

## Supplementary Information

**Table S1 Information of the 112 *P. sojae* isolates used in the study.**

Location	Code	Coordinates	Number	EC <sub>50</sub> range (μg/ml)	Year
Fujian	Ps1-8	24.78, 118.08	8	0.035-0.048	2008
Fujian	Ps9-27	24.37, 117.91	19	0.023-0.024	2002
Fujian	Ps28-39	24.33, 117.87	12	0.039-0.053	2004
Fujian	Ps40-49	24.77, 118.08	10	0.033-0.047	2005, 2006, 2007
Heilongjiang	LS-	45.12, 130.70	15	0.028-0.063	2010
Heilongjiang	HLYF-	46.89, 126.08	9	0.032-0.066	2010
Heilongjiang	SH-	46.65, 126.98	9	0.040-0.057	2010
Heilongjiang	CX-	46.03, 126.61	8	0.063-0.086	2010
Heilongjiang	DZT3-, JMS-	44.57, 129.63	16	0.046-0.067	2004, 2010
Anhui	AH-	32.36, 117.38	6	0.040-0.050	2010
<b>Total</b>			<b>112</b>	<b>0.023-0.086</b>	<b>2002-2010</b>

**Table S2 Concentrations used to determine the sensitivities of field isolates and resistant mutants of *P. sojae* to various fungicides**

Fungicide	Concentrations (μg/ml)
chlorothalonil	2.0, 4.0, 6.0, 8.0, 10.0
azoxystrobin	0.20, 0.40, 0.80, 1.0, 1.20
cymoxanil	0.10, 0.30, 0.50, 1.0, 3.0, 5.0
metalaxyl	0.15, 0.30, 0.60, 1.2, 2.4
flumorph	0.20, 0.30, 0.40, 0.50, 0.60, 0.80

**Table S3** Primers used in this study.

Primer name	Sequence 5'-3'	Purpose
Ps beta forward	GACGGAGAGGCCATACGAA	Amplification of the $\beta$ -tubulin gene in <i>P. sojae</i>
Ps beta reverse	AGATGCCGAGCCACTAAC	Amplification of the $\beta$ -tubulin gene in <i>P. sojae</i>
qRTHK-2F	CTCCAAGGGCTCGTCCAA	<i>P. sojae</i> housekeeping gene (rpS5) used as qRT-PCR reference
qRTHK-2R	GCCAGCATCCCTCCAAAG	<i>P. sojae</i> housekeeping gene (rpS5) used as qRT-PCR reference
PsACT qRT F	ACTGCACCTTCCAGACCATC	<i>P. sojae</i> actin gene used as qRT-PCR reference
PsACT qRT R	CCACCACCTTGATCTTCATG	<i>P. sojae</i> actin gene used as qRT-PCR reference
PsBeta_UTRF	GTGAGGGTATGGACGAGATGGA	qRT-PCR for validation of the endogenous $\beta$ -tubulin expression patterns
PsBeta_UTRR	TGAACAAAGGCGGTCAAGCAA	qRT-PCR for validation of the endogenous $\beta$ -tubulin expression patterns
PsBeta_qRTF	TACCCGGACCGTATCATGTG	qRT-PCR for validation of the total $\beta$ -tubulin expression patterns
PsBeta_qRTR	TCGTACAGGGCCTCGTTATC	qRT-PCR for validation of the total $\beta$ -tubulin expression patterns

