



Projet « *Funif-Col* »

*« De la récolte de l'échantillon à l'obtention d'une
séquence génétique »*

*Jérusalem Matthieu – Coordinateur
projet Funif-Col*



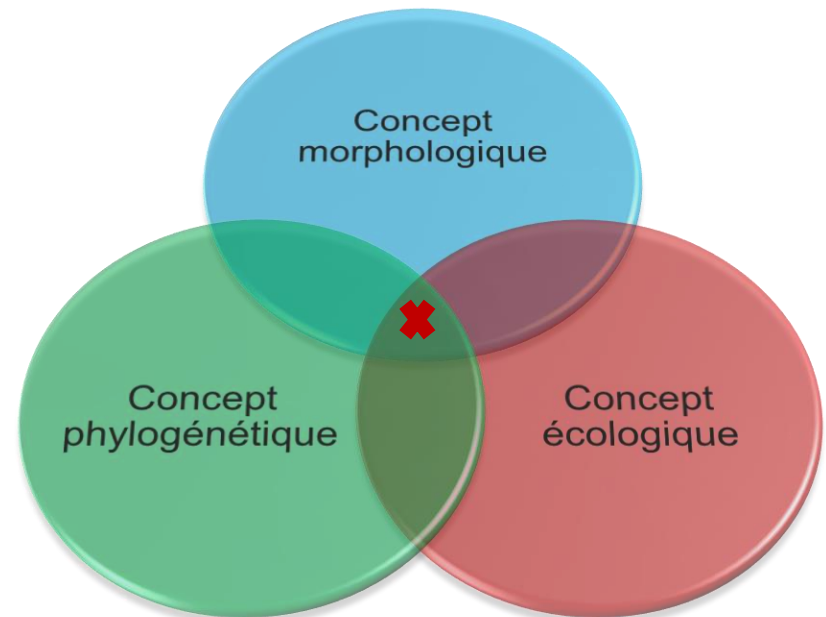
- Introduction – Les concepts d'espèces



Les espèces = « groupes de populations naturelles qui se **croisent** effectivement ou potentiellement, **isolées** des autres groupes sur le plan de la reproduction » (Mayr, 1942)



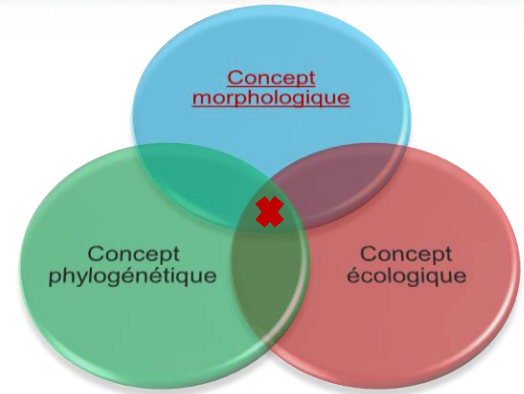
Nécessité d'utiliser un concept d'espèce « **consolidé** » pour délimiter les espèces



- Introduction – Les concepts d'espèces



1. *Morphological species concept (MSC)*



« Force »

- ✓ Largement appliqué dans le passé ainsi qu'actuellement
- Clés comparatives entre taxons

« Faiblesse »

- × Variations intraspécifiques / sp. cryptiques
- × Pertinence des caractères avec additions de nouvelles sp.
- × Concept basé sur l'interprétation humaine (subjectivité)

- Introduction – Les concepts d'espèces



1. *Morphological species concept (MSC)*



Young basidiomes



Intermediate basidiome



Mature basidiomes





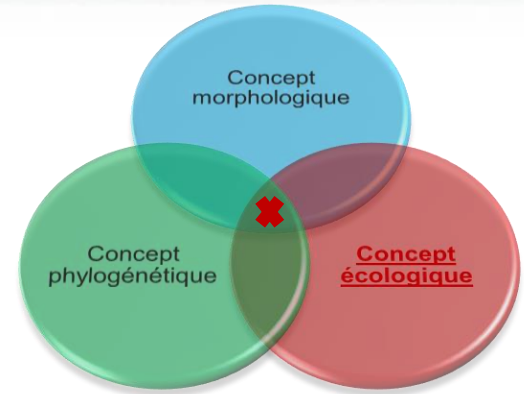
1. Morphology



- Introduction – Les concepts d'espèces



1. *Morphological species concept (MSC)*
2. *Ecological species concept (ESC)*



« Force »

- ✓ Spécificité d'hôte / niche écologique
- ✓ Prise en compte des zones biogéographiques et écosystèmes

« Faiblesse »

- × Présence possible chez d'autres hôtes sans dvlpmt de sporocarpes
- × Recouvrement de niche écologique
- × Switch possible si raréfaction de ressources (Host Jump)

- Introduction – Les concepts d'espèces



2. *Ecological species concept (ESC)*



Fomitiporia texana

Almost identical morphology

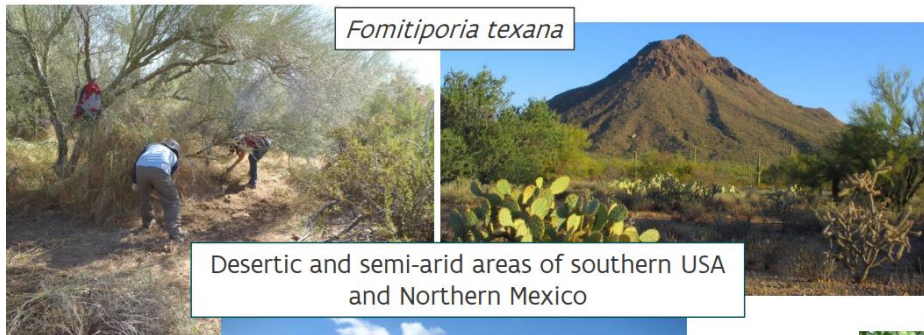


Fomitiporia sp. nov. PS19

- Introduction – Les concepts d'espèces



2. *Ecological species concept (ESC)*



- Introduction – Les concepts d'espèces



1. *Morphological species concept (MSC)*
2. *Ecological species concept (ESC)*
3. *Phylogenetic species concept (PSC)*

① **Barcoding moléculaire** = identification des espèces par des séquences génétiques uniques

DNA Barcoding:

a rapid method for species identification



cytochrome c oxidase sub. 1: *cox1*



matK and *rbcl*



ITS: internal transcribed spacers and
LSU: Ribosomal Large Subunit (28S)

DNA BARCODING



DNA extraction



Amplification of small piece
of genome (marker) using
universal primers (*COI*, *rbcl*,
matK, ITS etc.)

