7), LC(18), LJ(7), NJ(2), QJ(16), SC(15), WS(11), YX(16), ZT(2)
Yr2	123	98.4	CX(16), DL(6), HH(4), KM(8), LC(19), LJ(7), NJ(2), QJ(16), SC(15), WS(11), YX(18), ZT(1)
Yr(17,29)	123	98.4	CX(15), DL(7), HH(4), KM(8), LC(19), LJ(7), NJ(2), QJ(16), SC(15), WS(10), YX(18), ZT(2)

[*] Number in ( ) = number of isolates. Chuxiong (CX), Dali (DL), Honghe (HH), Kunming (KM), Lincang (LC), Lijiang (LJ), Nujiang (NJ), Qujing (QJ), Wenshan (WS), Yuxi (YX), Zhaotong (ZT), Sichuan (SC).

DISCUSSION

Stripe rust of wheat as the fungal disease is a significant yield-limiting factor in commercial wheat, incited by *P. striiformis* f. sp. *tritici*. Stripe rust considered a cosmopolitan disease due to the dynamic nature of its causal agent since it is converted from the disease of cold weather to the disease of variable ones. The annual survey of wheat stripe rust was conducted throughout the growing season 2017/18 of wheat crop in Yunnan and Sichuan provinces in China. Eighty-six virulence races characterized from 125 isolates were collected from 11 counties of Yunnan and one county of Sichuan, with the virulence frequencies ranged from 0.8–8.8%. Races v1 and v2 were the most widely distributed races and were detected in five counties owing to their highly aggressive. The rest of races appeared with lower frequencies. Similar results were reported by Ali et al[28] and Shahin et al[29], who confirmed the predominance of stripe rust races 0E0, 6E4, 70E20, and 128E28 in Egypt.

The predominance of stripe rust disease at Lincang and Yuxi was relatively high, and these high virulence frequencies could be attributed to the existence of weather conditions, being suitable for disease dispersal and dissemination. The obtained results indicated the excellent performance of *Yr5*, *Yr10*, since it could not be attacked by either of the tested races all over the growing season (with 100% efficacy); likewise, *Yr15* and *Yr24* occupied the second rank. Both *Yr5* and *Yr15* previously showed a high level of resistance to stripe rust in China, Iran, Turkey, North America, and Africa[2, 30].

Interestingly, the virulence frequencies for *Yr24* and *Yr26* were different, 0.8% and 95.2%, respectively. The *Yr24* and *Yr26* genes isolated independently were found to be located in the centromere region of chromosome 1B[31, 32], and were suggested to be a single gene. The significant difference in virulence frequencies to *Yr24* and *Yr26* indicated that these were not one gene but two linked genes. The *Yr10* was located on chromosome 1BL[33], while the *Yr5* gene existed in chromosome 2BL[34]. The perfect correlation between *Yr5* and *Yr10* genes despite being at different chromosomes suggests that posttranslational interaction between these two genes occur.

