BMSAB GENUS CHAPTER TEMPLATE WITH INSTRUCTIONS ON FORMAT AND INFORMATION TO INCLUDE

Use this template as an example for the format and content of your chapter. Feel free to include additional information that is available for the genus you are covering. Your text should be entered in place of the example information provided below in black text. Continuous line numbers should be maintained throughout the manuscript including any pages containing Tables or Figures. Heading in maroon text should not be removed or edited.

1. PHYLUM/CLASS/ORDER/FAMILY:

ENTER THE TAXONOMIC PATH IN ITALICS e.g.

_____

Proteobacteria/Gammaproteobacteria/Enterobacterales/Pectobacteriaceae/

_____

2. MANUSCRIPT NUMBER:

ENTER THE MANUSCRIPT NUMBER e.g.

_____

gbm02016

_____

3. CHAPTER TITLE:

ENTER THE CHAPTER TITLE IN ITALICS e.g.

Lonsdalea

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4. DEFINING PUBLICATION:

ENTER THE DEFINING PUBLICATION, EFFECTIVE PUBLICATION AND EMENDMENTS AS APPROPRIATE. THE PAGE NUMBER IS THE PAGE ON WHICH THE ACTUAL DESCRIPTION WAS PRINTED IN THE ORIGINAL PUBLICATION, NOT THE FIRST PAGE OF THAT PUBLICATION e.g.

Brady et al. 2012, 1599[VP]

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5. AUTHORS NAMES AND INSTITUTIONS:

ENTER THE NAMES, INSTITUTIONS, CITY AND COUNTRY OF AUTHORS. THE ADDRESS SHOULD BE IN ITALICS e.g.

Carrie L. Brady, *Department of Applied Science, University of the West of England, Bristol, UK*

Teresa A. Coutinho, *Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, South Africa*

6. ETYMOLOGY:

ENTER THE ETYMOLOGY AS PRESENTED IN THE ORIGINAL TAXONOMIC DESCRIPTION e.g.

Lons.da'le.a. N.L. fem. n. *Lonsdalea* named for David Lonsdale in honour of his contributions to British forest pathology.

7. ABSTRACT:

ENTER THE ABSTRACT OF THE CHAPTER. THE ABSTRACT SHOULD BE A SUMMARY OF THE INFORMATION CONTAINED IN THE MANUSCRIPT THAT GIVES THE READER AN OVERVIEW OF THE TAXON BEING COVERED. INFORMATION ON THE MORPHOLOGY, PHYSIOLOGY, PHYLOGENY AND ECOLOGY SHOULD BE INCLUDED e.g.

The genus *Lonsdalea* comprises species isolated from bacterial cankers of woody hosts including oak, poplar and willow. Cells are Gram-negative, facultativley anaerobic, motile, short rods which appear singly or rarely in pairs. Species are mesophilic, favouring growth temperatures of 28 – 34 °C. Carbon sources such as glucose, fructose, mannose, sucrose and *N*-acetylglucosamine are readily assimilated and fermented. Species form a monophyletic clade when phylogenetic analysis is based on 16S rRNA gene sequences, multilocus sequence analysis (MLSA) or whole genome sequences. Major fatty acids are $C_{14:0}$, $C_{16:0}$, $C_{17:0}$ cyclo and summed features 2 (iso-$C_{16:1}$

and/or $C_{14:0}$ 3-OH) and 3 ($C_{16:1}$ *ω7c* and/or iso-$C_{15:0}$ 2-OH) and the DNA G + C content is 55.0 – 55.6 mol % (genome analysis).

Type species: **Lonsdalea quercina** (Hildebrand & Schroth 1967) Brady et al. 2012[VP].

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8. KEYWORDS:

ENTER KEYWORDS THAT WILL DIRECT EXTRENAL SEARCHES TO THE CHAPTER e.g.

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facultative anaerobe, plant-associated, pathogenic, woody pathogens

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9. DESCRIPTION:

ENTER THE INFORMATION THAT DESCRIBES THE GENUS BEING CONSIDERED. IMPORTANT AND DEFINING CHARACTERISTICS SHOULD BE IN BOLD FONT. THE TYPE SPECIES AND DEFINING PUBLICATION, THE NUMBER OF VALIDLY PUBLISHED SPECIES AND THE FAMILY CLASSIFICATION SHOULD BE INCLUDED e.g.