Sanger sequencing

1 DNA sequence

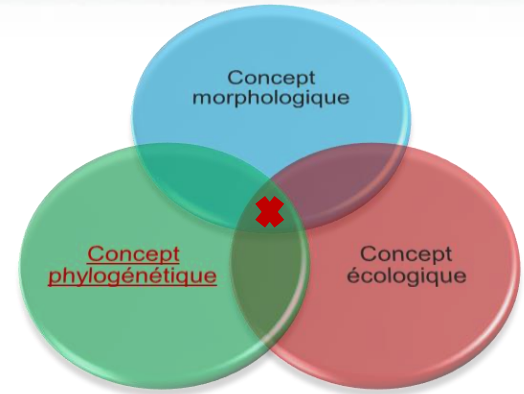
ATTCCGGATTCCAAGGTTCCAA

Fulvifomes kawakamii
(M.J. Larsen, Lombard &
Hodges) T. Wagner & M.
Fisch. 2002

- Introduction – Les concepts d'espèces



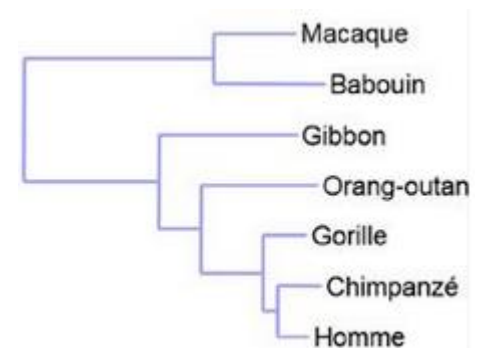
1. *Morphological species concept (MSC)*
2. *Ecological species concept (ESC)*
3. *Phylogenetic species concept (PSC)*



① **Barcoding moléculaire** = identification des espèces par des séquences génétiques uniques

② **Analyses phylogénétiques** (multigènes) = retracer l'histoire évolutive des taxons

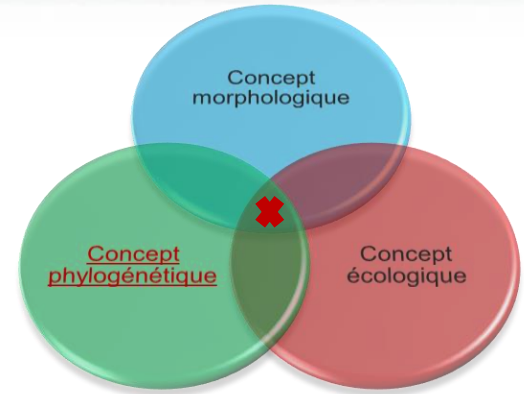
	Site constant	Site variable
Gibbon	AAGCTTTACAGGTGCAACCGTCCTCATAATCGCCACGGACTAACCTCTT	
Orang	AAGCTTCACCGGCGCAACCACCTCATGATTGCCCATGGACTCACATCCT	
Gorille	AAGCTTCACCGGCGCAGTTGTTCTTATAATTGCCACGGACTTACATCAT	
Homme	AAGCTTCACCGGCGCAGTCATTCTATAATCGCCACGGACTTACATCCT	
Chimpanzé	AAGCTTCACCGGCGCAATTATCCTCATAATCGCCACGGACTTACATCCT	
Macaque	AAGCTTTTCCGGCGCAACCATCCTTATGATCGCTCACGGACTCACCTCTT	
Babouin	AAGCTTCTCCGGTGCAACCATCCTTATGATTGCCACGGACTCACCTCTT	



- Introduction – Les concepts d'espèces



3. *Phylogenetic species concept (PSC)*



« Force »

- ✓ Identification universelle des espèces
- ✓ Reconstruction de l'histoire évolutive des espèces
- ✓ Diminution subjectivité humain

« Faiblesse »

- ✗ Utilisé seul, rend subjectif la délimitation des espèces !
- ✗ Incongruence phylogénétique
- ✗ Base de données internationales non-vérifiées et types (souvent) non-séquencés ou inexistants



Projet « *Funif-Col* »

*Code-barres moléculaires de référence pour les
Fungi (Eumycètes) français en collections*



- Projet “*Funif-Col*” -



DNA BARCODING



→ DNA extraction



→ Amplification of small piece of genome (marker) using universal primers (COI, rbcL, matK, ITS etc.)

→ Sanger sequencing

1 DNA sequence

ATTCGGGATTCCAAGGTTCCAA

→ *Fulvifomes kawakamii*
(M.J. Larsen, Lombard & Hodges) T. Wagner & M. Fisch. 2002

Diverses étapes successives :

- ① Extraction ADN
- ② Amplification PCR du gène d'intérêt
- ③ Séquençage
- ④ Correction des séquences
- ⑤ BLAST et analyse des séquences

- Matériel et Méthodes – Extraction ADN



innuPREP Plant DNA Kit

Protocol 1: gDNA isolation from plant material using Lysis Solution SLS

Recommended steps before starting

- Heat thermal mixer or water bath (65 °C)
- Prepare Washing Solution MS and Proteinase K according to the instruction

