

**Figure S1.** The information of pathogen (*Lophodermium piceae*). (a) The ascoma of *L. piceae* on the needle of *Picea asperata*; (b) The transverse section of *L. piceae* ascoma; (c) The ascospore of *L. piceae*; (d) The conidium of *L. piceae*. *L. piceae* characteristic sequence Genbank ID: KX573897.

**Table S1.** The details of the *Picea asperata* collection conditions on a forest farm of Erlang Mountain in Sichuan, China.

Time of	Precipitation/A	Humidity	Altitude	Мар	Percentage of needles infected	
collecting	nnual average	(%)		coordinates	by Lophodermium piceae (%)/The	
				(longitude	growth rate of infected needles	
				and latitude)	(%)	
					Healthy P.	Infected P.
					asperata	asperata
2018.05.25	625.18 mm	64	2830.00 m	N:	0/0	$45 \pm 0.08/0$
2018.07.26		47		25°51′34.66″	0/0	$52 \pm 0.06/15.56$
2018.09.25		51		E:	0/0	$68 \pm 0.11/30.77$
2018.11.27		60		102°16′30.96″	0/0	$76 \pm 0.18/11.76$

**Figure S2.** Nucleotide sequence and the deduced amino acid sequence of the *PaPAL* gene. The start codon and stop codon are indicated by bold font and an asterisk, respectively. The phenylalanine and histidine ammonia-lyase signature sequence is underlined. The deamination sites are shaded in grey. The catalytic active sites are shown in boxes.