Table S1. List of *Serpula himantioides* sequences

Area	Code	Origin	GenBank accession number: ITS	Reference
East Asia（Japan)	sawara1	Japan	LC038085 [a]	This study
	TUFC 12779	Japan	LC637886	This study
	UTCF3114221	Japan	LC630922	This study
	UTCF3114251	Japan	LC630921	This study
	WD2171	Japan	LC637887	This study
	WD2172	Japan	LC637888	This study
	WD2173	Japan	LC637889	This study
	WD2174	Japan	LC637890	This study
	WD2175	Japan	LC637891	This study
	WD2176	Japan	LC637892	This study
	WD2177	Japan	LC637893	This study
	WD2178	Japan	LC637894	This study
	WD2179	Japan	LC637895	This study
	WD2183	Japan	LC637896	This study
	WD2184	Japan	LC637897	This study
	WD2185	Japan	LC637898	This study
Africa	SH27	Zimbabwe	AM076507	Carlsen et al. [11]
East Asia	SH47	India	AJ557351	Kauserud et al. [41]
	SH48B	India	AJ557342	Kauserud et al. [41]
	SH127	China	HM135654	Carlsen et al. [11]
Europe	SH29	France	AM076509	Carlsen et al. [11]
	SH31	Norway	AM076495	Carlsen et al. [11]
	SH113	Norway	AM076497	Carlsen et al. [11]
	SH51	Denmark	AJ557329	Kauserud et al. [41]
	SH36	Estonia	AJ557325	Kauserud et al. [41]
North America	SH17	Canada	AM076494	Carlsen et al. [11]
	SH18	Canada	AJ557357	Kauserud et al. [41]
	SH20	Canada	AM076492	Carlsen et al. [11]
	SH141	USA	HM135655	Carlsen et al. [11]
	SH164	USA	AM076493	Carlsen et al. [11]
Oceania	SH114	New Zealand	AM076521	Carlsen et al. [11]
South America	SH168	Chile	HM135649	Carlsen et al. [11]
	SH169	Chile	HM135650	Carlsen et al. [11]
	SH171	Argentina	HM135690	Carlsen et al. [11]
	SH172	Argentina	HM135691	Carlsen et al. [11]

Table S2. Primer sequences, names, GC %, and melting temperatures

Primer	Name	Nucleotide sequences	GC%	Melting temperature (Tm) °C[1]
Forward	SHF	5'-CTCGCATCGATGAAGAAC-3'	50.0	59.5
Reverse	SHR	5'-CAAAACATTGTCTTACGACG-3'	40.0	58.3

[1] Melting temperatures were calculated using the nearest-neighbor method.

Table S3. *Serpula himantioides* strains and other fungal species used in end-point PCR

Fungal species	Isolate code	Isolate number	Host plant species	Source of isolation	Locality of source	Source[1]
Serpula himantioides	SH1	sawra1	*Chamaecyparis pisifera*	Decayed wood	Chichibu, Saitama, Japan	UTCF
	SH2	UTCF3114221	*C. pisifera*	Decayed wood	Chichibu, Saitama, Japan	UTCF
	SH3	WD2174	*C. pisifera*	Decayed wood	Mito, Ibaraki, Japan	FFPRI
	SH4	TUFC 12779	*Abies sachalinensis*	Decaying and decorticated branch	Sapporo, Hokkaido, Japan	TUFC
Serpula lacrymans	SL	NBRC30955	Unknown	Coniferous timber	Hokkaido, Japan	NBRC
Coniophora puteana	CP	WD1480	Unknown	Basidiospores	Tottori, Japan	FFPRI
Phaeolus schweinitzii	PS	NBRC6433	Unknown	Unknown	Japan	NBRC
Postia floriformis	PF	WD913	*Larix kaempferi*	Decay of butt	Shizuoka, Japan	FFPRI
Veluticeps berkeleyi	VB	WD26	Unknown	Decayed wood	Nagano, Japan	FFPRI
Lenzites betulinus	LB	WD1351	Unknown	Unknown	Yamagata, Japan	FFPRI

[1] UTCF, The University of Tokyo Chichibu Forest, Japan; FFPRI, Forestry and Forest Products Research Institute, Japan; TUFC, Fungus/Mushroom Resource and Research Center, Tottori University, Japan; NBRC, Biological Resource Center, NITE, Japan.

