Table S1. Primers used in this study to amplify and sequence barcode regions in molecular identification.

Gene	Primer	Sequence	References
The small subunit (18S) of the nuclear rDNA (SSU)	NS1	5′-GTAGTCATATGCTTGTCTC-3′	White et al. 1990 [45]
	NS4	5′-CTTCCGTCAATTCCTTTAAG-3′	
Internal transcribed spacer (ITS)	ITS1-F	5′-CTTGGTCATTTAGAGGAAGTAA-3′	Gardes and Bruns. 1993 [49]
	ITS4	5′-TCCTCCGCTTATTGATATGC-3′	White et al. 1990 [45]
The large subunit (28S) of the nuclear rDNA (LSU)	LR0R	5′-ACCCGCTGAACTTAAGC-3′	Rehner and Samuels 1994 [47]
	LR6	5′-CGCCAGTTCTGCTTACC-3′	Vilgalys and Hester 1990 [46]
Translation elongation factor 1-α (TEF1)	EF1-983F	5′-GCYCCYGGHCAYCGTGAYTTYAT-3′	Rehner and Buckley 2005 [48]
	EF-2218R	5′-ATGACACCRACRGCRACRGTYTG-3′	

Table S2. Presence of septa in *Hendersonia* conidia produced on *Pinus mugo* needles in situ in pycnidia (A) and in vitro on agar medium (B), according to their location or age. (A) a – conidia within pycnidia embedded in *P. mugo* needles; b – conidia aggregated in a crust above the ostiole on the surface of *P. mugo* needles. (B) c – conidia produced in young colonies (up to 6 weeks old); d – conidia produced in older colonies (3–4 months old).

Origin of Conidia	Biological Units	Percentage of Conidia With a Certain Number of Septa [1]						Number of Conidia Analysed
		0	1	2	3	4	5	
Aa	T1e68	3	6	74 [a]	15 [b]	1	1	100
Aa	Pm436E	0	2	59 [a]	39 [b]	0	0	100
Aa	T1e84	0	1	75 [a]	24 [b]	0	0	100
Aa	T1h1	0	1	76 [a]	23 [b]	0	0	100
Aa in total		0.8	2.5	71	25.3	0.2	0.2	400
Ab	T1g87	0	2	41 [a]	53 [a]	4	0	100
Ab	T1e49	0	0	50 [a]	46 [a]	3	1	100
Ab	Pm440E	0	1	57 [a]	41 [a]	1	0	100
Ab	T1e69	0	0	49 [a]	51 [a]	0	0	100
Ab in total		0	0.8	49.2	47.8	2	0.2	400
Bc	Pm441E	2	8	79 [a]	10 [b]	1	0	100
Bc	T1g71	0	2	96 [a]	2 [b]	0	0	100
Bc	T1g74	0	4	73 [a]	21 [b]	1	1	100
Bc	Pm439E	0	8	80 [a]	11 [b]	1	0	100
Bc in total		0.5	5.5	82	11	0.8	0.2	400
Bd	Pm379E	0	0	60 [a]	39 [b]	1	0	100
Bd	Pm421E	0	7	86 [a]	7 [b]	0	0	100
Bd	T2a71	0	1	83 [a]	14 [b]	1	1	100
Bd	T1s1	0	2	66 [a]	29 [b]	2	1	100
Bd in total		0	2.5	73.7	22.3	1	0.5	400

[1] Different lower-case letters within each row indicate statistically significant differences in the relative frequency of type 2 conidia compared with type 3 conidia ($p < 0.05$), based on a one-sided exact binomial test with the Benjamini–Hochberg correction.

Table S3. Selected morphological characteristics of pycnidia and conidia for three *Hendersonia* species on pine (*Pinus* sp.) needles.