Cells are Gram-negative short rods (0.5 – 1.0 x 1.0 – 2.0 μm) occurring singly, in pairs or in groups. Motile by peritrichous flagella. Facultatively anaerobic, oxidase negative but catalase positive. Optimum temperature is 28 – 34 °C. Colonies are white to cream on tryptone soya agar, small (approx. 1 mm in diameter after 48 hours incubation), round, convex and smooth with entire margins. Negative for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and tryptophan deaminase activity. Acetoin production is variable. Citrate is

utilised but H_2S, urease, indole and gelatinase are not produced. Nitrates are not reduced to nitrites. Acid is produced from *N*-acetylglucosamine, aesculin ferric citrate, arbutin, D-fructose, D-glucose, D-mannose, methyl-αD-glucopyranoside, D-ribose, salicin and D-sucrose. The following carbon sources are utilized at 28 °C: *N*-acetyl-D-glucosamine, D-fructose, D-galactose, D-glucose, D-mannitol, D-mannose, *β*-methyl-D-glucoside, D-psicose, sucrose, turanose, citric acid, D-gluconic acid, bromosuccinic acid, L-aspartic acid, glycerol and D-glucose-6-phosphate. Major fatty acids are $C_{14:0}$, $C_{16:0}$, $C_{17:0}$ cyclo and summed features 2 (iso-$C_{16:1}$ and/or $C_{14:0}$ 3-OH) and 3 ($C_{16:1}$ *ω7c* and/or iso-$C_{15:0}$ 2-OH). Members of the genus *Lonsdalea* form a phylogenetic clade as determined by both 16S rRNA gene sequence analysis and MLSA based on four housekeeping genes. *Lonsdalea* species cause disease on oak trees including drippy nut and bud disease and bark canker, as well as bark canker on poplar hybrids, and may be associated with Acute Oak Decline.

*DNA G + C content (mol %)***:** 55.0 – 55.6 (genome analysis).

Type species: ***Lonsdalea quercina*** (Hildebrand & Schroth 1967) Brady et al. 2012.

Number of species with validly published names: 4.

Family classification: The genus *Lonsdalea* is classified within the family *Enterobacteriaceae*.

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10. NUMBER OF SPECIES WITH VALIDLY PUBLISHED NAMES:

ENTER THE NUMBER OF SPECIES THAT HAVE VALIDLY PUBLISHED NAMES e.g.

4

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11. FURTHER DESCRIPTIVE INFORMATION:

A. CELL MORPHOLOGY AND ULTRASTRUCTURE

ENTER INFORMATION ON THE MORPHOLOGY AND ULTRASTRUCTURE OF THE GENUS BEING CONSIDERED. THIS SHOULD INCLUDE CELL SHAPES AND SIZES, UNIQUE MORPHOLOGICAL CHARACTERISTICS AND THE DESCRIPTION OF ULTRASTRUCTURE SUCH AS CELL WALL STRUCTIURE ETC. REFERENCE SHOULD BE MADE TO PHOTOMICROGRAPHS AND OTHER INCLUDED FIGURES e.g.

Four species are currently classified in the genus *Lonsdalea*, all of which have been isolated from woody hosts including oak, poplar and willow. Cells are Gram-negative, short rods (0.5 – 1.0 x 1.1 – 2.0 µM) with rounded ends and occur singly or rarely in pairs. All species are motile by peritrichous flagella (Fig. 1a and b).

B. COLONIAL AND CULTURAL CHARACTERISTICS

ENTER INFORMATION ON THE SHAPES, SIZES AND CHARACTERISTICS OF COLONIES ON SOLID MEDIA AS WELL AS GROWTH CHARACTERISTICS IN LIQUID CULTURE e.g.

All *Lonsdalea* species produce white to ivory colonies on tryptone soy agar (TSA) following incubation for ~48 hours at 30 °C. Colonies are small, approximately 1 – 1.5 mm in diameter. They

are circular, smooth with entire margins and slightly convex. On eosin methylene blue (EMB) agar, species produce small metallic green colonies. Weak growth is observed in liquid culture.

C. NUTRITION AND GROWTH CONDITIONS

ENTER INFORMATION PHYSIOLOGY OF THE ORGANISMS AS WELL AS THE CONDITIONS FOR GROWTH. THESE SHOULD INCLUDE PH, TEMPERATURE RANGES AND OPTIMA FOR GROWTHAS WELL AS NUTRIENT REQUIREMENTS LIKE NaCl ETC, e.g.