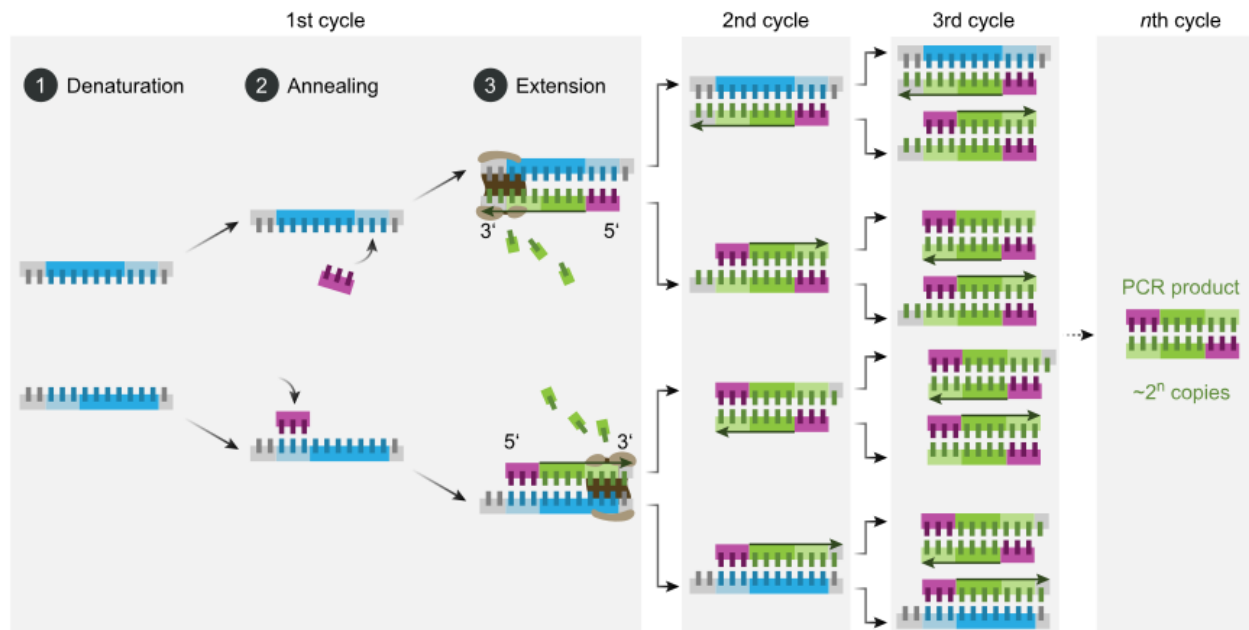
1. Starting material	▪ Plant material ▪ Wet plant material	▪ 50–100 mg ▪ 120–180 mg
2. Homogenization	▪ Homogenizer ▪ Pestle ▪ Grinding	▪ SpeedMill (innuSPEED Plant DNA Kit) ▪ Liquid N₂ ▪ Sand
3. Lysis		▪ Add 400 µl SLS and 20 µl PK ▪ Vortex: 5 sec ▪ Incubation: 65 °C, 30 min
4. Pre-filtration		▪ Add Prefilter to a Receiver Tube ▪ Add sample to Prefilter ▪ 11,000 x g (~11,000 rpm): 1 min NOTE Don't discard the Receiver Tube with the filtrate!
5. Optional: RNA removal		▪ 100 mg/ml RNase A; vortex ▪ Incubation: 5 min @ RT
6. Binding of DNA		▪ 200 µl SBS to the filtrate ▪ Mix: pipetting up and down ▪ Add Spin Filter to Receiver Tube ▪ Add sample to Spin Filter ▪ 11,000 x g (~11,000 rpm): 2 min

7. Washing		▪ Add 650 µl MS ▪ 11,000 x g (~11,000 rpm): 1 min ▪ Add 650 µl MS ▪ 11,000 x g (~11,000 rpm): 1 min
8. Remove Ethanol		▪ Discard filtrate ▪ Add Spin Filter to Receiver Tube ▪ Centrifuge: max speed, 2 min
9. Elution (Repeat 2x)		▪ Add Spin Filter to an Elution Tube ▪ Add 100–200 µl Elution Buffer ▪ Incubation: 1 min @ RT ▪ 11,000 x g (~11,000 rpm): 1 min

Order No.:	845-KS-1060010	10 reactions
	845-KS-1060050	50 reactions
	845-KS-1060250	250 reactions

ADN extrait : 100 ou 200 µL
→ 5 µL / amplification PCR nécessaire

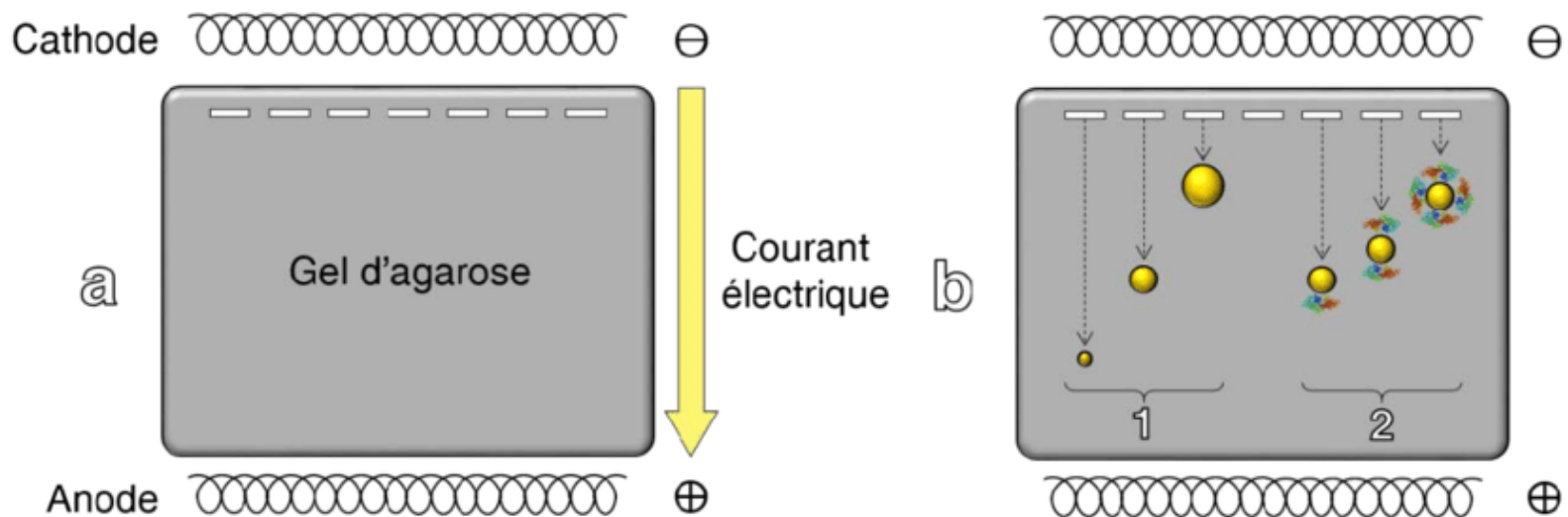
- Matériel et Méthodes – Amplification PCR



