



## ***Lecanicillium uredinophilum* known from rusts, also occurs on animal hosts with chitinous bodies**

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### **Abstract**

Two isolates of *Lecanicillium uredinophilum* were obtained from an infected insect collected in Yunnan Province, China. *L. uredinophilum* was initially discovered on a rust fungus in Korea. The identity was supported by combined analyses of the internal transcribed spacer (ITS1, 5.8s and ITS2), large subunit (LSU) and small subunit (SSU) of the ribosomal RNA gene and protein loci of elongation factor-1 alpha (*tef1-a*), RNA polymerase II largest subunits (RPB1 and RPB2). This is the first report of *L. uredinophilum* in China and from an insect host. This species and perhaps other *Lecanicillium* species are likely to infect various hosts with chitinous bodies. A description of *L. uredinophilum* from China is accompanied by illustrations of macro- and micromorphological characters, and a discussion of related taxa is provided.

**Key words** – China – *Cordycipitaceae* – verticillium-like – entomogenous – phylogeny – taxonomy

### **Introduction**

The genus *Lecanicillium* W. Gams & Zare is currently referred to *Cordycipitaceae* Kreisel in the order *Hypocreales* Lindau, based on multi-gene phylogenetic analyses (Sung et al. 2007, Maharachchikumbura et al. 2016, Wijayawardene et al. 2017). *Lecanicillium* and *Torrubiella* Boud. were treated as synonyms of *Akanthomyces* Lebert by Kepler et al. (2017) and this was followed by Wijayawardene et al. (2018). Connections between the asexual morph of *Lecanicillium* and its sexual morph have been established, i.e. *L. araneorum* (Petch) Zare & W. Gams linked to *Torrubiella alba* Petch (Petch 1932), *L. lecanii* (Zimm.) Zare & W. Gams linked to *Cordyceps confragosa* (Mains) G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora (Evans & Samson 1982, Gams & Zare 2001, Bischoff & White 2004), and *L. wallacei* (H.C. Evans) H.C. Evans & Zare linked to *Torrubiella wallacei* H.C. Evans (Gams 2017). *Verticillium* is extremely heterogeneous and divide into four sharply delimited groups and have correlated with host range based on ITS analysis and morphologic study (Zare et al. 2000). Subsequently, the parsimony analyses of many representative taxa within *Verticillium* section *Prostrata* Nees based on SSU and LSU sequence data showed that *Prostrata* appeared to be paraphyletic rather than monophyletic (Sung &

Spatafora 2001). Consequently, most taxa classified in *Verticillium* (section *Prostrata*) were accommodated in the genus *Lecanicillium* based on the integration of morphological observation and molecular analyses (Zare & Gams 2008).

*Lecanicillium* infects various hosts, including arthropods, nematodes, plants and even fungi (Zare & Gams 2001, Sukarno et al. 2009). For example, *L. araneogenum* Wan H. Chen, Y.F. Han, J.D. Liang, Z.Q. Liang & D.C. Jin and *L. araneorum* on spiders (Evans & Samson 1987, Chen et al. 2017), *L. antillanum* (R.F. Castañeda & G.R.W. Arnold) Zare & W. Gams occurs on the eggs of nematode *Meloidogyne incognita* (Nguyen et al. 2007), *L. flavidum* (W. Gams & Zaayen) W. Gams & Zare on decaying needles of *Abies alba* (Zaayen & Gams 1982) and *L. uredinophilum* M.J. Park, S.B. Hong & H.D. Shin on rust fungi and agarics (Mijeong et al. 2015, Spatafora et al. 2007). Therefore, this genus was considered to be entomopathogenic, fungicolous and nematophagous and could be developed as bio-control agents (Goettel et al. 2008). Chiriví-Salomón et al. (2015) discovered that *L. sabanense* Chir-Salom, S. Restrepo & T.I. Sanjuan plays an important role in suppressing the development of soft scale insects (e.g. *Pulvinaria caballeroramosae*), which are harmful to the health of ornamental trees e.g. *Ficus soatensis* (Moraceae). In addition, both *L. attenuatum* Zare & W. Gams and *L. longisporum* (Petch) Zare & W. Gams are controlling agents of aphids and *Sphaerotheca fuliginea* (Goettel et al. 2008). Hajji-Hedfi et al. (2017) showed that *Lecanicillium* sp. had antagonistic activity against the nematode *Meloidogyne javanica* and Xie et al. (2018) suggested that *L. attenuatum* may be useful in controlling nematodes. With the development of science and technology, an increasing number of microbial agents will be used against insect pests.