Lonsdalea species can grow at temperatures between 8 and 40 °C, although the optimum temperature is 28 – 30 °C for most species (*Lonsdalea populi* grows optimally at 30 – 34 °C). All species produce acid from the fermentation of D-glucose, D-fructose, D-mannonse, arbutin, aesculin ferric citrate, salicin and sucrose. As for many bacteria belonging to the Enterobacterales, D-glucose and D-saccharose can be utilized as sole carbon sources. Additionally, *Lonsdalea* species can assimilate *N*-acetyl-D-glucosamine, D-fructose, D-galactose, D-mannitol, D-mannose, *β*-methyl-D-glucoside, D-psicose, D-gluconic acid, bromosuccinic acid, L-aspartic acid, glycerol and D-glucose-6-phosphate. *Lonsdalea* species can be differentiated by their reactions to carbon sources (Table 1). There is no information reported for pH range or salt tolerance.

D. CHEMOTAXONOMIC CHARACTERISTICS

ENTER INFORMATION ON THE CHEMOTAXONOMIC CHARACTERISTICS OF THE GENUS INCLUDING FATTY ACIDS, POLAR LIPIDS, QUINONES AS APPROPRIATE e.g.

Lonsdalea species contain $C_{14:0}$, $C_{16:0}$, $C_{17:0}$ cyclo and summed features 2 (iso-$C_{16:1}$ and/or $C_{14:0}$ 3-OH) and 3 ($C_{16:1}$ *ω7c* and/or iso-$C_{15:0}$ 2-OH) as major fatty acids. As with *Brenneria* species (see gbm01136), hexadecanoic acid ($C_{16:0}$) constitutes the highest component in the whole-cell fatty acid composition for *Lonsdalea*, with an average of 32.8 %. Tetradecanoic acid ($C_{14:0}$) and the cyclopropane fatty acid, $C_{17:0}$, are present in amounts ranging from 10.3 – 11.7 % and 8.7 – 16.2 %, respectively. The fatty acid profiles of Lonsdalea are similar to those of related genera *Brenneria* (see gbm01136.pub2) and *Pectobacterium* (see gbm01158) with the exception of trace amounts of dodecanoic acid ($C_{12:0}$) present in *Lonsdalea*, and $C_{17:0}$ cyclo typically absent in *Pectobacterium*. Polar lipids and quinones have not been determined for species belonging to the genus *Lonsdalea*.

E. GENOME FEATURES

ENTER INFORMATION ON THE AVAILABLE GENOME SEQUENCES FOR SPECIES OF THE GENUS. PROVIDE INFORMATION ON GENOME SIZE AND COMPOSITION AS WELL AS THE PRESENCE OF GENES RELATED TO THE CHARACTERISTIC AND PHYSIOLOGY OF THE ORGANISM. IF INFORMATION IS AVAIALABLE INCLUDE A COMPARATIVE TABLE OF THE GENOME CHARACTERISTICS FOR EACH SPECIES e.g.

Genome sequences are available for all four validly described *Lonsdalea* species (Li et al., 2017). The genomes are similar in size and range from 3.7 Mb (*L. populi*) to 3.9 Mb (*L. quercina* and *L. britannica*) with median predicted protein-encoding genes of 3108 (*L. iberica*) to 3363 (*L. britannica*). See Table 2 for a comparison of *Lonsdalea* species genomes.

Virulence factors have been described for *L. britannica* (Doonan et al., 2019) and *L. populi* (Li & He, 2019) with both species containing a complete Type III Secretion System (T3SS) as well as effectors, harpins and two-component signal transduction systems.

F. ECOLOGY

ENTER INFORMATION ON THE ECOLOGY OF THE GENUS INCLUDING HABITATS FROM WHICH STRAINS HAVE BEEN ISOLATED AS WELL AS INFORMATION ON THE DETECTION OF MEMBERS OF THE GENUS IN THE ENVIRONMENT BASED ON ENVIRONMENTAL DNA STUDIES e.g.

Lonsdalea species are associated with diseases on woody hosts, specifically oak and poplar. The type species of the genus, *L. quercina*, is the causal agent of drippy nut and shoot blight of coast live oak (*Quercus agrifolia*) and interior live oak (*Q. wislizeni*). The disease was first reported in California, USA in the 1960's (Hildebrand & Schroth, 1967), however, there are no further recorded incidences of the disease. *L. quercina* is also responsible for a second, more recent disease in the USA, drippy blight of northern red oak (*Q. rubra*), pin oak (*Q. palustris*) and Shumard oak (*Q. shumardii*) (Sitz et al., 2018). In the 1990's bark canker, drippy bud and drippy nut were observed on holm oak (*Q. ilex*) and Pyrenean oak (*Q. pyrenaica*) in Spain (Biosca et al., 2003, Poza-Carrión et al., 2008). The disease in Spain was thought to be caused by *L. quercina* (syn. *Brenneria quercina*) but following multilocus sequence analysis of *Brenneria* species and the creation of the genus *Lonsdalea* (Brady et al., 2012), these strains were identified as *L. iberica*.

