

**Supplementary Table 1.** Geographical distribution of isolated samples and their identification through different genes

Geographical location	Isolate	Source	Year	<i>Xanthomonas euvesicatoria</i> <i>hrpB1</i> gene	<i>X. euvesicatoria</i> <i>hrpB2</i> gene	<i>X. euvesicatoria</i> <i>recQ</i> gene
Hailun	Sh1	<i>Physalis pubescens</i>	2018	+	+	+
Hailun	Sh2	<i>P. pubescens</i>	2018	+	+	+
Hailun	Sh3	<i>P. pubescens</i>	2018	+	+	+
Hailun	Sh4	<i>P. pubescens</i>	2018	+	+	+
Hailun	Sh5	<i>P. pubescens</i>	2018	+	+	+
Hailun	Sh6	<i>P. pubescens</i>	2018	+	+	+
Hailun	Sh7	<i>P. pubescens</i>	2018	+	+	+
Hailun	Sh8	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq1	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq2	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq3	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq4	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq5	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq6	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq7	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq8	<i>P. pubescens</i>	2018	+	+	+
Qinggang	Sq9	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz1	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz2	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz3	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz4	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz5	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz6	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz7	<i>P. pubescens</i>	2018	+	+	+
Zhaodong	Sz8	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm1	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm2	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm3	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm4	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm5	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm6	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm7	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm8	<i>P. pubescens</i>	2018	+	+	+
Mulan	Hm9	<i>P. pubescens</i>	2018	-	-	-
Fangzheng	Hf1	<i>P. pubescens</i>	2018	+	+	+
Fangzheng	Hf2	<i>P. pubescens</i>	2018	+	+	+
Fangzheng	Hf3	<i>P. pubescens</i>	2018	+	+	+
Fangzheng	Hf4	<i>P. pubescens</i>	2018	+	+	+
Fangzheng	Hf5	<i>P. pubescens</i>	2018	+	+	+
Fangzheng	Hf6	<i>P. pubescens</i>	2018	+	+	+
Fangzheng	Hf7	<i>P. pubescens</i>	2018	+	+	+
Fangzheng	Hf8	<i>P. pubescens</i>	2018	+	+	+

(Continued)

Supplementary Table 1. Continued

Geographical location	Isolate	Source	Year	<i>Xanthomonas euvesicatoria</i> <i>hrpB1</i> gene	<i>X. euvesicatoria</i> <i>hrpB2</i> gene	<i>X. euvesicatoria</i> <i>recQ</i> gene
Shuang cheng	Hs1	<i>P. pubescens</i>	2018	+	+	+
Shuang cheng	Hs2	<i>P. pubescens</i>	2018	+	+	+
Shuang cheng	Hs3	<i>P. pubescens</i>	2018	+	+	+
Shuang cheng	Hs4	<i>P. pubescens</i>	2018	+	+	+
Shuang cheng	Hs5	<i>P. pubescens</i>	2018	+	+	+
Shuang cheng	Hs6	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg1	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg2	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg3	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg4	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg5	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg6	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg7	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg8	<i>P. pubescens</i>	2018	+	+	+
Gannan	Qg9	<i>P. pubescens</i>	2018	+	+	+
Fuyu	Qf1	<i>P. pubescens</i>	2018	+	+	+
Fuyu	Qf2	<i>P. pubescens</i>	2018	+	+	+
Fuyu	Qf3	<i>P. pubescens</i>	2018	+	+	+
Fuyu	Qf4	<i>P. pubescens</i>	2018	+	+	+
Fuyu	Qf5	<i>P. pubescens</i>	2018	+	+	+
Fuyu	Qf6	<i>P. pubescens</i>	2018	+	+	+
Fuyu	Qf7	<i>P. pubescens</i>	2018	+	+	+
Baiquan	Qb1	<i>P. pubescens</i>	2019	+	+	+
Baiquan	Qb2	<i>P. pubescens</i>	2019	+	+	+
Baiquan	Qb3	<i>P. pubescens</i>	2019	+	+	+
Baiquan	Qb4	<i>P. pubescens</i>	2019	+	+	+
Baiquan	Qb5	<i>P. pubescens</i>	2019	+	+	+
Baiquan	Qb6	<i>P. pubescens</i>	2019	+	+	+
Baiquan	Qb7	<i>P. pubescens</i>	2019	+	+	+
Fujin	Jf1	<i>P. pubescens</i>	2019	+	+	+
Fujin	Jf2	<i>P. pubescens</i>	2019	+	+	+
Fujin	Jf3	<i>P. pubescens</i>	2019	+	+	+
Fujin	Jf4	<i>P. pubescens</i>	2019	+	+	+
Fujin	Jf5	<i>P. pubescens</i>	2019	+	+	+
Fujin	Jf6	<i>P. pubescens</i>	2019	+	+	+
Fujin	Jf7	<i>P. pubescens</i>	2019	+	+	+
Huanan	Jh1	<i>P. pubescens</i>	2019	+	+	+
Huanan	Jh2	<i>P. pubescens</i>	2019	+	+	+
Huanan	Jh3	<i>P. pubescens</i>	2019	+	+	+
Huanan	Jh4	<i>P. pubescens</i>	2019	+	+	+
Huanan	Jh5	<i>P. pubescens</i>	2019	+	+	+