In this study, we describe a new host and new country record for *L. uredinophilum* based on morphological observations and molecular analyses to enrich the resource of entomopathogenic fungi.

## Materials & Methods

### Sample collection, morphological studies and isolation

Infected insect specimens attached to lower leaf surface of a pear tree were collected from Pingbian, Yunnan Province, China. Strain KUN 101466 and KUN 10149 were isolated from two specimens and cultured on potato dextrose agar (PDA, 1 % w/v peptone), and incubated at room temperature. Macromorphological characters of these two isolates were examined using a stereoscope (Olympus SZ61). Squash mounts were prepared prior to study of micromorphology with a compound microscope (Nikon ECLIPSE Ni); important characteristics such as conidiophores, phialides and conidia were captured with a digital camera (Canon EOS 600D). Whenever possible, more than 30 measurements were made. The lengths and widths were measured using the Tarosoft (R) Image Frame Work program and images used for figures processed with Adobe Photoshop CS3 Extended v. 10.0 (Adobe®, San Jose, CA).

### DNA extraction, PCR amplification and sequencing

The total genomic DNA was extracted from mycelium scraped from the edges of the growing cultures. DNA was extracted using a DNA extraction kit (Biospin Fungus Genomic DNA Extraction Kit, BioFlux®, China) following the instructions of the manufacturer. Extracted DNA products were deposited at -20 °C for long term storage.

DNA sequence data was obtained from the partial sequences of six genes, including the internal transcribed spacers (ITS1-5.8S-ITS2), large subunit rDNA (28S, LSU), small subunit rDNA (18S, SSU), translation elongation factor 1-alpha gene (*tef1- $\alpha$* ), RNA polymerase II largest subunit 1 (RPB1) and RNA polymerase II largest subunit 2 (RPB2). ITS was amplified using the primers ITS4/ITS5 (White et al. 1990), LSU was amplified using the primers LR0R and LR5 (Vilgalys & Hester 1990). SSU was amplified using the primers NS1 and NS4 (White et al. 1990). *tef1- $\alpha$*  was amplified using primers EF1-983F and EF1-2218R (Rehner & Buckley 2005), RPB1

was amplified using the primers RPB1-Cr and RPB1-Ac primer (Castlebury et al. 2004) and RPB2 was amplified using the primers fRPB2-5f and fRPB2-7cR (Liu et al. 1999, Matheny 2005).

### Sequences alignments and phylogenetic analyses

Forward and reverse sequences were verified and assembled with Finch TV version 1.4.0 (Mccredden 2016) and Seqman software (Swindell & Plasterer 1997), respectively. Sequences generated from LSU rRNA, SSU rRNA, *tef1- $\alpha$* , RPB2, RPB1 and ITS were analyzed with other sequences retrieved from GenBank (Table 3). The related sequences were obtained from BLAST searches and recently published data (Sung & Spatafora 2001, Spatafora et al. 2007, Mijeong et al. 2015, Chen et al. 2017). The sequences were automatically aligned in MAFFT v. 7 at the web server (<http://mafft.cbrc.jp/alignment/server>) (Kuraku et al. 2013, Katoh & Standley 2013, Katoh et al. 2017). The alignments were edited where necessary with MEGA6 (Tamura et al. 2013). The final alignment (combined LSU, SSU, *tef1- $\alpha$* , RPB2, RPB1 and ITS loci) included 41 strains. *Simplicillium lanosoniveum* (CBS 704.86) was selected as the outgroup taxon. The phylogenetic analyses of concatenated data-set were performed for maximum-likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI). The alignment properties for the individual genes are shown in Table 1.