L. britannica is isolated sporadically from pedunculate (*Quercus robur*) and sessile oak (*Q. petraea*) suffering from acute oak decline (AOD) in the UK (Denman et al., 2018), and is considered an infrequent component of the pathobiome (Doonan et al., 2019). Additionally, *L. britannica* has been isolated from the skin microbiome of the lesser horseshoe bat in the Czech Republic (Kovacova et al., 2017). *L. populi*, causing bacterial canker of *Populus x euramericana* and other poplar hybrids, appears to be the most frequently isolated *Lonsdalea* species with reports of the disease in Hungary (Tóth et al., 2013), China (Li et al., 2014), Spain (Berruete et al., 2016), Portugal (Abelleira et al., 2019) and Serbia (Zlatković et al., 2020). Recently, *L. populi* has

also been identified as the causal agent of bacterial canker disease of corkscrew willow (*Salix matsudana*) in China (Li et al., 2019).

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12. ENRICHMENTS AND ISOLATION PROCEDURES

ENTER INFORMATION ON THE METHODS AND PRECEDURES USED FOR THE ISOLATION OF STRAINS OF THIS GENUS e.g.

Isolation of *Lonsdalea* species is as for most plant pathogenic bacteria from woody hosts. Infected material is surface sterilized by dipping in 70 % ethanol for 30 sec to 1 min, submerging in a 1-3 % (v/v) solution of sodium hypochlorite (NaClO) for a further 1 to 2 mins and rinsing thoroughly in sterile distilled water at least twice. Small chips of tissue (5 mm x 5 mm) are cut from the lesion margin with a sterile scalpel and placed on solid media (Denman et al., 2016). Alternatively, the tissue is shaken in sterile water or buffer for 10 mins. The resulting suspension can be streaked onto solid media, or diluted further then streaked out (Li et al., 2014). Nutrient agar (NA), tryptone soy agar (TSA) or peptone yeast glucose agar (PYGA) are most commonly used for isolation. Inoculated media is incubated at 28 – 30 °C for 24 – 48 hours until growth is observed. Single colonies can be sub-cultured further.

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13. MAINTENANCE PROCEDURES

ENTER INFORMATION ON THE PROCEDURES USED TO MAINTAIN STRAINS OF THIS GENUS BOTH SHORT AND LONG TERM e.g.

Lonsdalea strains should be grown on a standard media of choice (TSA supports good growth of all species) at 28 – 30 °C for 24 – 48 hours (or until good growth occurs). Cultures on solid media can be maintained short-term in a refrigerator (4 – 5 °C). Strains can be grown in liquid culture, although it typically takes > 6 hours for species to reach an optical density (OD_{600}) of 0.6.

For long-term storage, strains can be lyophilized by freeze-drying a cell suspension in cryopreservation buffer. Strains have also been stored on cryopreservation beads and in glycerol at – 80 °C.

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14. PROCEDURES FOR TESTING SPECIAL CHARACTERISTICS

SOME GENERA MAY BE VERY SPECIALIZED AND SO HAVE UNQUE CHARACTERISTICS THAT REQUIRE SPECIAL APPROACHES. ENTER INFORMATION ON THESE SPECIAL PROCEDURES e.g.

N/A

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15. DIFFERENTIATION OF THE GENUS XXXXX FROM OTHER GENERA

ENTER INFORMATION ON THE CHARACTERISTICS THAT DIFFERENTIATE THIS GENUS FROM RELATED GENERA. A TABLE SHOULD PROVIDED THAT SHOWS THE KEY DIFFERENTIATING CHARACTERISTICS e.g.

Phylogenetically, the closest relatives of *Lonsdalea* are *Brenneria* and *Pectobacterium* although it is difficult to phenotypically differentiate between these genera. Species of *Brenneria* (see gbm01136.pub2) and *Pectobacterium* (see gbm01158) share many common phenotypic

characteristics with those of *Lonsdalea*. The limited differential characteristics for distinguishing between these three genera are listed in Table 3.