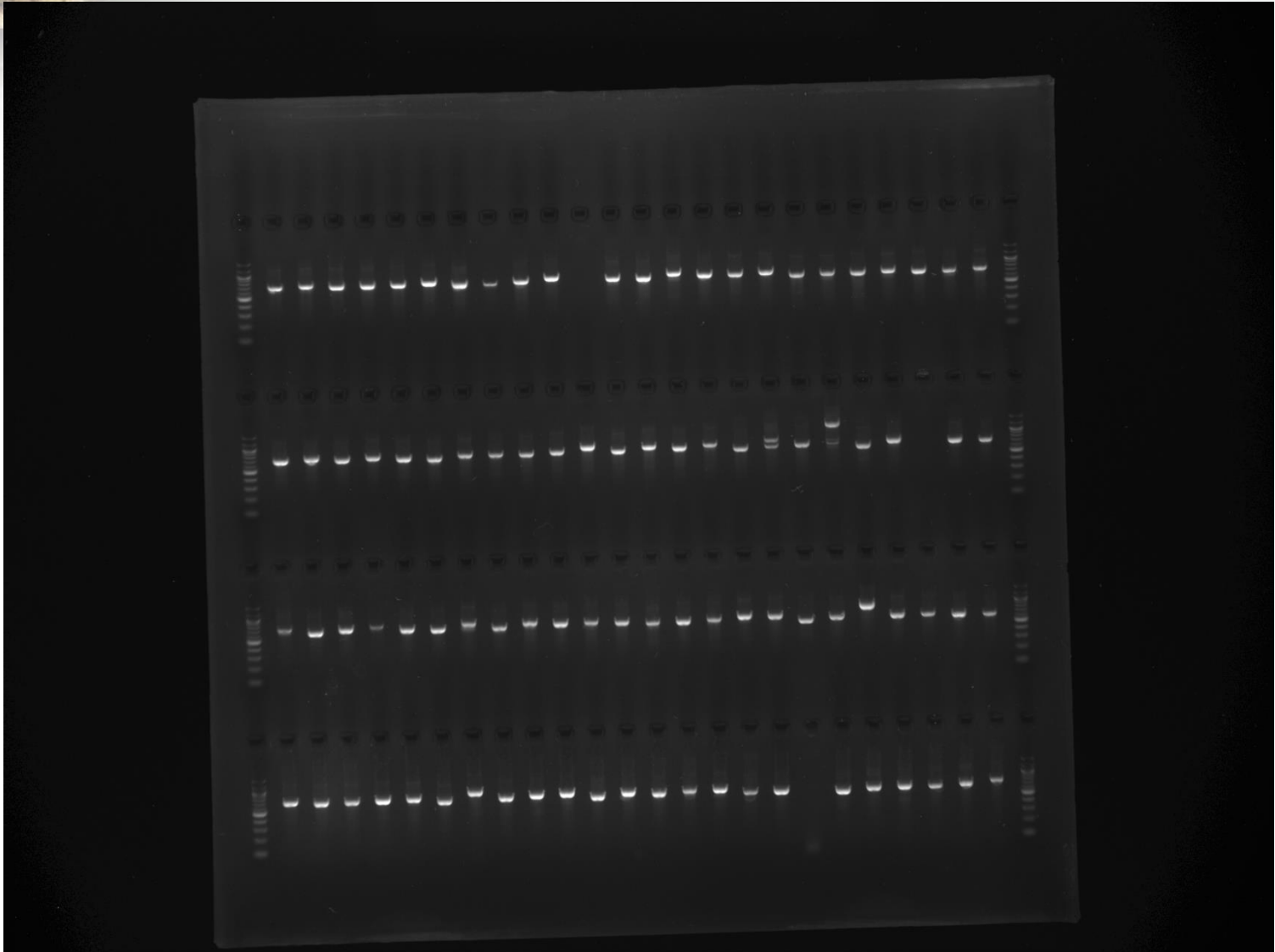
- Matériel et Méthodes – Migration sur gel



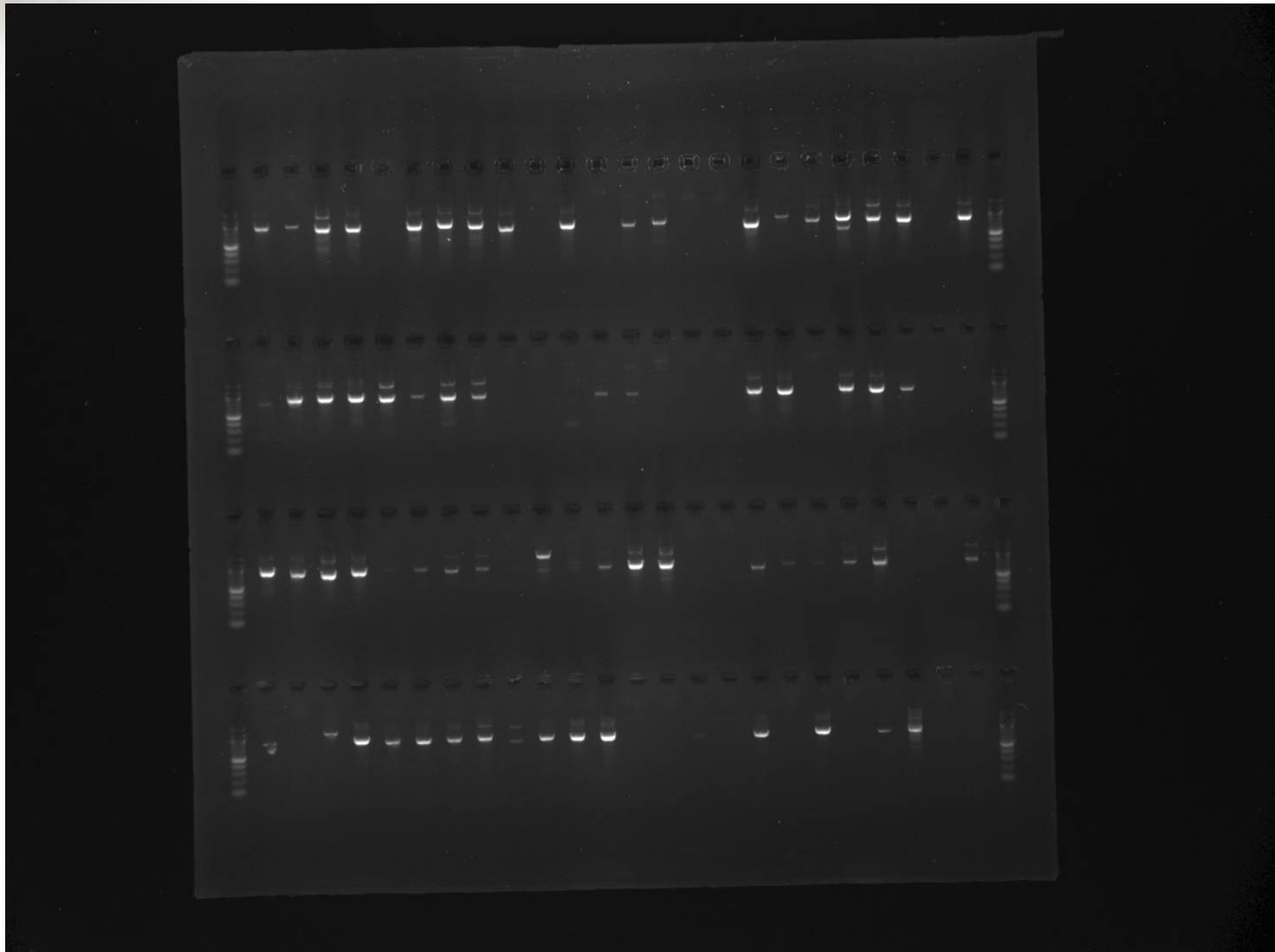
Rôle = Vérifier que l'amplification
PCR a fonctionné correctement !