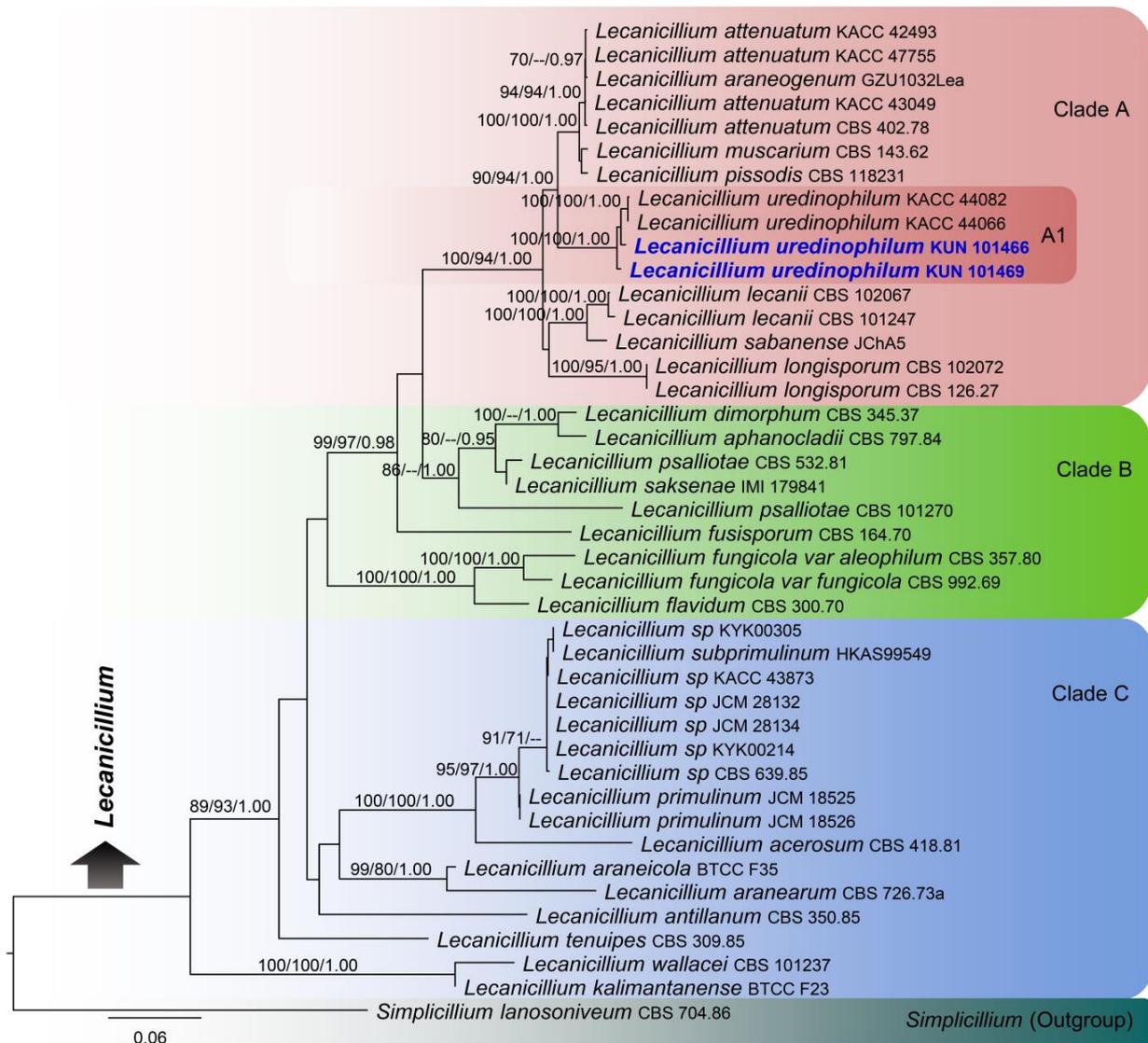
The sequence alignments were converted to NEXUS format (.nex) for MP and BI using ClustalX2 v. 1.83 (Thompson et al. 1997, Kohli & Bachhawat 2003). For the RAxML analysis, sequence alignments were converted to PHYLIP format (.phy) using ALTER (<http://sing.ei.uvigo.es/ALTER/>, 2018). MP was carried out with PAUP v. 4.0b10 (Swofford 2002). The trees were inferred using the heuristic search option with TBR branch swapping algorithm. Related parameters were set as follow: all characters have equal weight; random taxon addition; gaps are treated as “missing” where they occurring in relatively conserved region; branches collapsed if minimum branch length is zero; tree length (TL), consistency index (CI), homoplasy index (HI), retention index (RI) and rescaled consistency index (RC) were calculated for the MP. Clade stability was assessed using bootstrap (BT) analyses with 1000 replicates, each with 10 replicates of random stepwise of taxa. Bootstrap values that equal or are more than 70% are shown at each node (Fig. 1). The evolutionary models for Bayesian analysis and ML were selected independently for each locus using MrModeltest v. 2.3 (Nylander et al. 2008) under the Akaike Information Criterion (AIC) performed in PAUP v. 4.0b10 (Ronquist & Huelsenbeck 2003). The best-fit models for each locus in both Bayesian and ML analyses were given in Table 1. The Bayesian analysis was performed in MrBayes v. 3.1.2 (Rannala & Yang 1996, Zhaxybayeva & Gogarten 2002) to evaluate posterior probabilities (PP) under Markov Chain Monte Carlo sampling (MCMC). Bayesian analysis was run for 725000 generations, with trees sampled every 1000 generations. The temperature value was lowered to 0.15, all sampled topologies beneath the asymptote (25%) were discarded as part of a burn-in procedure, the remaining trees were used for calculating posterior probabilities in the majority rule consensus tree and the critical value for the topological convergence diagnostic set to 0.01. PP equal or greater than 0.95 are given near to each node (Fig. 1). ML analysis was performed with RAxML implemented in raxmlGUI v.0.9b2 using a GTR+I+G model and bootstrap support were obtained by running 1000 pseudo replicates (Silvestro & Michalak 2012, Stamatakis 2014). Phylogenetic trees were visualized with FigTree v1.4.0 (Rambaut 2006) and edited in Adobe Illustrator CS5.