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16. TAXONOMIC COMMENTS

ENTER INFORMATION ON THE TAXONOMIC POSITION OF THE GENUS AND THE SPECIES IT CONTAINS INCLUDING THE 16S rRNA GENE BASED PHYLOGENY, THE WHOLE-GENOME BASED PHYLOGENY FROM GTDB AND ANY DIFFERENCES OBSERVED BETWEEN THESE PHYLOGENIES AND RESULTING CLASSIFICATIONS. PHYLOGENTIC TREES AND ANI/AAI VALUES SHOULD BE INCLUDED AS APPROPRIATE AND AVAILABLE. A 16S rRNA BASED PHYLOGENETIC TREE SHOULD BE PRESENTED e.g.

The genus *Lonsdalea* was proposed to include strains of *Brenneria quercina* following a taxonomic study of the genera *Brenneria*, *Pectobacterium* and *Dickeya* (Brady et al., 2012) which are all polyphyletic based on 16S rRNA sequence analysis (Fig. 2). Multilocus sequence analysis (MLSA) based on partial sequencing of four housekeeping genes (*gyrB*, *rpoB*, *infB* and *atpD*), revealed that *B. quercina* belongs to a distinctly separate lineage (Fig. 3) and was subsequently transferred to the novel genus *Lonsdalea* as *Lonsdalea quercina* comb. nov. MLSA was also used in the same study to support the description of two novel subspecies of *L. quercina*, *L. quercina* ssp. *britannica* and *L. quercina* ssp. *iberica* for strains isolated from symptomatic oak in Great Britain and Spain. Despite clear clustering of the oak strains from *L. quercina* reference strains in phylogenetic analyses, their DNA-DNA hybridization values were considered borderline (~ 58 – 70 %) and could not be described as novel species at that time. A fourth subspecies of *L. quercina* was later described in 2013 for strains causing bark canker of poplar, *L. quercina* ssp. *populi* (Tóth et al., 2013). When the whole genomes for the subspecies of *L. quercina* were sequenced and compared in 2017, average nucleotide identity (ANI) values were observed that were below the proposed species boundary ANI cut-off of 95 – 96 %. Consequently, three subspecies of *L.*

quercina were elevated to the species level as *L. britannica*, *L. iberica* and *L. populi* (Li et al., 2017). *Lonsdalea* is one of the few genera in the Enterobacterales that is monophyletic in phylogenies based on 16S rRNA gene sequences, protein-encoding sequences and whole genome sequences (Fig. 4). The clear delineation of the four species of *Lonsdalea* in the whole genome phylogeny is reflected in the lower DNA-DNA similarity values, based on ANIm and *is*DDH, between their genomes (Table 4).

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17. LIST OF SPECIES OF THE GENUS

ENTER INFORMATION ON EACH OF THE SPECIES OF THE GENUS WITH NAMES THAT HAVE BEEN VALIDLY PUBLISHED. INCLUDE THE DEFINING PUBLICATION AND THE ETYMOLOGY. MAINTAIN A SIMILAR FORMAT AND INFORMATION CONTENT ORDER FOR EACH SPECIES ENTRY. INCLUDE THE DNA G+C CONTENT, TYPE STRAIN AND CULTURE COLLECTION, THE ACCESSION NUMBERS FOR THE 16S rRNA GENE AND WHOLE GENOME SEQUENCES. SPECIES DESCRIPTION SHOULD NOT BE COPIED VERBATUM FROM THE ORIGINAL PUBLICATIONS, e.g.

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1. ***Lonsdalea quercina*** (Hildebrand & Schroth 1967) Brady et al. 2012[VP].

quer.ci'na. L. fem. adj. *quercina* of or pertaining to oak

The characteristics are as given for the genus with the following additions. Cells are short rods (0.5 – 1.0 x 1.0- 2.0 µm). The acetoin reaction is variable. Acid is produced from D-galactose (weaker reaction), D-mannitol (variable reaction), D-turanose and potassium gluconate in addition to those listed for the genus description. L-histidine and L-leucine are utilised as carbon sources along with those listed for the genus description. Additional distinguishing characteristics are listed in Table 1.

Causes drippy nut disease and shoot blight of *Quercus* (oak) species, with copious oozing of sap from acorns in later summer; as well as drippy blight of red oak with leaf scorching, dieback and cankers with copious gummosis.

The type strain was isolated from *Quercus* spp. (live oak) in the USA.

DNA G + C content (mol %): 55.1 (Genome analysis).

Type strain: ATCC 29181, ATCC 29281, CCUG 48867, CFBP 3617, CIP 105201, DSM 4561, ICMP 1845, LMG 2724, NCPPB 1852.