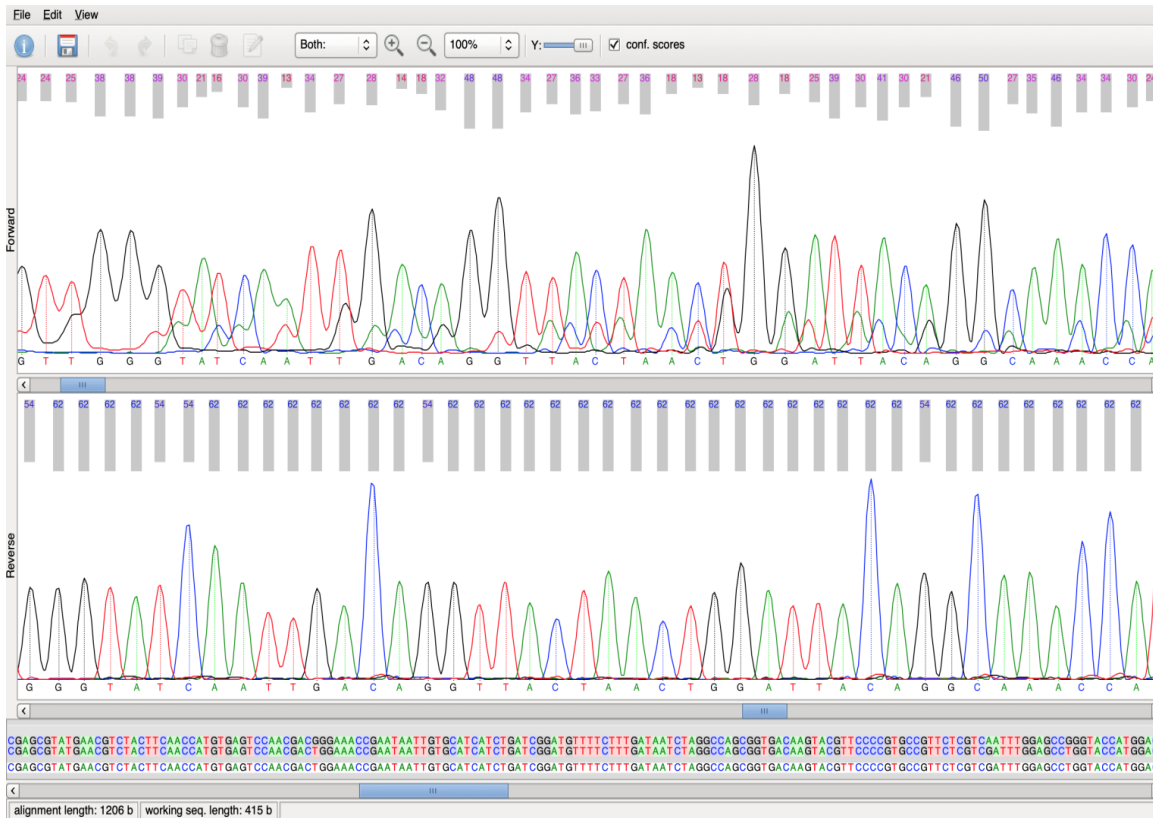
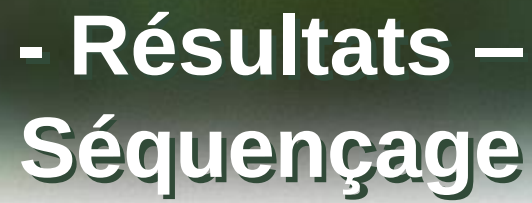


- Matériel et Méthodes – Révélation gel



- Matériel et Méthodes – Révélation gel





Nucleotide

The diagram shows a single nucleotide with three components: a **Base** (pink rectangle), a **Sugar** (yellow circle), and a **Phosphate** (orange circle). The sugar and phosphate are connected by a bond, and the base is attached to the sugar.

Bases

- Adenine (pink)
- Cytosine (blue)
- Guanine (teal)
- Thymine (yellow)

The DNA double helix is shown with the sugar-phosphate backbone on the outside and the nitrogenous bases on the inside. The bases are paired: Adenine (pink) pairs with Thymine (yellow), and Cytosine (blue) pairs with Guanine (teal). The strands are labeled with 5' and 3' ends, indicating antiparallel orientation.