In cluster analysis, the races were divided into two clusters. Cluster-I comprises two races v29 and v30 that had relatively narrow virulence spectra while Cluster-II comprises 84 races that had broad virulence spectra. The φ coefficient of associa-
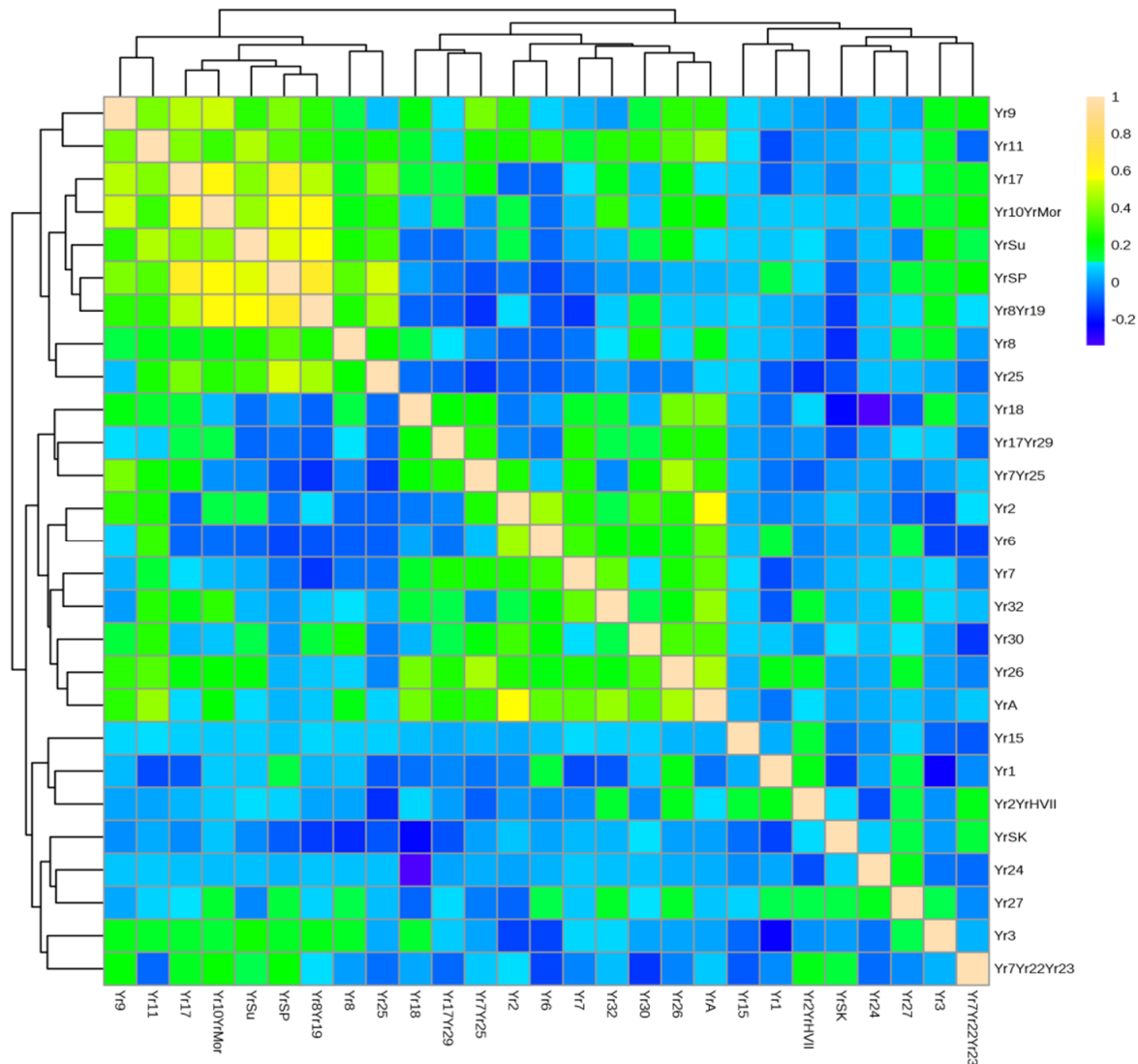
Fig. 2 Correlation coefficients between 27 avirulence/virulence loci of *P. striiformis* f. sp. *tritici*. The avirulence genes are represented by their corresponding resistance *Yr* genes.

tion between virulence to the 29-*Yr*-gene differentials showed highly positive correlation identified between virulence to *YrSP* and *Yr(8,19)* or *Yr17*; *Yr(10,Mor)* and *Yr17*, *Yr(8,19)* or *YrSP*. The remaining pairwise associations were moderate or have negative correlation except for *Yr5* and *Yr10* that were highly associated and resistant to virulence races. Similar results were reported by Li et al [35, 36]. The virulence patterns revealed from this study can guide the wheat breeding program to develop resistant cultivars.