EMBL/GenBank accession (16S rRNA gene): AJ223469

EMBL/GenBank accession (genome): NZ_JIBO00000000

2. ***Lonsdalea britannica*** (Brady et al. 2012) Li et al. 2017^{VP}.

bri.tan'ni.ca. L. fem. adj. *Britannica*, Britannic, British, referring to the origin where these strains were first isolated.

The characteristics are as given for the genus with the following additions. Cells are short rods (0.5 – 0.7 x 1.1 – 2.0 μm). Acetoin is not produced. Acid is produced from glycerol, D-trehalose (variable), D-turanose (variable) and potassium gluconate (variable) in addition to those listed for the genus description. D-trehalose, formic acid (weakly), α-ketoglutaric acid (weakly), D,L-lactic acid (weakly), succinic acid and L-glutamic acid (weakly) are utilised as carbon sources along with those listed for the genus description. Utilisation of D-raffinose, L-aspargine and L-glutamic acid are variable. Additional distinguishing characteristics are listed in Table 1.

Associated with acute oak decline (AOD) of mature *Quercus* (oak) species. Affected trees are characterized by stem bleeding from vertical cracks and the underlying tissues are stained and necrotic.

The type strain was isolated from *Quercus robur* in Britain.

DNA G + C content (mol %): 55.1% (genome analysis).

Type strain CFCC 10822, FRB 18, LMG 26267, NCPPB 4481.

EMBL/GenBank accession (16S rRNA gene): JF311442.

EMBL/GenBank accession (genome): LUTN00000000.

3. ***Lonsdalea iberica*** (Brady et al. 2012) Li et al. 2017[VP].

i.be'ri.ca. L. fem. adj. *iberica* Iberic, Spanish, referring to the origin of the first strains to be isolated.

The characteristics are as given for the genus with the following additions. Cells are short rods (0.7 – 0.9 x 1.5 – 2.0 μm). Acetoin is produced. Acid is produced from glycerol and D-galactose in addition to those listed for the genus description. D-raffinose (weakly), D-trehalose, formic acid (weakly), α-ketoglutaric acid (weakly), D,L-lactic acid (weakly) and succinic acid are utilised as carbon sources along with those listed for the genus description. Additional distinguishing characteristics are listed in Table 1.

Causes bark canker, drippy nut and drippy bud of *Quercus ilex* (holm oak) and *Quercus pyrenaica* (Pyrenean oak). Longitudinal cankers are seen on the trunk bark with necrotic outer and inner tissues and exudate. Buds and acorns ooze in spring and summer.

The type strain was isolated from *Quercus ilex* in Spain

DNA G + C content (mol %): 55.0% (genome analysis).

Type strain: CFCC 10824, LMG 26264, IVIA-1915-14, NCPPB 4490

EMBL/GenBank accession (16S rRNA gene): JF311441.

EMBL/GenBank accession (genome): LUTP00000000.

4. ***Lonsdalea populi*** (Tóth et al. 2013) Li et al. 2017[VP].

po'pu.li. L. gen. n. *populi* of poplar, the principal host trees of the bacterium.

The characteristics are as given for the genus with the following additions. Cells are short rods (0.5 – 0.1 x 1.0 – 2.0 μm). Acetoin is produced. Acid is produced from glycerol, D-mannitol, D-galactose, trehalose and potassium gluconate in addition to those listed for the genus description. D-trehalose, pyruvic acid methyl ester, succinic acid, are utilised as carbon sources along with those listed for the genus description. Utilisation of α-ketoglutaric acid, L-glutamic acid and cellobiose are variable. Additional distinguishing characteristics are listed in Table 1.

Causes bark canker of *Populus* x *euramericana* (poplar). Symptomatic trees have vertical cracks in the bark with sticky, frothy brown fluid oozing from the cankers.

The type strain was isolated from *Populus* x *euramericana* in Hungary

DNA G + C content (mol %): 55.4% (genome analysis).

Type strain: CFCC 13125, DSM 25466, LMG 27349, NCAIM B.02483, NY060

EMBL/GenBank accession (16S rRNA gene): JQ291575

EMBL/GenBank accession (genome): LUTM00000000.

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18. OTHER SPECIES

ENTER INFORMATION ON OTHER SPECIES THAT HAVE BEEN DESCRIBED IN THE LITERATURE BUT DO NOT HAVE VALIDLY PUBLISHED NAMES. MAINTAIN A SIMILAR FORMAT AND INFORMATION CONTENT ORDER FOR EACH SPECIES ENTRY. INCLUDE THE DNA G+C CONTENT, TYPE STRAIN AND CULTURE COLLECTION, THE ACCESSION NUMBERS FOR THE 16S rRNA GENE AND WHOLE GENOME SEQUENCES e.g.