Literature	Tree Species	Number of Septa in Conidia	Constriction at the Septa	Dimensions of Conidia (µm) Length × Width	Diameter of pycnidia (µm)
		***Hendersonia montana* – Europe**			
Saccardo 1899 [28]	*P. mugo*	3, less frequently 2–4	–	29–34 (–42) × 3.5–4	–
Kalandra 1938 [29]	*P. sylvestris, P. mugo*	0–4, mainly 3	slightly constricted	24–55 × 3–6 (mostly 27–36 × 4–5)	82–168 (except. 256–352)
Moriondo 1963 [30]	*P. sylvestris*	1–3	–	15–40 × 2.5–5	120–300
		***Hendersonia pinicola* – North America**			
Wehmeyer 1946 (holotype) [33]	*P. murrayana*	0 – at first, becoming 3-septate	not constricted	14–20 × 5–7	100–150
Chao 1969 [34]	*P. banksiana*, *P. contorta*	3	not constricted	15–17 × 5–5.5	up to 200
James 1984 [35]	*P. contorta*	3 (90%), 1–2 (<10%)	slight at each septum	15.5–22.0 × 5.5–6.8 average 19.6 × 6.3 (crust on needles)	125–150
Stahl et al. 1988 [37]	*P. contorta*	3 – typically, can be 1–6	not constricted	(13–) 17–21 (–29) × (4.5–)5–7.5(–9)	–
		***Hendersonia acicola* – Europe**			
Münch and Tubeuf 1910, 1911 [21,22]	*P. sylvestris*	1–3, mostly 2	constricted	11–15 × 4–5, mostly 14–15 × 4–5	ca. 140
Lagerberg 1910 [23]	*P. sylvestris*	1–3, mostly 2	constricted	11–15 × 4–5	–
Kujala 1950 [42]	*P. sylvestris*	2–3	–	13–15 × 5–6,5	82–168
Ellis and Ellis 1985 [43]	*P. nigra var. maritima*, *P. sylvestris*	1–3, mostly 2	–	11–15 × 4–5	150
		***Hendersonia acicola* – Asia**			
Bingzhang et al. 1994 [27]	*P. sylvestris* var. *mongolica*	2–3 (rarely 1), at first 0	constricted	10.2–13.6 × 4.3–6.8	209.5–323.5 × 153–269.5

Table S4. Colony radius reduction of *Hendersonia acicola* and fungi isolated from *Pinus mugo* needles assessed in three weeks old dual cultures.

Taxon	Representative Strain [1]	Reduction in Growth of Test Fungi (%) Mean (Min–Max)	*Hendersonia acicola* Growth Reduction (%) [2] Mean (Min–Max)
Aureobasidium pullulans	PZ734645	38.1 (27.6–60.0)	1.3 (0.0–7.6)
Biscogniauxia nummularia	PZ734646	48.3 (35.0–62.3)	10.3 (0.0–17.6)
Botrytis cinerea	PZ734647	60.3 (51.8–67.2)	4.4 (0.0–14.3)
Epicoccum nigrum	PZ734650	58.0 (49.1–70.6)	35.7 (0.0– 48.1)
Lophodermium conigenum	PZ734652	58.3 (50.0–66.7)	15.3 (0.0–30.0)
Lophodermium corconticum	PZ734666	58.0 (51.5–70.0)	7.9 (0.0–14.5)
Lophodermium sp.	PZ734671	16.0 (6.3–25.0)	15.3 (6.3–23.1)
Nemania serpens	PZ734672	40.1.(35.7–46.4)	4.7 (0.0–20.0) (+11.5) [2]
Sydowia polyspora	PZ734673	58.1 (54.0–61.4)	10.6 (0.0– 25.0) (+12.8) [2]
Xylaria sp.	PZ734674	48.9 (44.4– 54.3)	6.3 (0.0–11.1)

[1] Explanations as in Table 2. [2] One culture of *N. serpens* showed faster growth by 11.5%, and one culture of *S. polyspora* by 12.8%.