(Continued)

**Supplementary Table 1.** Continued

Geographical location	Isolate	Source	Year	<i>Xanthomonas euvesicatoria</i> <i>hrpB1</i> gene	<i>X. euvesicatoria</i> <i>hrpB2</i> gene	<i>X. euvesicatoria</i> <i>recQ</i> gene
Huanan	Jh6	<i>P. pubescens</i>	2019	+	+	+
Huanan	Jh7	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh1	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh2	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh3	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh4	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh5	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh6	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh7	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh8	<i>P. pubescens</i>	2019	+	+	+
Hailin	Mh9	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn1	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn2	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn3	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn4	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn5	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn6	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn7	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn8	<i>P. pubescens</i>	2019	+	+	+
Ningan	Mn9	<i>P. pubescens</i>	2019	+	+	+

**Supplementary Table 2.** Mean loci for each population of 13 regions through BOX-PCR

Population	No. of samples	No. of different alleles	No. of effective alleles	Shannon's information index	Diversity	Unbiased diversity
Hailun	8.000	1.100	1.377	0.310	0.211	0.241
Qinggang	9.000	1.100	1.364	0.303	0.205	0.231
Zhaodong	8.000	1.200	1.326	0.303	0.198	0.227
Mulan	9.000	1.100	1.361	0.327	0.212	0.239
Fangzheng	8.000	1.000	1.410	0.310	0.217	0.248
Shuang cheng	6.000	0.600	1.228	0.181	0.125	0.150
Gannan	9.000	0.900	1.321	0.256	0.175	0.197
Fuyu	7.000	1.100	1.278	0.272	0.176	0.205
Baiquan	7.000	0.700	1.195	0.180	0.118	0.138
Fujin	7.000	1.300	1.370	0.335	0.220	0.257
Huanan	7.000	1.100	1.283	0.277	0.180	0.210
Hailin	9.000	1.300	1.427	0.337	0.227	0.258
Ningan	9.000	1.200	1.271	0.269	0.170	0.192

