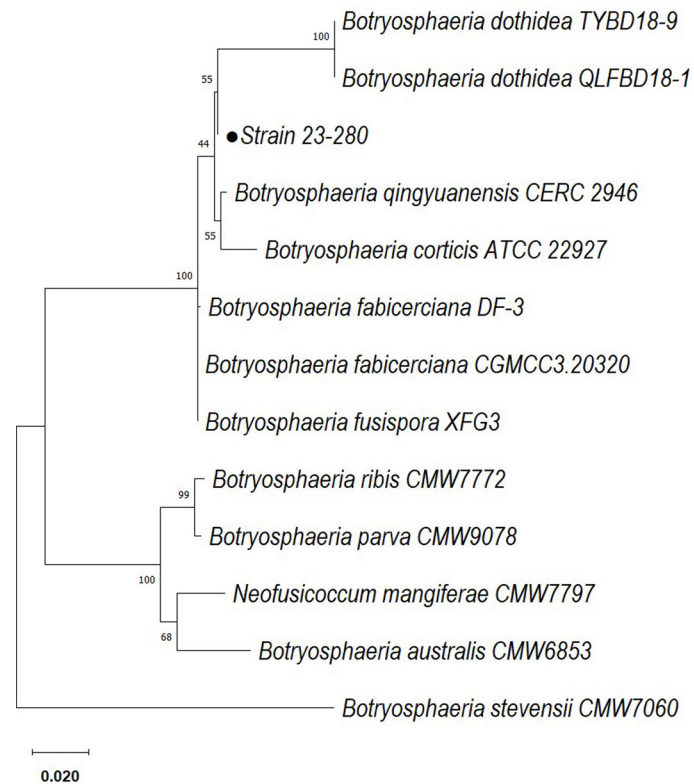


Supplementary Table 1. *Botryosphaeria* species used in this study for phylogenetic analyses and GenBank accession numbers

Species	Isolates	GenBank accession no.		
		ITS	<i>EF-1α</i>	TUB2
<i>Botryosphaeria dothidea</i>	23-280	OR751622	OR759418	OR901329
<i>Botryosphaeria dothidea</i>	TYBD 18-9	MW561961.1	MW561776.1	MW561872.1
<i>Botryosphaeria dothidea</i>	QLFBD18-1	MW561903.1	MW561717.1	MW561814.1
<i>Botryosphaeria qingyuanensis</i>	CERC 2946	KX278000.1	KX278105.1	KX278209.1
<i>Botryosphaeria corticis</i>	ATCC 22927	DQ299247.1	EU673291.1	EU673108.1
<i>Botryosphaeria fabicerciana</i>	DF-3	OP729178.1	OP758196.1	OP758199.1
<i>Botryosphaeria fabicerciana</i>	CGMCC3.20320	MW642163.2	MW651965.1	MW651966.1
<i>Botryosphaeria fusispora</i>	XFG3	MZ831293.1	MZ851774.1	MZ851777.1
<i>Botryosphaeria ribis</i>	CMW 7772	AY236935.1	AY236877.1	AY236906.1
<i>Botryosphaeria parva</i>	CMW 9078	AY236940.1	AY236885.1	AY236914.1
<i>Neofusicoccum mangiferae</i>	CMW 7797	AY615186.1	DQ093220.1	AY615173.1
<i>Botryosphaeria australis</i>	CMW 6853	AY339263.1	AY339271.1	AY339255.1
<i>Botryosphaeria stevensii</i>	CMW 7060	AY236955.1	AY236904.1	AY236933.1



Supplementary Fig. 1. Phylogenetic relationship based on ITS, *EF-1 α* , *TUB2* sequences of *Botryosphaeria dothidea*. DNA sequences from the NCBI nucleotide database were aligned using the ClustalW program in MEGA 6, and constructed using the maximum likelihood method with 1,000 bootstrap replicates. The scale bar indicates the number of differences in nucleotide substitutions per sequences.