CONCLUSION

Survey of wheat yellow rust pathotypes using 29-*Yr*-gene differential lines is significant in characterizing virulence variation, the geographical distribution of virulence isolates, and the way yellow rust isolates change in response to host selection. Out of 86 characterized *Pst* races, two races (v1 and v2) were widely distributed in Yunnan and Sichuan provinces of China. Based on the virulence spectrum, the 86 races were grouped into two clusters. Cluster-I included only two races (v29 and v30) with a narrow virulence spectrum and cluster-II comprised 84 races with broad virulence spectrum. The four

Yr genes (*Yr5, Yr10, Yr15*, and *Yr24*) were found to be effective against all tested virulent *Pst* races. This activity should be carried out in all wheat growing seasons using rust survey and planting of wheat rust trap nurseries at different locations in Yunnan province; this will supply timely warning to wheat breeders about the change in the virulence of *P. striiformis* pathotypes. Thus, it will be essential to avert future yellow rust epidemics and reduce yearly losses of the commercial wheat varieties grown in Yunnan, China.

Appendix A. Supplementary data

Supplementary data associated with this article can be found at http://dx.doi.org/10.2306/scienceasia1513-1874.2019.45.572.

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Appendix A. Supplementary data

Table S1 Races of *P. striiformis*, their virulence formula, frequencies (%), and distributions.

Race	Virulence formula	Freq.	Distribution[†]
v1	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	8.8	KM, LC, QJ(3), WS(3), YX(3)
v2	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	8.0	LC(3), NJ(2), QJ(3), WS, YX
v3	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	2.4	SC, ZT, KM
v4	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	2.4	QJ(2), SC
v5	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	2.4	SC(3)
v6	*Yr2, Yr6, Yr7, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, Yr(7,25), Yr(17,29)*	2.4	CX, LC, KM
v7	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	1.6	LC, SC
v8	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	1.6	QJ(2)
v9	*Yr1, Yr2, Yr3, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	1.6	KM, YX
v10	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, Yr26, Yr30, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	1.6	KM, CX
v11	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	1.6	LC, KM
v12	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(7,25), Yr(2,HVII), Yr(17,29)*	1.6	YX(2)
v13	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	1.6	CX, YX
v14	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	1.6	HH, SC
v15	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	1.6	LC, YX
v16	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	1.6	LC(2)
v17	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	1.6	SC, LC
v18	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	1.6	QJ, WS
v19	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, Yr26, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	DL
v20	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	QJ
v21	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	LC
v22	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	SC
v23	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	QJ
v24	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr18, Yr26, Yr27, Yr30, YrA, YrSK, YrSP, YrSu, Yr(7,25), Yr(2,HVII), Yr(17,29)*	0.8	LJ
v25	*Yr1, Yr2, Yr3, Yr6, Yr7, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	CX
v26	*Yr1, Yr2, Yr3, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	YX
v27	*Yr1, Yr2, Yr3, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	LC
v28	*Yr1, Yr2, Yr3, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	LC
v29	*Yr1, Yr2, Yr6, YrSK, Yr(7,25), Yr(17,29)*	0.8	CX
v30	*Yr1, Yr2, Yr6, Yr25, YrSP, YrSu, Yr(8,19)*	0.8	WS
v31	*Yr1, Yr2, Yr6, Yr7, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSu, Yr(7,25), Yr(17,29)*	0.8	LJ
v32	*Yr1, Yr2, Yr6, Yr7, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, Yr(7,25), Yr(2,HVII), Yr(17,29)*	0.8	LJ
v33	*Yr1, Yr2, Yr6, Yr7, Yr11, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, YrSu, Yr(7,25), Yr(2,HVII), Yr(17,29)*	0.8	LJ
v34	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSP, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	LC
v35	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr17, Yr25, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(10,Mor), Yr(17,29)*	0.8	LC
v36	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, Yr(7,25), Yr(17,29)*	0.8	CX
v37	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr18, Yr26, Yr30, Yr32, YrA, Yr(7,25), Yr(17,29)*	0.8	LJ
v38	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, Yr(7,25), Yr(2,HVII), Yr(17,29)*	0.8	CX
v39	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	WS
v40	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	LJ
v41	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr11, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, (8,19), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	SC