## Results

### Phylogenetic analyses

Forty-one *Lecanicillium* isolates and one outgroup isolate were included in the phylogenetic analyses. The most parsimonious tree in MP demonstrated that TL=2975, CI=0.501, RI=0.670, RC=0.336, HI=0.499. Phylogenetic tree topologies obtained from BI and MP analyses were congruent to those obtained in ML analysis. Multigene phylogenetic analyses showed that our new

isolates (KUN 101466 and KUN 101469) have a close phylogenetic affinity to *L. uredinophilum* with strong bootstrap support (100%, ML/ 1.00, PP/ 100%, MP, Fig. 1).



**Fig. 1** – RAxML (ML) phylogenetic tree generated from analysis of a combined LSU, SSU, *tef1- $\alpha$* , RPB2, RPB1 and ITS sequences dataset for 41 isolates of *Lecanicillium* and *Simplicillium lanosoniveum* (outgroup). ML support values greater than 70% (left), MP bootstrap value higher than 70% (middle) and Bayesian posterior probabilities greater than 0.95 (right) are indicated near the nodes. Strains generated in this study are in blue bold.

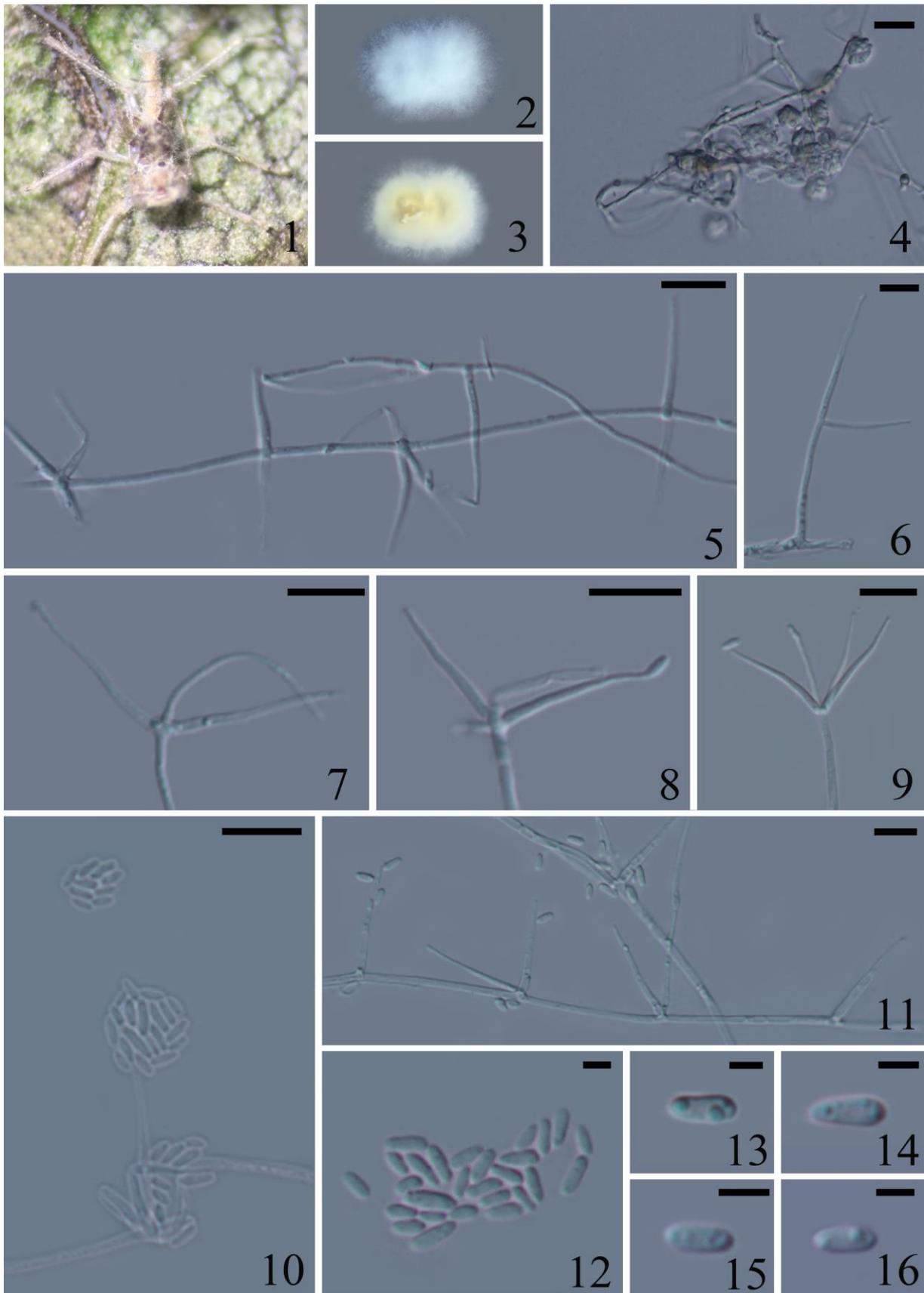
## Taxonomy

*Lecanicillium uredinophilum* M.J. Park, S.B. Hong & H.D. Shin, Mycotaxon 130(4): 1002 (2016) [2015]