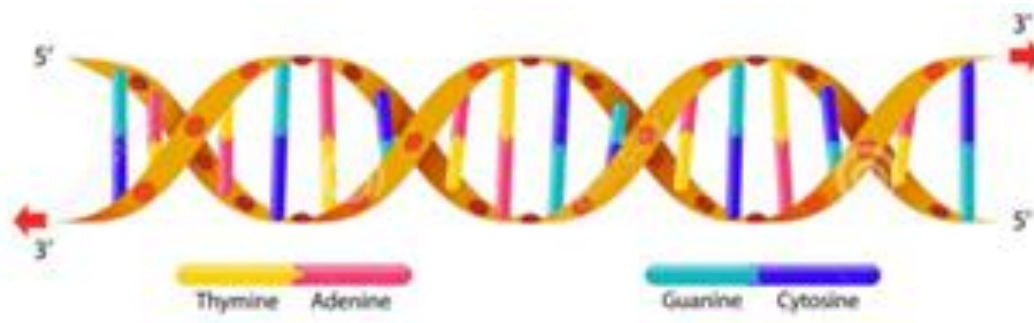


- Résultats – Séquençage



Méthodologie de correction des séquences (chromatogramme)

- **Etape 1:** Charger les séquences dans un programme de correction de séquences (Bioedit, Geneious, Sequencher,....)
- **Etape 2:** Retourner le brin « Reverse » pour obtenir le complémentaire du brin « Forward »





- Résultats – Séquençage



Méthodologie de correction des séquences (chromatogramme)

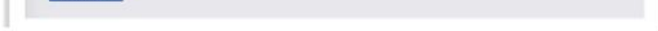
- **Etape 1:** Charger les séquences dans un programme de correction de séquences (Bioedit, Geneious, Sequencher,...)
- **Etape 2:** Retourner le brin « Reverse » pour obtenir le complémentaire du brin « Forward »
- **Etape 3:** « Contiger » les deux brins pour obtenir une séquence « consensus »
- **Etape 4:** Correction de la séquence « consensus »

Initiation séquences :

ITS1/4: ATCATTA...

LSU: TAACAAGG...

N	A or C or G or T
M	A or C
R	A or G
W	A or T
S	C or G
Y	C or T
K	G or T
V	Not T
H	Not G
D	Not C
B	Not A



!!! Le BLAST est une comparaison, pas une identification !!!

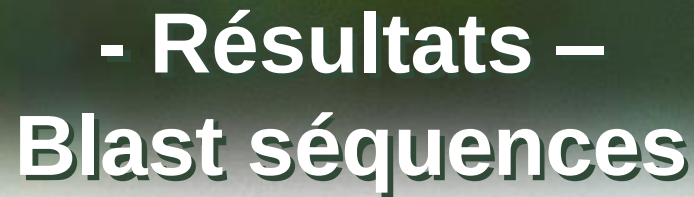


- Résultats – Blast séquences

1^{er} cas: Similarité 100% à plusieurs séquences étiquetées sous un même nom de taxon

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
☐ Alternaria tenuissima isolate SaX224-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012286.1
☐ Alternaria tenuissima isolate HeB249-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012285.1
☐ Alternaria tenuissima isolate FJ215-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012284.1
☐ Alternaria tenuissima isolate FJ209-4-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012283.1
☐ Alternaria tenuissima isolate XJ306-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012282.1
☐ Alternaria tenuissima isolate SX298-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012281.1
☐ Alternaria tenuissima isolate SX292-4 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012280.1
☐ Alternaria tenuissima isolate SX304-2 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012279.1
☐ Alternaria tenuissima isolate SX295-6 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012278.1
☐ Alternaria tenuissima isolate SX299-6 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012277.1
☐ Alternaria tenuissima isolate SD321-2 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012276.1
☐ Alternaria tenuissima isolate QH343-6 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012275.1
☐ Alternaria tenuissima isolate NX335-2 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012274.1
☐ Alternaria tenuissima isolate NX266-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012273.1
☐ Alternaria tenuissima isolate NX281-5 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012272.1
☐ Alternaria tenuissima isolate LN325-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012271.1
☐ Alternaria tenuissima isolate LN305-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012270.1
☐ Alternaria tenuissima isolate LN342-3 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012269.1
☐ Alternaria tenuissima isolate JX309-10 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012268.1
☐ Alternaria tenuissima isolate JX229-4 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012267.1
☐ Alternaria tenuissima isolate JL276-5 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012266.1
☐ Alternaria tenuissima isolate JL275-1 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene	991	991	100%	0.0	100%	MG012265.1



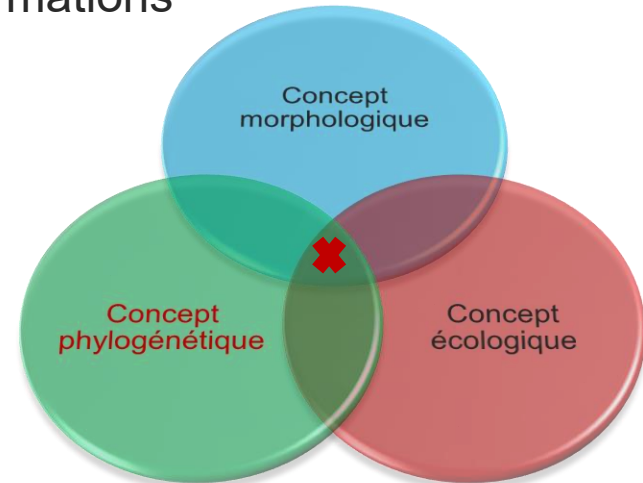
	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Volucrispora graminea strain CBS 114630 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inter	550	550	99%	2e-152	98%	MH062967.1
☐	Uncultured fungus clone 8-106 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed space	550	550	99%	2e-152	98%	KC884358.1
☐	Fungal sp. strain S187P internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S	546	546	99%	2e-151	98%	KU839102.1
☐	Fungal sp. strain S184T internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S	546	546	99%	2e-151	98%	KU839098.1
☐	Phialophora sp. Pr27 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, comp	546	546	99%	2e-151	98%	KU886586.1
☐	Rhoxocerosporidium sp. CSTC4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;	546	546	99%	2e-151	98%	KU504554.1
☐	Rhoxocerosporidium sp. CSTC3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;	546	546	99%	2e-151	98%	KU504553.1
☐	Rhoxocerosporidium sp. CSTC1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;	546	546	99%	2e-151	98%	KU497674.1
☐	Uncultured Helotiales clone 12137_B_vivipara_A2_A8 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and in	546	546	99%	2e-151	98%	KF000642.1
☐	Uncultured fungus genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, clone 3-113	546	546	99%	2e-151	98%	FN812810.2
☐	Uncultured fungus genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, clone 3-23	546	546	99%	2e-151	98%	FN812809.2
☐	Cadophora sp. E 7R3-1-8 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RN	546	546	99%	2e-151	98%	GU212388.1
☐	Cadophora sp. 6e51-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, com	546	546	99%	2e-151	98%	DQ3717329.1
☐	Fungal endophyte strain C327K internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; a	545	545	99%	2e-151	98%	KT203010.1
☐	Uncultured Volucrispora clone IVK4-24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	544	544	99%	8e-151	98%	EU516740.1
☐	Uncultured Helgardia clone IIK2F40 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	543	543	98%	3e-150	98%	FJ197857.1
☐	Fungal sp. strain S232A internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S	542	542	99%	3e-150	98%	KU839386.1
☐	Fungal sp. strain J246T internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S	542	542	99%	3e-150	98%	KU838425.1
☐	Fungal sp. strain J238Q internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S	542	542	99%	3e-150	98%	KU838365.1
☐	Fungal sp. strain N131J internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S	542	542	99%	3e-150	98%	KU837315.1
☐	Fungal sp. strain N131I internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S r	542	542	99%	3e-150	98%	KU837314.1
☐	Uncultured Cadophora clone IIK3-7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	542	542	99%	3e-150	98%	EU516830.1
☐	Leptodontidium orchidicola small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	542	542	99%	3e-150	98%	KF646097.1