N/A

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19. REFERENCES

ENTER FULL REFERENCE FOR EACH CITATION IN THE CHAPTER INCLUDING THOSE CITED IN TABLES AND FIGURE LEGENDS. REFERENCES SHOULD BE LISTED IN ALPHABETICAL ORDER BASED ON THE NAME OF THE FIRST AUTHORS. THE FORMAT PROVIDED BELOW SHOULD BE FOLLOWED EXACTLY. DOIs SHOULD BE INCLUDED WHEN AVAILABLE e.g.

Abelleira A, Moura L, Aguín O, & Salinero C. (2019) First report of *Lonsdalea populi* causing bark canker disease on poplar in Portugal. *Plant Dis* **103**: 2121. doi:10.1094/PDIS-12-18-2230-PDN

450 Berruete IM, Cambra MA, Collados R, Monterde, A, López, MM, Cubero J, & Palacio-Bielsa A.
451 (2016) First report of bark canker disease of poplar caused by *Lonsdalea quercina* subp. *populi*
452 in Spain. *Plant Dis* **100**: 2159. doi:10.1094/PDIS-03-16-0405-PDN
453
454 Biosca EG, González R, López- López MJ, Soria S, Montón C, Pérez-Laorga E, & López MM. (2003)
455 Isolation and characterization of *Brenneria quercina*, causal agent for bark canker and drippy nut
456 of *Quercus* spp. in Spain. *Bacteriol* **93**: 485-492
457
458 Brady CL, Cleenwerck I, Denman S, Venter SN, Rodríguez-Palenzuela P, Coutinho TA, & De Vos P.
459 (2012) Proposal to reclassify *Brenneria quercina* (Hildebrand and Schroth 1967) Hauben *et al*.
460 1999 into a new genus, *Lonsdalea* gen. nov., as *Lonsdalea quercina* comb. nov., descriptions of
461 *Lonsdalea quercina* subsp. *quercina* comb. nov., *Lonsdalea quercina* subsp. *iberica* subsp. nov.
462 and *Lonsdalea quercina* subsp. *britannica* subsp. nov., emendation of the description of the genus
463 *Brenneria*, reclassification of *Dickeya dieffenbachiae* as *Dickeya dadantii* subsp. *dieffenbachiae*
464 comb. nov., and emendation of the description of *Dickeya dadantii*. *Int J Syst Evol Microbiol* **62**:
465 1592-1602. doi:10.1099/ijs.0.035055-0
466
467 Denman S, Plummer S, Kirk S, Peace A, & McDonald JE. (2016) Isolation studies reveal a shift in
468 the cultivable microbiome of oak affected with Acute Oak Decline. *Systematic and Applied*
469 *Microbiol* **39:** .484-490. doi: 10.1016/j.syapm.2016.07.002
470
471

472 Denman S, Doonan J, Ransom-Jones E, Broberg M, Plummer S, Kirk S, Scarlett K, Griffiths AR,
473 Kaczmarek M, Forster J, Peace A, Golyshin PN, Hassard F, Brown N, Kenny JG, & McDonald JE.
474 (2018) Microbiome and infectivity studies reveal complex polyspecies tree disease in Acute Oak
475 Decline. *ISME Journal*. **12**: 386-399. doi: 10.1038/ismej.2017.170
476
477 Doonan J, Denman S, Pachebat JA, & McDonald JE. (2019) Genomic analysis of bacteria in the
478 Acute Oak Decline pathobiome. *Microb Genomics* **5**: 0-15. doi: 10.1099/mgen.0.000240
479
480 Hildebrand DC, & Schroth MN. (1967) A new species of *Erwinia* causing the drippy nut disease of
481 live oaks. *Phytopathol* **57**: 250-253.
482
483 Hou J, Wu Q, Zuo T, Guo L, Chang J, Chen J, Wang Y, & He W.(2016) Genome-wide transcriptomic
484 profiles reveal multiple regulatory responses of poplar to *Lonsdalea quercina* infection. *Trees -*
485 *Struct Funct* **30**: 1389-1402. doi:10.1007/s00468-016-1376-7
486
487 Kovacova V, Kolarik M, Bandouchova H, Bartonicka T, Berkova H, Havelkova B, Hrudova E,
488 Kohoutova L, Martinková N, Zukal J, & Pikula J. (2018) Recovery of a phytopathogenic bacterium
489 *Lonsdalea quercina* from a lesser horseshoe bat in Moravian karst, Czech Republic. *For Pathol* **48**:
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20. TABLES AND FIGURES

PROVIDE TABLES AND FIGURES IN THE FORMAT PROVIDED BELOW

Table 1. Characteristics for differentiation of described species of the genus *Lonsdalea* (data from Brady et al., 2012; Tóth et al., 2013; Li et al., 2017).