Table S4. Size of decayed *Chamaecyparis pisifera* tree

Tree number	**CP1**	**CP2**
Age at time of cutting	88	90
Diameter of breast height（cm）	24.5	25.5
Tree height（m）	28.0	27.8

Table S5. Details of the decayed wood samples

Sample name	Collected tree	Sampling height(m)	Wood discoloration[1]
DWS_1	CP1	1.8	Moderate discoloration
DWS_2	CP1	1.9	Moderate discoloration
DWS_3	CP1	2.0	Moderate discoloration
DWS_4	CP1	2.2	Non-discoloration
DWS_5	CP1	2.3	Non-discoloration
DWS_6	CP1	2.4	Non-discoloration
DWS_7	CP2	2.7	Severe discoloration
DWS_8	CP2	2.9	Severe discoloration
DWS_9	CP2	3.1	Severe discoloration

Table S6. Absolute quantification of *Serpula himantioides* in decayed wood samples

Sample name	Concentration of DNA (ng/μL)	Number of DNA copies (/μL)
DWS_1	0.49	4.53×10^{6}
DWS_2	0.42	3.46×10^{6}
DWS_3	0.25	2.36×10^{6}
DWS_4	0.12	1.51×10^{6}
DWS_5	0.22	1.66×10^{6}
DWS_6	0.11	3.21×10^{4}
DWS_7	0.29	1.99×10^{5}
DWS_8	0.44	3.01×10^{6}
DWS_9	0.04	7.78×10^{3}

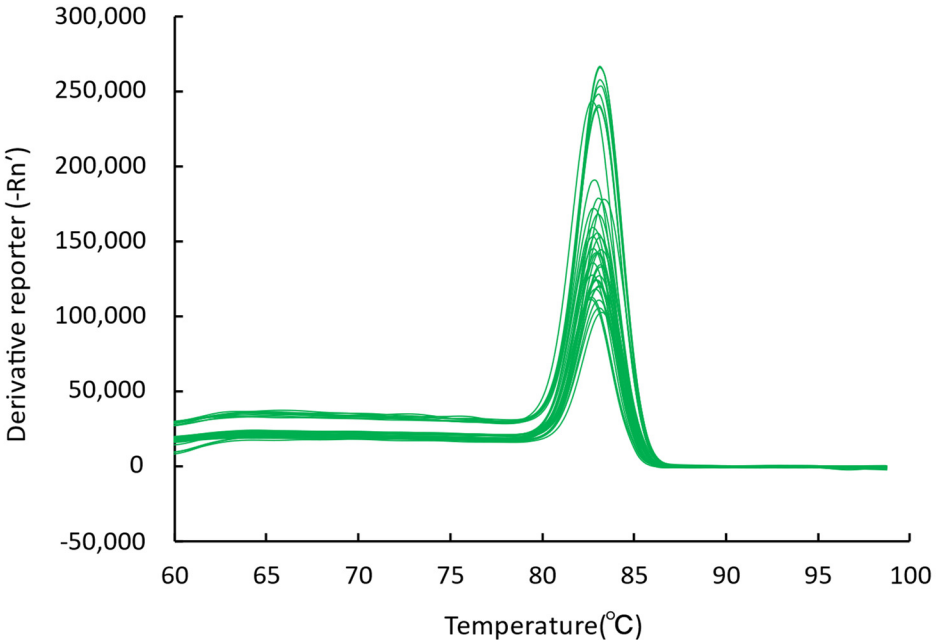

Figure S1. Melting curves of DNA extracted from decayed wood samples as measured by real-time PCR. The derivative reporter, displayed on the y-axis, was calculated as the negative first derivative of the normalized fluorescence (Rn) generated by the reporter during PCR amplification.