- Résultats – Blast séquences

2^{eme} cas: Similarité à >97%

- Comparaison des séquences et revérification des chromatogrammes (ambiguïté)
- Littérature (genre + séquences sur GenBank)
- Séquençage d'autres gènes pour recouper les informations
- Vérification morphologique





- Résultats – Blast séquences

3^{eme} cas: Similarité à 100% pour plusieurs séquences étiquetées sous des noms de taxons différents

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Penicillium bifforme strain KAS8028 beta-tubulin gene, partial cds	693	693	100%	0.0	100%	KY469085.1
☐	Penicillium bifforme strain KAS8027 beta-tubulin gene, partial cds	693	693	100%	0.0	100%	KY469084.1
☐	Penicillium commune strain 5i15 beta-tubulin 2 (tub2) gene, partial cds	693	693	100%	0.0	100%	KX928914.1
☐	Penicillium commune strain 5i20 beta-tubulin 2 (tub2) gene, partial cds	693	693	100%	0.0	100%	KX928911.1
☐	Penicillium commune strain UBOCC-A-116003 beta-tubulin 2 (tub2) gene, partial cds	693	693	100%	0.0	100%	KX928909.1
☐	Penicillium commune strain 5i24 beta-tubulin 2 (tub2) gene, partial cds	693	693	100%	0.0	100%	KX928908.1
☐	Penicillium commune strain 5i30 beta-tubulin 2 (tub2) gene, partial cds	693	693	100%	0.0	100%	KX928898.1
☐	Penicillium commune culture-collection MUT<ITA>:4856 beta-tubulin (Tub) gene, partial cds	693	693	100%	0.0	100%	KT313385.1
☐	Penicillium bifforme strain DTO_269E2 beta-tubulin (tub2) gene, partial cds	693	693	100%	0.0	100%	KJ775117.1
☐	Penicillium commune isolate IS22 beta-tubulin gene, partial cds	693	693	100%	0.0	100%	JQ217372.1
☐	Penicillium commune strain 5i17b beta-tubulin 2 (tub2) gene, partial cds	691	691	99%	0.0	100%	KX928917.1

Causes :

- Mauvaises annotations GenBank
- Séquences géniques peu variables au sein de ce genre (littérature !)
- Nécessité de séquencer d'autres gènes appropriés selon groupe taxonomique



- Résultats – Blast séquences

4^{eme} cas: Similarité à < 97% ! → probabilité forte d'une *sp. nov* !

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Uncultured Phoma genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10D70C66 (SMOTU224)	472	472	99%	4e-129	92%	HG937104.1
☐	Pezizomycotina sp. strain W82 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; an	468	468	99%	5e-128	91%	MF614988.1
☐	Uncultured fungus clone ZBJ201308-46 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	468	468	99%	5e-128	91%	KX515399.1
☐	Uncultured Ascomycota clone 5_12_NE_3 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	468	468	99%	5e-128	91%	KX499281.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10S70C02 (MOTU4)	468	468	99%	5e-128	91%	HG935441.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10S50C26 (MOTU4)	468	468	99%	5e-128	91%	HG935439.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10S10C59 (MOTU4)	468	468	99%	5e-128	91%	HG935437.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10S10C01 (MOTU4)	468	468	99%	5e-128	91%	HG935436.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10J70C52 (MOTU4)	468	468	99%	5e-128	91%	HG935435.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10J50C71 (MOTU4)	468	468	99%	5e-128	91%	HG935434.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10J50C41 (MOTU4)	468	468	99%	5e-128	91%	HG935433.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10J10C92 (MOTU4)	468	468	99%	5e-128	91%	HG935431.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10J10C61 (MOTU4)	468	468	99%	5e-128	91%	HG935430.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 10J10C15 (MOTU4)	468	468	99%	5e-128	91%	HG935429.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09S50C44 (MOTU4)	468	468	99%	5e-128	91%	HG935415.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09S50C19 (MOTU4)	468	468	99%	5e-128	91%	HG935414.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09S10C40 (MOTU4)	468	468	99%	5e-128	91%	HG935413.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09S10C38 (MOTU4)	468	468	99%	5e-128	91%	HG935412.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09JWuC87 (MOTU4)	468	468	99%	5e-128	91%	HG935408.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09JWuC29 (MOTU4)	468	468	99%	5e-128	91%	HG935407.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09JWuC08 (MOTU4)	468	468	99%	5e-128	91%	HG935406.1
☐	Uncultured Psiloglonium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone 09J10C71 (MOTU4)	468	468	99%	5e-128	91%	HG935403.1

- Récoltes JMHA 2023 -

1) XC23-093 : *Entoloma lucidum* / *sericeum* ?