Fig. 2

Facesoffungi number: FoF04115

*Colonies* grow on PDA reaching 2 cm diameter after 12 days at room temperature (about 26°C), white, velvety-cottony, irregular, umbonate; pale yellow from below. Asexual morph: *Conidiophores* arising from prostrate hyphae and bearing up to 1–4 whorls of phialides. *Phialides* 15–35 × 0.5–2 ( $\bar{x}$  = 22 × 1.2, n = 30)  $\mu$ m, gradually tapering towards the apex, aseptate, phialidic, hyaline, occasionally producing secondary branch. *Conidia* 3–6 × 1.1–2.3  $\mu$ m ( $\bar{x}$  = 4.5 × 1.6, n = 30), oval to cylindrical, aseptate, smooth-walled, hyaline, aggregating in slimy head on the tip of phialides. Sexual morph: Undetermined.



**Fig. 2** – *Lecanicillium uredinophilum*. 1, 4–9, 15, 16 KUN 101469. 2, 3, 10–14 KUMCC 18-0024 1 Host. 2, 3 Upper and reverse view of cultures on PDA after 12 days incubation. 4 Conidia mass. 5, 7, 8, 9 Verticillate phialides. 6 Secondary producing phialide. 10. Conidia mass on the tip of phialides. 11 Phialides produced from procumbent hypha. 12–16 Conidia. – Scale bars: 4 – 11 = 10  $\mu$ m, 12 – 16 = 3  $\mu$ m.