**Supplementary Table 3.** Pairwise population matrix of Nei genetic distance through BOX-PCR

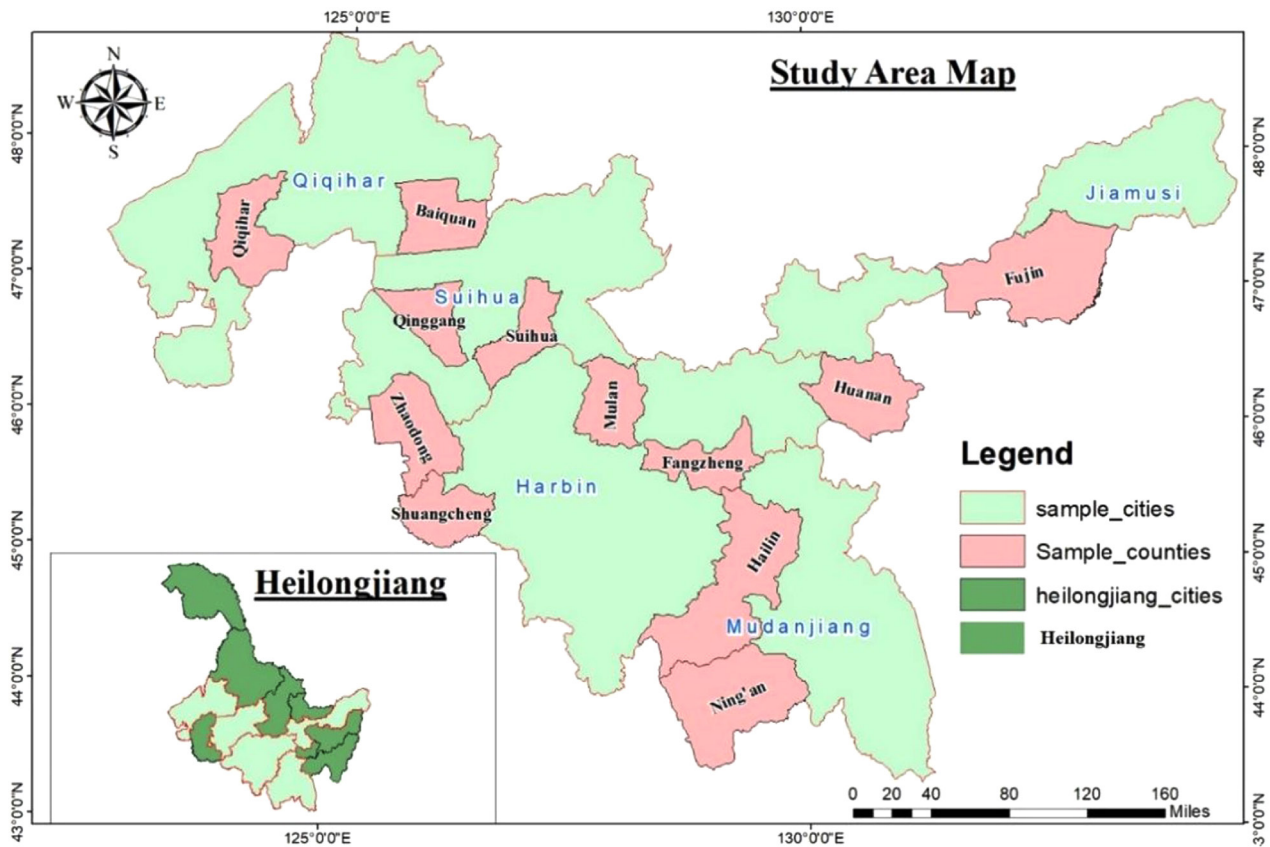
Population	Sh	Sq	Sz	Hm	Hf	Hs	Qg	Qf	Qb	Jf	Jh	Mh	Mn
Hailun (Sh)	0.000												
Qinggang (Sq)	0.048	0.000											
Zhaodong (Sz)	0.052	0.038	0.000										
Mulan (Hm)	0.060	0.078	0.057	0.000									
Fangzheng (Hf)	0.123	0.099	0.097	0.095	0.000								
Shuang cheng (Hs)	0.097	0.076	0.048	0.088	0.096	0.000							
Gannan (Qg)	0.139	0.106	0.114	0.131	0.100	0.166	0.000						
Fuyu (Qf)	0.076	0.079	0.047	0.099	0.109	0.044	0.116	0.000					
Baiquan (Qb)	0.084	0.119	0.078	0.063	0.120	0.063	0.133	0.048	0.000				
Fujin (Jf)	0.072	0.061	0.049	0.098	0.147	0.061	0.183	0.057	0.072	0.000			
Huanan (Jh)	0.074	0.071	0.042	0.069	0.104	0.041	0.124	0.073	0.068	0.064	0.000		
Hailin (Mh)	0.142	0.102	0.077	0.110	0.056	0.078	0.044	0.078	0.084	0.125	0.090	0.000	
Ningan (Mn)	0.075	0.076	0.034	0.075	0.067	0.039	0.105	0.045	0.061	0.060	0.032	0.055	0.000