Ovis aries	MREIVHICAGQCGNQIGAKRFWEVISDEHGIDPTGSYHGDSLQLERINVYYNEAT	GKYYVFRALIIVDLEPGTMDSVRSGPFQGIFRPDNFVFGQSGAGNNW	KGHYTEGAELIDSVLDVVRBESCDCLQGFQIAHSLGGGTG-GMGLT	150
Drosophila melanogaster	MREIVVNLCAGQCGNQIGAKRFWEIISERHIDSNGIIVCDSDLQLERVSYYNEASVTRSSGGKYYVFRAILLDEPGTMDSVRSGPYQJLFRPDNFVYGGSGAGNNW	KGHYTEGAELIDSVLDVVRBECNCDCLGQFQIAHSLGGGTG-GMGLT	155	
Arabidopsis thaliana	MREILHLIQGGCGNQIGAKRFWEVVAEHRGIDSTGRYQGFDLQLERVNYYNEAS	CGRFVFRAVIMDLEPGTMDSVRSGPYQJLFRPDNFVYGGSGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQVCHSLGGGTG-GMGLT	150
Botrytis cinerea	MREIVBLQTCQCGNQIGAAFWQTISGEHGLDGSVYNGTSDLQLERMNYYNEAS	GKYYVFRALIIVDLEPGTMDAVRAGFFGQLFRPDRNFVFGQSGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
Monilinia fructicola	MREIVBLQTCQCGNQIGAAFWQTISGEHGLDGSVYNGTSDLQLERMNYYNEAS	GKYYVFRALIIVDLEPGTMDAVRAGFFGQLFRPDRNFVFGQSGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
Cercospora beticola.seq	MREIVBLQTCQCGNQIGAAFWQTISGEHGLDGSVYNGTSDLQLERMNYYNEAS	GKYYVFRALIIVDLEPGTMDAVRAGFFGQLFRPDRNFVFGQSGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
Fusarium fujikuroi	MREIVBLQTCQCGNQIGAAFWQTISGEHGLDGSVYNGTSDLQLERMNYYNEAS	GKYYVFRALIIVDLEPGTMDAVRAGFFGQLFRPDRNFVFGQSGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
Magnaporthe oryzae	MREIVBLQTCQCGNQIGAAFWQTISGEHGLDGSVYNGTSDLQLERMNYYNEAS	GKYYVFRALIIVDLEPGTMDAVRAGFFGQLFRPDRNFVFGQSGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
P. sojae	MREIVBLQTCQCGNQIGAAFWQTISGEHGLDGSVYNGTSDLQLERMNYYNEAS	GKYYVFRALIIVDLEPGTMDAVRAGFFGQLFRPDRNFVFGQSGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
P. infestans	MREIVBLQTCQCGNQIGAKRFWEVISDEHVDPGTSYHGDSLQLERINVYYNEAT	GGRYVFRALIIMDLEPGTMDSVRAGPYQJLFRPDRNFVFGQTGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
P. capsici	MREIVBLQTCQCGNQIGAKRFWEVISDEHVDPGTSYHGDSLQLERINVYYNEAT	GGRYVFRALIIMDLEPGTMDSVRAGPYQJLFRPDRNFVFGQTGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
Py. macrosporum	MREIVBLQTCQCGNQIGAKRFWEVISDEHVDPGTSYHGDSLQLERINVYYNEAT	GGRYVFRALIIMDLEPGTMDSVRAGPYQJLFRPDRNFVFGQTGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
Py. sulcatum	.....DQCGNQIGAKRFWEVISDEHVDPGTSYHGDSLQLERINVYYNEAT	GGRYVFRALIIMDLEPGTMDSVRAGPYQJLFRPDRNFVFGQTGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	140
Py. sylvaticum	.....HGDSDLQLERINVYYNEAT	GGRYVFRALIIMDLEPGTMDSVRAGPYQJLFRPDRNFVFGQTGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	48
Py. ultimum	MREIVBLQTCQCGNQIGAKRFWEVISDEHVDPGTSYHGDSLQLERINVYYNEAT	GGRYVFRALIIMDLEPGTMDSVRAGPYQJLFRPDRNFVFGQTGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	114
Py. aphanidermatum	MREIVBLQTCQCGNQIGAKRFWEVISDEHVDPGTSYHGDSLQLERINVYYNEAT	GGRYVFRALIIMDLEPGTMDSVRAGPYQJLFRPDRNFVFGQTGAGNNW	KGHYTEGAELIDSVLDVVRBEPNCDCLGQFQIAHSLGGGTG-GMGLT	150
Consensus	mreivh q gqcgncqgkfwies ehg d tg yhgdslqlerinvyyneat	ggryvprailmdlepgtdmsvragpygqlfrpdnfvfgqsgagnnwakhytegaelidsvldvvrkeaeescdclqgfithsllgggtsgmgtl	ggryvprailmdlepgtdmsvragpygqlfrpdnfvfgqsgagnnwakhytegaelidsvldvvrkeaeescdclqgfithsllgggtsgmgtl	150
Ovis aries	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTYSDNEALYDICRTLKLITPQYGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Drosophila melanogaster	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTYCDNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	310		