Material examined – CHINA, Yunnan Province, Pingbian County (N 22°69', E 103°69'), on a decayed insect attached to lower surface of leaf on a pear tree, 22 Sept. 2017, *De-Ping Wei*, PB06 (KUN 101469, KUMCC 18-0024, living culture); *ibid.* PB03 (KUN 101466; KUMCC 18-0021, living culture).

Notes – The genus *Lecanicillium* delineated by Zare & Gams (2001) was characterised by having conidiophores arising from aerial or prostrate hyphae, phialides which are solitary or verticillate, slender, discrete, tapering towards the apex, occasionally, presenting secondary branch and conidia adhering in slimy masses or fascicles at right angles to phialide apex at maturity. Solitary conidia produced on each phialide have been observed in a few species of this genus. Chlamydospores, dictyochlamydospores or swollen hyphal portions are absent in *Lecanicillium*. Ellipsoidal to cylindrical and fusiform to falcate conidia are more common in the genus.

**Table 1** Comparison of alignment properties of genes and nucleotide substitution models used in *Lecanicillium* phylogenetic analyses.

	LSU <sup>1</sup>	SSU <sup>2</sup>	<i>tef1</i> <sup>3</sup>	RPB2 <sup>4</sup>	RPB1 <sup>5</sup>	ITS <sup>6</sup>	Combined LSU, SSU, <i>tef1</i> , RPB2, RPB1 and ITS
Number of characters included in analysis (including gaps)	793	974	884	789	583	502	4543
Number of constant characters	731	940	650	466	324	342	3471
Number of parsimony informative characters (%)	31 (4%)	13 (1%)	160 (73%)	276 (59%)	188 (32%)	108 (26%)	776 (17%)
Number of uninformative and variable characters	31	21	74	47	71	52	296
Nucleotide substitution model	GTR+I+G	GTR+I	GTR+I+G	GTR+I+G	GTR+G	GTR+G	GTR+I+G

<sup>1</sup>LSU: partial 28S nrDNA; <sup>2</sup>SSU: partial 18S nrDNA; <sup>3</sup>*tef1*: translation elongation factor 1-alpha gene; <sup>4</sup>RPB2: RNA polymerase II largest subunit 2 gene; <sup>5</sup>RPB1: RNA polymerase II largest subunit 1 gene; <sup>6</sup>ITS: Internal transcribed spacers gene.

**Table 2** Morphological comparison between strains KUN 101466, KUN 101469 and *L. uredinophilum* (KACC 44082).

Strain	Colonies on PDA	Phialides	Conidia	Host	Location
<b>KACC 44082</b>	velvety to cottony, margin entire, white to cream colored, reverse cream, 25–30 mm diameter in 10 days	hyaline, tapering towards apex, arising from prostrate hyphae, solitary or up to 3–4 per node; secondary phialides present, 15–50 × 1–3 µm.	hyaline, cylindrical to oblong or narrowly ellipsoid, aseptate, 3–6 × 1.5–3 µm	rust	North Chungcheong Province, KOREA
<b>KUN 101466</b>	velvety, irregular, umbonate, white, yellowish white reverse, 17–20 mm in diameter after 12 days	hyaline, tapering towards apex, aseptate, solitary or up to 4 whorls produced per node. secondary phialides produced from internode of original phialides, 20.3–43.4 × 1.2–1.9 µm	hyaline, oval to cylindrical, aseptate, smooth-walled, 3.9–9.5 × 1.3–2.3 µm	insect	Yunnan Province, CHINA
<b>KUN 101469</b>	velvety, irregular, umbonate, white, yellowish white reverse, 13–19 mm in diameter after 12 days	hyaline, tapering towards apex, aseptate, solitary or up to 4 whorls produced per node. secondary phialides produced from internode of original phialides, 15.2–36.1 × 0.5–1.9 µm	hyaline, oval to cylindrical, aseptate, smooth-walled, 3.1–5.9 × 1.1–2.3 µm	insect	Yunnan Province, CHINA