v42	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr11, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	KM
v43	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, Yr25, Yr26, Yr27,32, YrA, YrSK, YrSP, Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	WS
v44	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, Yr25, Yr26, Yr30, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(7,22,23), Yr(17,29)*	0.8	KM
v45	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	LJ
v46	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	DL
v47	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	SC
v48	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	LC
v49	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, Yr(8,19), Yr(7,25), Yr(17,29)*	0.8	HH
v50	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	QJ
v51	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	QJ
v52	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	YX
v53	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	YX
v54	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr32, YrA, YrSK, YrSP, YrSu, Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	CX
v55	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	WS
v56	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, YrA, YrSK, YrSP, YrSu, Yr(7,25), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	CX
v57	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	HH
v58	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr24, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	CX
v59	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	CX
v60	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr15, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	SC
v61	*Yr1, Yr2, Yr6, Yr7, Yr8, Yr9, Yr11, Yr15, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	SC
v62	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr17, Yr18, Yr25, Yr26, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	WS
v63	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr17, Yr18, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	HH
v64	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr18, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	CX
v65	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	YX
v66	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSP, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	YX
v67	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	YX
v68	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	CX
v69	*Yr1, Yr2, Yr6, Yr7, Yr9, Yr11, Yr17, Yr18, Yr26, Yr27, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	YX
v70	*Yr1, Yr2, Yr6, Yr8, Yr11, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	SC
v71	*Yr1, Yr2, Yr6, Yr8, Yr11, Yr18, Yr26, Yr25, Yr30, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(17,29)*	0.8	WS
v72	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr17, Yr18, Yr25, Yr26, Yr27, Yr30, YrA, YrSK, YrSP, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	LC
v73	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr18, Yr25, Yr32, YrA, YrSP, Yr(8,19), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	DL
v74	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	SC
v75	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr17, Yr25, Yr26, Yr27, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	LC
v76	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr18, Yr26, Yr30, YrA, Yr(7,25), Yr(17,29)*	0.8	CX
v77	*Yr1, Yr2, Yr6, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23)*	0.8	CX
v78	*Yr1, Yr2, Yr7, Yr8, Yr17, Yr18, Yr25, Yr26, Yr32, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	DL
v79	*Yr1, Yr2, Yr8, Yr9, Yr17, Yr18, Yr25, Yr26, Yr30, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	DL
v80	*Yr1, Yr2, Yr8, Yr9, Yr18, Yr25, Yr26, YrA, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	DL
v81	*Yr1, Yr2, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	QJ
v82	*Yr1, Yr2, Yr9, Yr17, Yr25, Yr26, Yr30, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(2,HVII), Yr(10,Mor), Yr(7,22,23), Yr(17,29 0.8*		CX
v83	*Yr1, Yr3, Yr8, Yr17, Yr18, Yr25, Yr26, Yr27, Yr32, YrSP, YrSu, Yr(8,19), Yr(2,HVII), Yr(10,Mor), Yr(17,29)*	0.8	ZT
v84	*Yr1, Yr8, Yr17, Yr18, Yr25, YrSP, Yr(7,25), Yr(17,29)*	0.8	DL
v85	*Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr26, Yr30, Yr32 YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(17,29)*	0.8	YX
v86	*Yr2, Yr3, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, Yr25, Yr30, Yr32, YrA, YrSK, YrSP, YrSu, Yr(8,19), Yr(7,25), Yr(10,Mor), Yr(7,22,23), Yr(17,29)*	0.8	YX

† Distribution item in the table without number means one isolate. Chuxiong (CX), Dali (DL), Honghe (HH), Kunming (KM), Lincang (LC), Lijiang (LJ), Nujiang (NJ), Qujing (QJ), Wenshan (WS), Yuxi (YX), SZhaotong (ZT), Sichuan (SC).