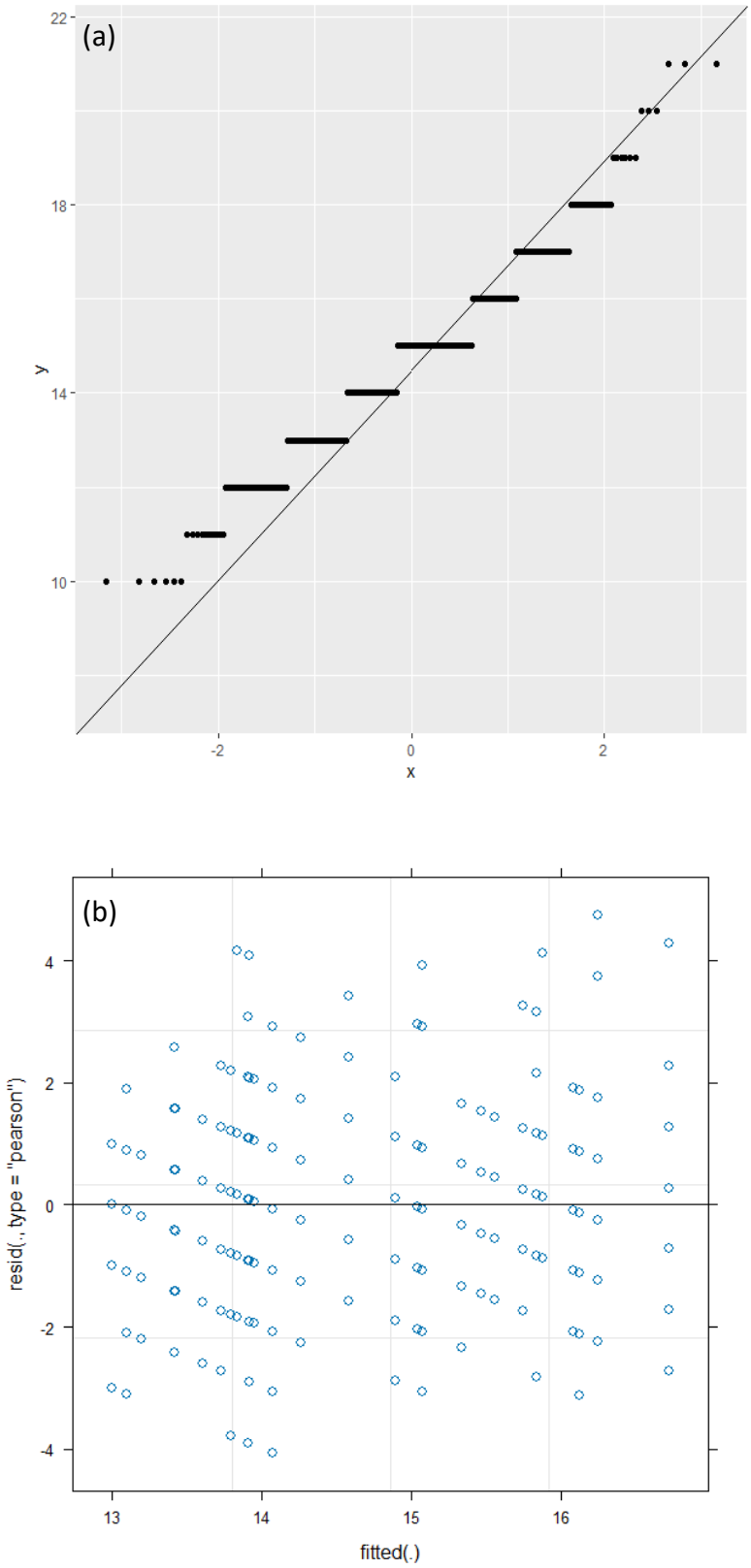


Figure S1. Residual diagnostic plots for the linear mixed-effects model of *Hendersonia* sp. conidium length ($n = 640$): (**a**) normal quantile–quantile (Q–Q) plot of the model residuals, evaluating the assumption of normality; (**b**) residuals-versus-fitted values plot, assessing the homogeneity of residual variance (homoscedasticity) and model linearity.