**Supplementary Table 4.** Mean loci for each population of 13 regions using ERIC-PCR

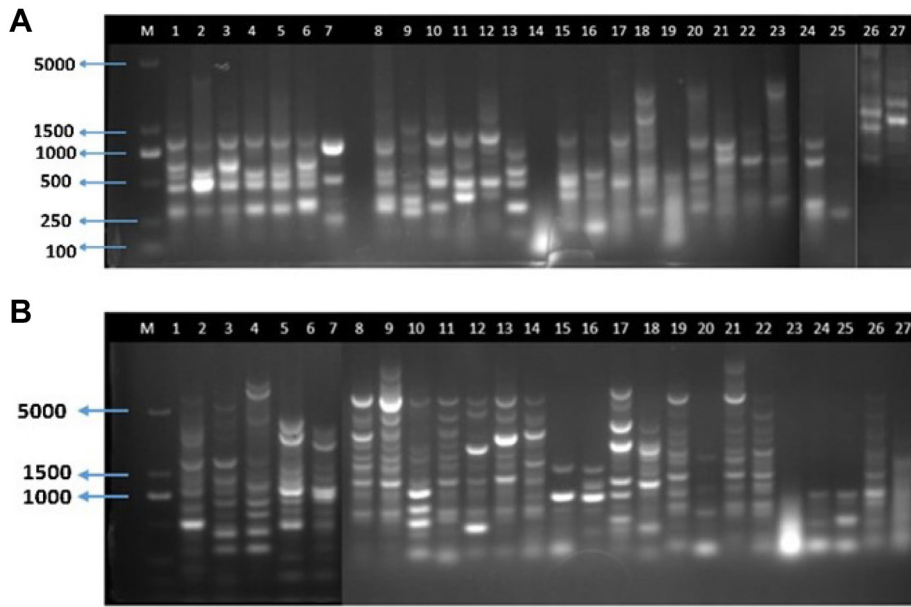
Population	No. of samples	No. of different alleles	No. of effective alleles	Shannon's information index	Diversity	Unbiased diversity
Hailun	8.000	0.923	1.314	0.265	0.180	0.206
Qing gang	9.000	1.154	1.456	0.355	0.247	0.278
Zhaodong	8.000	1.385	1.456	0.384	0.260	0.297
Mulan	9.000	1.154	1.424	0.342	0.236	0.265
Fang Zheng	8.000	1.154	1.431	0.347	0.239	0.273
Shuang cheng	6.000	1.385	1.449	0.390	0.263	0.303
Gannan	9.000	1.346	1.362	0.327	0.215	0.241
Fuyu	7.000	1.154	1.397	0.328	0.223	0.260
Baiquan	7.000	1.308	1.398	0.358	0.239	0.278
Fujin	7.000	1.462	1.426	0.384	0.254	0.297
Huanan	7.000	1.115	1.388	0.316	0.217	0.253
Hailin	9.000	1.538	1.461	0.405	0.270	0.315
Ning An	9.000	0.923	1.311	0.257	0.175	0.197