Characteristic	*L. quercina*	*L. britannica*	*L. iberica*	*L. populi*
Acetoin production	v	-	+	+
Acid from:				
Glycerol	-	+	+	+
D-galactose	+	-	v	+
D-trehalose	-	v	-	+
D-turanose	+	+	+	-
Potassium gluconate	+	v	-	+
Assimilation of:				
D-raffinose	-	v	+	-
D-trehalose	-	+	+	+
Turanose	+	+	+	-

Citric acid	+	+	+	-
Formic acid	-	+	+	-
α-ketoglutaric acid	-	+	+	+
D,L-lactic acid	-	+	+	-
Succinic acid	-	+	+	+
L-glutamic acid	-	+	-	v
L-histidine	+	-	-	-

+, positive; -, negative; v, variable

Table 2. Genome metrics of species belonging to the genus *Lonsdalea* (data from Li et al., 2017)

	L. quercina	*L. britannica*	*L. iberica*	*L. populi*
Chromosome size (bp)	3.8	3.9	3.8	3.7-3.8
G + C content (mol %)	55.1-55.6	55.1	55.0	55.4
Median protein count	3246	3363	3108	3148

539 **Table 3.** Characteristics differentiating *Lonsdalea* from related genera within the family

540 *Pectobacteriaceae* (data from Brady et al., 2012)

Characteristic	*Lonsdalea*	*Brenneria*	*Pectobacterium*
β-galactosidase	-	v	+
Citrate utilization	+	v	+
H_2S production	-	v	v
Gelatinase	-	-	+
Acid from:			
Amygdalin	-	v	+
Cellobiose	-	v	+
Inulin	-	-	v
L-rhamnose	-	v	+
D-xylose	-	v	+
G + C content	55.0 – 55.6	51.1 – 56.1	50.4 – 52.2

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542 +, positive; -, negative; v, variable

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549 **Table 4.** DNA-DNA similarity values between species belonging to the genus *Lonsdalea* and the
550 type species of related genera within the family *Pectobacteriaceae*. Similarity values are based
551 on ANIm (JSpecieWS Online Service) and *is*DDH (Genome-to-Genome Distance Calculator 2.1).

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*is*DDH / ANIm	*L. quercina*	*L. britannica*	*L. iberica*	*L. populi*	*B. salicis*	*P. carotovorum*
L. quercina	100	35.7	44.3	37.4	20.1	20.3
L. britannica	89.4	100	36.9	39.8	20.3	20.4
L. iberica	91.9	89.9	100	36.7	20.0	20.3
L. populi	89.9	90.6	89.7	100	20.5	20.3
B. salicis	83.9	83.8	83.9	84.0	100	22.3
P. carotovorum	84.0	83.9	84.1	83.9	84.0	100

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21. FIGURE CAPTIONS

Figure 1. Transmission electron micrograph showing pertrichous flagella of **(a)** *Lonsdalea britannica* LMG 26267^T; bar, 1 µm **(b)** *Lonsdalea iberica* LMG 26264^T; bar, 2 µm. Photo credit: C. Brady

Figure 2. Maximum likelihood tree based on almost complete 16S rRNA gene sequences of all validly described *Lonsdalea* species and their closest phylogenetic relatives. Bootstrap values after 1000 replicates are expressed as percentages. *Plesiomonas shigelloides* NCIMB 9242^T was used as an outgroup. GenBank accession numbers are indicated after strain numbers. The scale bar indicates the fraction of nucleotide substitutions per site.

Figure 3. Maximum likelihood tree based on concatenated partial *gyrB*, *rpoB*, *infB* and *atpD* gene sequences of all validly described *Lonsdalea* species and their closest phylogenetic relatives. Bootstrap values after 1000 replicates are expressed as percentages. *Cronobacter sakazakii* ATCC BAA894 was used as an outgroup (not shown). The scale bar indicates the fraction of nucleotide substitutions per site.

Figure 4. Phylogenomic tree calculated from all available genome sequences of validly described *Lonsdalea* species and their closest phylogenetic relatives. Pseudo-bootstrap support values 100 replications are expressed as percentages, the tree was rooted at the midpoint. GenBank genome assembly accession numbers are indicated after strain numbers.