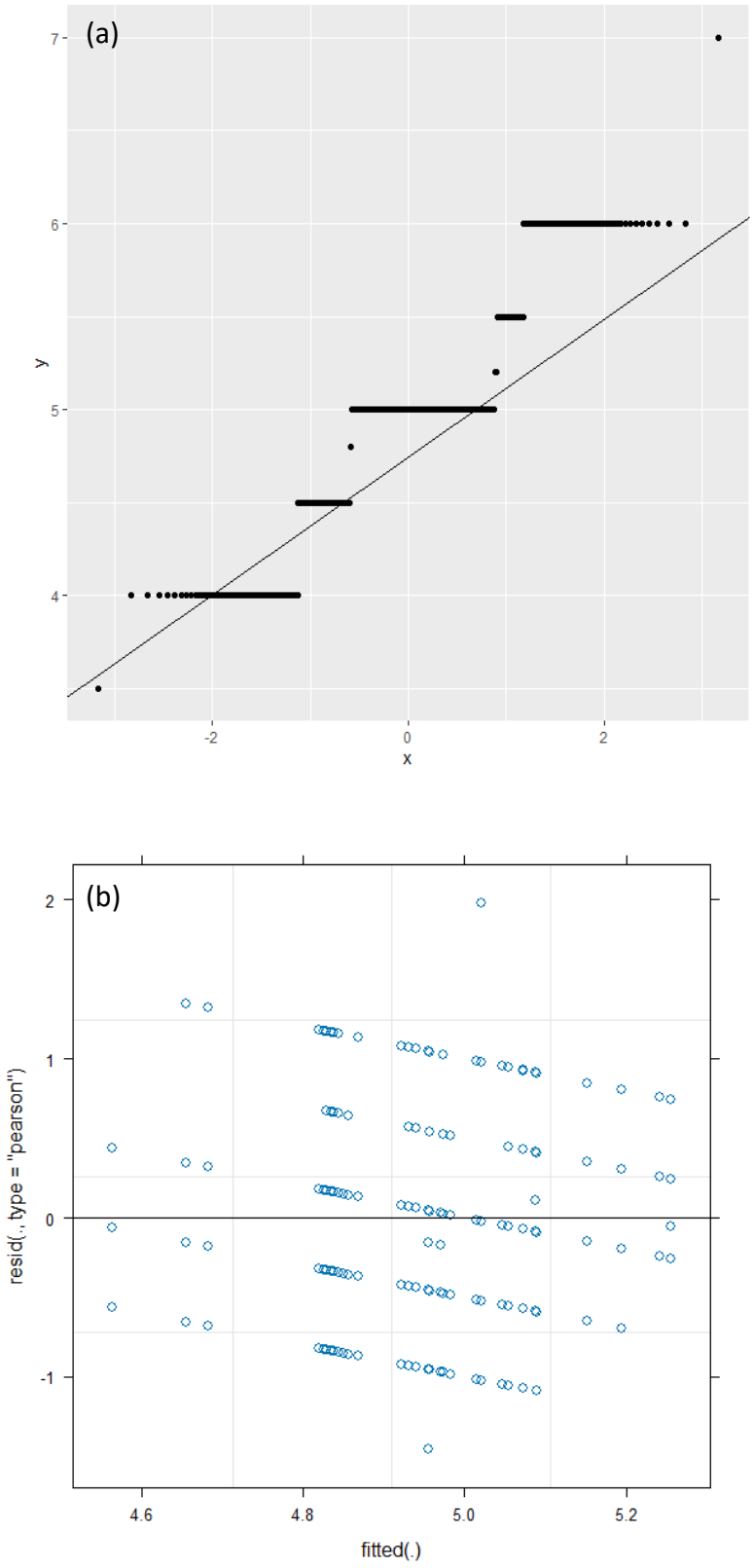


Figure S2. Residual diagnostic plots for the linear mixed-effects model of *Hendersonia* sp. conidium width (n = 640): (**a**) normal quantile–quantile (Q–Q) plot of the model residuals, evaluating the assumption of normality; (**b**) residuals-versus-fitted values plot, assessing the homogeneity of residual variance (homoscedasticity) and model linearity.