Arabidopsis thaliana	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLITPQSGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Botrytis cinerea	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Monilinia fructicola	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Cercospora beticola.seq	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Fusarium fujikuroi	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Magnaporthe oryzae	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
P. sojae	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
P. infestans	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
P. capsici	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Py. macrosporum	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Py. sulcatum	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	295		
Py. sylvaticum	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	203		
Py. ultimum	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	269		
Py. aphanidermatum	LISKIREEDPDRMNTSVPSPFKVSDTVVEPYNATLSHQIVENADTCVLNEALYDICRTLKLSPNSPQGDINLISVMSMGTQCLRLKAVNTPPFRLHFFMGEAPLTSRGSCQYRAIDPELTQCMDRNMPAADF	305		
Consensus	liskireeypdrimctysvcpspkvsvdtvvepynatlsvhqlvenadevmclnealycdftrtlkltpygdlnhvcamaamsgittcrlfpqqlnsdrklavnlipfprlhffmgfapltsrgsqyraltvplqqfdaknmmcaadp	305		
Ovis aries	RGRYLTAACMRGMSKMEVKDEOMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSATFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	445		
Drosophila melanogaster	RGRYLTAACMRGMSKMEVKDEOMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFSMFRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEFPENVEEVGDCI	453		
Arabidopsis thaliana	RGRYLTAACMRGMSKMEVKDEOMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFSMFRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEFPENVEEVGDCI	449		
Botrytis cinerea	RGRYLTCASIERRGVSMEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	447		
Monilinia fructicola	RGRYLTCASIERRGVSMEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	447		
Cercospora beticola.seq	RGRYLTCASIERRGVSMEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	398		
Fusarium fujikuroi	RGRYLTCASIERRGVSMEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	447		
Magnaporthe oryzae	RGRYLTCASIERRGVSMEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	447		
P. sojae	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	446		
P. infestans	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	446		
P. capsici	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	446		
Py. macrosporum	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	446		
Py. sulcatum	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	257		
Py. sylvaticum	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	363		
Py. ultimum	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	446		
Py. aphanidermatum	RGRYLTAACMRGMSKTEKVEDQMLNVCNRNSYYFEWIPLNNVRAISCDIPKGLRMSSTFIGNSTAIQELFLRRISEQFTAMFRRRAFLHWYTGEGMDEMEFTAEESNNNDIVSEYQQYQDATADE...EEGFEEDEAPLEGEE...	446		
Consensus	rhgrylttaamfrgmrstkevdqeqlnvqcnknssyfiewiplnnikasvcodipkgklkms tfignstaiqemfkrvseqftamfrrraflhwytgegmdeftaeesnmndlvseyqqyqdatae e e e e e e	446		

Figure S1 Multiple alignment of the β-tubulin amino acid sequences in *Ovis aries* (PDB: D0VWY9-1), *Drosophila melanogaster* (GenBank: NP\_001286835.1), *Arabidopsis thaliana* (GenBank: AAK96884.1), *Botrytis cinerea*, *Monilinia fructicola*, *Cercospora beticola*, *Fusarium fujikuroi*, *Magnaporthe grisea*, *P. sojae*, *P. infestans*, *P. capsici*, *Py. macrosporum* (GenBank: BAJ79093.1), *Py. sulcatum* (GenBank: AJD08746.1), *Py. sylvaticum* (GenBank: ADJ39244.1), *Py. ultimum* and *Py. aphanidermatum*. The red asterisk (★) indicates the amino acid residue at the codon 239.