**Supplementary Table 5.** Pairwise population matrix of Nei genetic distance using ERIC-PCR

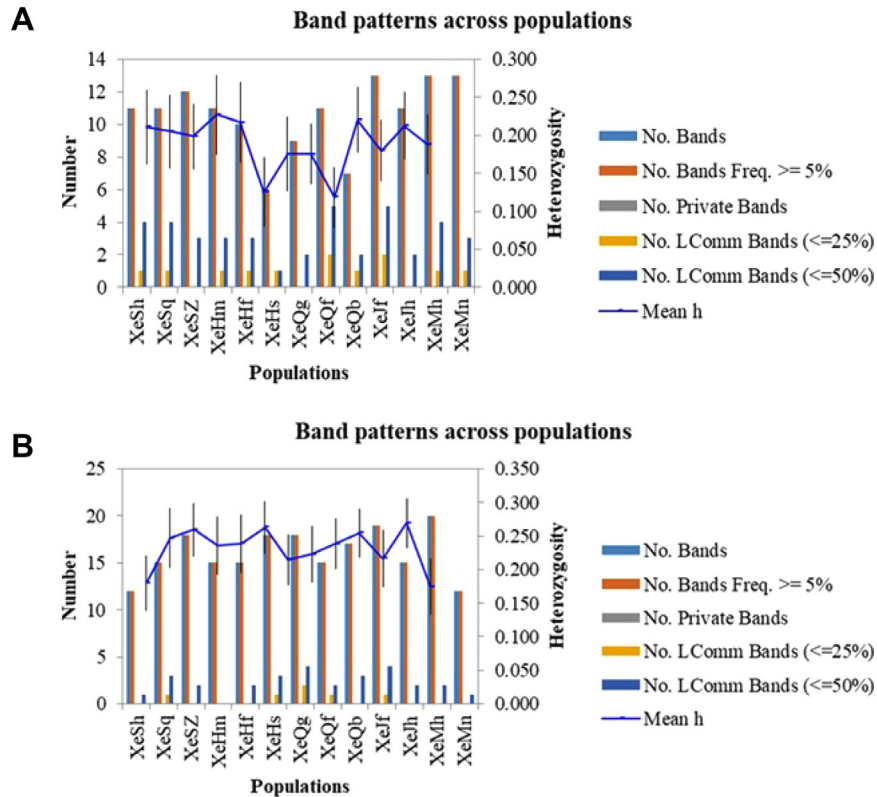
Population	Sh	Sq	Sz	Hm	Hf	Hs	Qg	Qf	Qb	Jf	Jh	Mh	Mn
Hailun (Sh)	0.000												
Qinggang (Sq)	0.104	0.000											
Zhaodong (Sz)	0.139	0.104	0.000										
Mulan (Hm)	0.090	0.087	0.066	0.000									
Fangzheng (Hf)	0.200	0.159	0.175	0.137	0.000								
Shuang cheng (Hs)	0.231	0.117	0.130	0.159	0.158	0.000							
Gannan (Qg)	0.311	0.175	0.201	0.164	0.185	0.123	0.000						
Fuyu (Qf)	0.299	0.160	0.200	0.141	0.167	0.098	0.076	0.000					
Baiquan (Qb)	0.154	0.118	0.170	0.096	0.114	0.138	0.143	0.117	0.000				
Fujin (Jf)	0.202	0.124	0.122	0.127	0.105	0.108	0.127	0.106	0.148	0.000			
Huanan (Jh)	0.152	0.154	0.134	0.104	0.193	0.121	0.232	0.186	0.136	0.208	0.000		
Hailin (Mh)	0.200	0.135	0.221	0.128	0.177	0.112	0.064	0.104	0.108	0.168	0.155	0.000	
Ningan (Mn)	0.215	0.185	0.207	0.137	0.180	0.156	0.183	0.135	0.132	0.227	0.114	0.110	0.000



**Supplementary Fig. 1.** Study map of 13 counties and 5 main cities of Heilongjiang province.



**Supplementary Fig. 2.** An examination of the *Xanthomonas euvesicatoria* strains using gel electrophoresis analysis of BOX-PCR (A) and ERIC-PCR (B) fingerprinting profiling, with lane M representing the molecular marker and lane 1 to 27 representing the bacterial samples that were isolated.



**Supplementary Fig. 3.** Comparison of BOX-PCR (A) and ERIC-PCR (B) fingerprinting patterns of bacterial isolates, with the y-axis representing the number of bands, the x-axis representing regional populations such as Hailun (XeSh), Qinggang (XeSq), Zhaodong (XeSZ), Mulan (XeHm), Fangzheng (XeHf), Shuang cheng (XeHs), Gannan (XeQg), Fuyu (XeQf), Baiquan (XeQb), Fujin (XeJf), Huanan (XeJh), Hailin (XeMh), and Ningan (XeMn), and a third axis indicating heterozygosity.