**Table 3** Strains and GenBank accession numbers collected from related references

Species	Voucher	GenBank accession No					
		LSU	SSU	<i>tef1-a</i>	RPB2	RPB1	ITS
<i>Lecanicillium acerosum</i>	<b>CBS 418.81</b>	KM283786	KM283762	KM283810	KM283852	KM283832	EF641893
<i>Lecanicillium antillanum</i>	<b>CBS 350.85</b>	AF339536	AF339585	DQ522350	DQ522450	DQ522396	AJ292392
<i>Lecanicillium aphanocladii</i>	CBS 797.84	KM283787	KM283763	KM283811	KM283853	KM283833	_
<i>Lecanicillium araneorum</i>	<b>CBS 726.73a</b>	AF339537	AF339586	EF468781	EF468934	EF468887	AJ292464
<i>Lecanicillium araneicola</i>	<b>BTCC-F35</b>	_	_	_	_	_	AB378506
<i>Lecanicillium araneogenum</i>	GZU1032Lea	_	_	KX845698	KX845702	KX845700	_
<i>Lecanicillium attenuatum</i>	CBS 402.78	AF339565	AF339614	EF468782	EF468935	EF468888	AJ292434
<i>Lecanicillium attenuatum</i>	KACC 47755	KM283779	KM283755	KM283803	KM283845	KM283825	_
<i>Lecanicillium attenuatum</i>	KACC 43049	KM283781	KM283757	KM283805	KM283847	KM283827	_
<i>Lecanicillium attenuatum</i>	KACC 42493	KM283780	KM283756	KM283804	KM283846	KM283826	_
<i>Lecanicillium dimorphum</i>	CBS 345.37	KM283788	KM283764	KM283812	KM283854	KM283834	_
<i>Lecanicillium flavidum</i>	CBS 300.70D	KM283789	KM283765	KM283813	KM283855	_	EF641877
<i>Lecanicillium fungicola</i> var. <i>aleophilum</i>	<b>CBS 357.80</b>	KM283791	KM283767	KM283815	KM283856	KM283835	NR_111064
<i>Lecanicillium fungicola</i> var. <i>fungicola</i>	<b>CBS 992.69</b>	KM283792	KM283768	KM283816	KM283857	_	NR_119653
<i>Lecanicillium fuisporum</i>	<b>CBS 164.70</b>	AF339549	AF339598	EF468783	AJ292428	EF468889	KR064302
<i>Lecanicillium kalimantanense</i>	<b>NBRC 105406</b>	_	_	_	_	_	AB360356
<i>Lecanicillium lecanii</i>	CBS 101247	KM283794	KM283770	DQ522359	KM283859	KM283837	JN049836
<i>Lecanicillium lecanii</i>	CBS 102067	KM283795	KM283771	KM283818	KM283860	KM283838	_
<i>Lecanicillium longisporum</i>	<b>CBS 126.27</b>	AF339556	AF339605	_	_	KR064300	KR064303
<i>Lecanicillium longisporum</i>	CBS 102072	KM283796	KM283772	KM283819	_	_	_
<i>Lecanicillium muscarium</i>	<b>CBS 143.62</b>	_	_	KR064305	_	KR064301	KR064304
<i>Lecanicillium pissodis</i>	CBS 118231	KM283799	KM283775	KM283822	KM283864	KM283842	_
<i>Lecanicillium primulinum</i>	<b>JCM 18525</b>	AB712263	_	_	_	_	AB712266
<i>Lecanicillium primulinum</i>	JCM 18526	AB712264	_	_	_	_	AB712267
<i>Lecanicillium psalliotae</i>	CBS 532.81	AF339560	AF339609	EF469067	_	_	JN049846
<i>Lecanicillium psalliotae</i>	CBS 101270	EF469081	EF469128	EF469066	EF469113	EF469095	_
<i>Lecanicillium sabanense</i>	JChA5	KC875225	KC633251	KC633266	KC633249	_	KC633232

**Table 3** Continued.

Species	Voucher	GenBank accession No					
		LSU	SSU	<i>tef1-a</i>	RPB2	RPB1	ITS
<i>Lecanicillium saksenae</i>	<b>IMI 179841</b>	–	–	–	–	–	NR111102
<i>Lecanicillium</i> sp.	CBS 639.85	KM283801	KM283777	KM283824	KM283865	KM283843	AJ292386
<i>Lecanicillium</i> sp.	KACC 43873	KM283785	KM283761	KM283809	KM283851	KM283831	–
<i>Lecanicillium</i> sp.	JCM 28134	–	–	–	–	–	LC145294
<i>Lecanicillium</i> sp.	JCM 28132	–	–	–	–	–	LC145292
<i>Lecanicillium</i> sp.	KYK00305	–	–	–	–	–	AB378529
<i>Lecanicillium</i> sp.	KYK00214	–	–	–	–	–	AB378528
<i>Lecanicillium tenuipes</i>	CBS 309.85	AF339526	AF339576	DQ522341	–	DQ522387	DQ522439
<i>Lecanicillium uredinophilum</i>	KACC 44066	KM283784	KM283760	KM283808	KM283850	KM283830	–
<i>Lecanicillium uredinophilum</i>	KACC 44082	KM283782	KM283758	KM283806	KM283848	KM283828	–
<b><i>Lecanicillium uredinophilum</i></b>	KUN 101466	MG948307	MG948309	MG948315	MG948313	MG948311	MG948305
<i>Lecanicillium uredinophilum</i>	KUN 101469	MG948308	MG948310	MG948316	MG948314	MG948312	MG948306
<i>Lecanicillium wallacei</i>	<b>CBS 101237</b>	AY184967	AY184978	EF469073	EF469119	EF469102	EF641891
<i>Simplicillium lanosoniveum</i>	CBS 704.86	AF339553	AF339602	DQ522358	DQ522464	DQ522406	AJ292396

Voucher number of ex-type strains and species names of new isolates from this study are indicated in bold.

## Discussion

Twenty-seven epithets of *Lecanicillium* are listed in Index Fungorum (2018). In our phylogenetic analyses, we have included all available sequences data for *Lecanicillium* species from GenBank. The maximum likelihood tree generated based on sequence analysis of the combined dataset recovered a monophyletic clade containing our new isolates and *L. uredinophilum*. This is strongly supported in all analyses. Phylogenetically, *L. uredinophilum* has a close affinity to *L. araneogenum*, *L. attenuatum*, *L. lecanii*, *L. longisporum*, *L. muscarium*, *L. pissodis* and *L. sabanense*. Morphologically, the two new isolates (KUN 101466 and KUN 101469) are similar to *L. uredinophilum*, *L. araneogenum*, *L. lecanii* and *L. muscarium* (Petch) Zare & W. Gams in having verticillate conidiophores, gradually tapering phialides, and ellipsoidal to oblong-oval aseptate conidia (Zare & Gams 2001, Mijeong et al. 2015, Chen et al. 2017). Even though molecular data of *L. evansii* and *L. nodulosum* is not available, *L. evansii* differs from our isolates in having slightly curved conidia (Zare & Gams 2001). *L. nodulosum* can be distinguished from our isolates by swelling nodules which may produce up to 6 phialides or hypha and the smaller conidia (Zare & Gams 2001).

Interestingly, the comparison between our two isolates and *L. uredinophilum* (KACC 44082) shows that they differ from the previously known *L. uredinophilum* collections, mainly in their appearance on insects and geographical distribution (Table 2). Previously it was only recorded from rust fungi in Korea. Therefore, these two generated isolates are introduced as new host and a new country record. The discovery of *L. uredinophilum* on insects indicates that this species has the potential to be developed as a microbial agent against pests in agriculture and forestry and may be found on any animal or micro-organism with chitinous bodies.

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### Accessibility of data

Specimen KUN 101469 (KUMCC 18-0024, living culture) and KUN 101466 (KUMCC 18-0021, living culture) were deposited in Herbarium of Cryptogams Kunming Institute of Botany, Academia Sinica. Generated sequences data in this study (including ITS, LSU, SSU, *tefl-α*, RPB1 and RPB2) were submitted to GenBank sequence database, and the accession number are listed in the Table 3. The novel taxonomic descriptions and nomenclature was submitted to Faces of Fungi as outlined in Jayasiri et al. (2015). The final alignment and tree were deposited in TreeBASE, submission ID: 22339 (<http://www.treebase.org/>).

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