→ BLAST séquence ITS

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Entoloma sericeum isolate BF8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and inte...	Entoloma sericeum	1157	1157	100%	0.0	100.00%	1280	KY706153.1
✓	Entoloma sericeum internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcri...	Entoloma sericeum	1157	1157	100%	0.0	100.00%	672	KF897025.1
✓	Entoloma sericeum strain Battistin 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S...	Entoloma sericeum	1153	1153	99%	0.0	100.00%	641	JX454815.1
✓	Entoloma sericeum voucher LE302051 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Entoloma sericeum	1110	1110	96%	0.0	100.00%	601	OL338254.1
✓	Entoloma sericeum voucher MQ17229-QFB29737 small subunit ribosomal RNA gene, partial sequence; internal tr...	Entoloma sericeum	1153	1153	100%	0.0	99.84%	706	MN992584.1
✓	uncultured fungus genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gen...	uncultured fungus	1151	1151	100%	0.0	99.84%	1584	OU939303.1
✓	Entoloma sericeum voucher KR-M-0053201 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA ...	Entoloma sericeum	1151	1151	100%	0.0	99.84%	730	PP868373.1
✓	Entoloma sericeum strain JVG 1060831-8 18S ribosomal RNA gene, partial sequence; internal transcribed spacer...	Entoloma sericeum	1149	1149	99%	0.0	99.84%	641	JX454851.1
✓	Entoloma sericeum strain MEN 1048 (L) 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1...	Entoloma sericeum	1147	1147	99%	0.0	99.84%	641	JX454814.1
✓	Entoloma sericeum strain JVG 960816-7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer ...	Entoloma sericeum	1146	1146	99%	0.0	99.84%	640	JX454869.1
✓	Uncultured fungus clone 3993_431 small subunit ribosomal RNA gene, partial sequence; internal transcribed spac...	uncultured fungus	1140	1140	99%	0.0	99.84%	666	MW214974.1
✓	Entoloma sericeum voucher MQ18R381-QFB30897 internal transcribed spacer 1, partial sequence; 5.8S ribosom...	Entoloma sericeum	1129	1129	98%	0.0	99.84%	639	MN992142.1
✓	Entoloma sericeum voucher GC13091816 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA ge...	Entoloma sericeum	1123	1123	97%	0.0	99.84%	760	OL338087.1
✓	Entoloma sericeum voucher GC99100110 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA ge...	Entoloma sericeum	1122	1122	97%	0.0	99.84%	760	OL338105.1
✓	Entoloma sericeum var. sericeum voucher 256129141 small subunit ribosomal RNA gene, partial sequence; intern...	Entoloma sericeu...	1114	1114	96%	0.0	99.83%	648	OQ586341.1
✓	Entoloma sericeum voucher GC14112812 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA ge...	Entoloma sericeum	1112	1112	96%	0.0	99.83%	755	OL338090.1
✓	Entoloma sericeum voucher PDD86974 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Entoloma sericeum	1110	1110	96%	0.0	99.83%	753	OL338382.1

- Récoltes JMHA 2023 -

1) XC23-093 : *Entoloma lucidum* / *sericeum* ?

→ BLAST séquence *LSU*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Entoloma sericeum voucher GLM 45918 28S large subunit ribosomal RNA gene, partial sequence	Entoloma sericeum	1947	1947	99%	0.0	100.00%	1078	AY207197.1
✓	Nolanea sericea strain CBS 237.50 large subunit ribosomal RNA gene, partial sequence	Entoloma sericeum	1927	1927	98%	0.0	99.90%	1109	AF223170.1
✓	Entoloma sericeum isolate HMJAU60927 large subunit ribosomal RNA gene, partial sequence	Entoloma sericeum	1825	1825	94%	0.0	99.80%	1000	ON041704.1
✓	Entoloma sp. strain G0104 large subunit ribosomal RNA gene, partial sequence	Entoloma sp.	1901	1901	98%	0.0	99.52%	1284	MK278045.1
✓	Entoloma farinolens strain G1604 large subunit ribosomal RNA gene, partial sequence	Entoloma farinol...	1901	1901	99%	0.0	99.43%	1286	MK277986.1
✓	Entoloma alboubonatum strain G1803 large subunit ribosomal RNA gene, partial sequence	Entoloma albou...	1895	1895	98%	0.0	99.43%	1284	MK277958.1
✓	Entoloma cf. solstitialis strain G1415 large subunit ribosomal RNA gene, partial sequence	Entoloma cf. sols...	1849	1849	96%	0.0	99.41%	1259	MK278034.1
✓	Entoloma minutum strain G0395 large subunit ribosomal RNA gene, partial sequence	Entoloma minutum	1875	1875	98%	0.0	99.32%	1275	MK278007.1
✓	Nolanea sericea strain CBS 153.46 large subunit ribosomal RNA gene, partial sequence	Entoloma sericeum	1844	1844	96%	0.0	99.31%	1081	AF223171.1
✓	Entoloma farinolens isolate CONTIG_SL18 large subunit ribosomal RNA gene, partial sequence	Entoloma farinol...	1890	1890	99%	0.0	99.24%	1241	OL688355.1
✓	Entoloma farinolens isolate CONTIG_SL10 large subunit ribosomal RNA gene, partial sequence	Entoloma farinol...	1890	1890	99%	0.0	99.24%	1241	OL688347.1
✓	Entoloma aromaticum strain G1672 large subunit ribosomal RNA gene, partial sequence	Entoloma aromat...	1890	1890	99%	0.0	99.24%	1286	MK277965.1
✓	Entoloma fibropileatum strain G1625 large subunit ribosomal RNA gene, partial sequence	Entoloma fibroso...	1888	1888	99%	0.0	99.24%	1285	MK277987.1
✓	Entoloma conferendum strain G0703 large subunit ribosomal RNA gene, partial sequence	Entoloma confer...	1879	1879	98%	0.0	99.23%	1280	MK278032.1
✓	Entoloma brunneosericeum isolate HMJAU60945 large subunit ribosomal RNA gene, partial sequence	Entoloma brunne...	1814	1814	95%	0.0	99.21%	1011	ON042432.1
✓	Entoloma llimonae isolate HMJAU60966 large subunit ribosomal RNA gene, partial sequence	Entoloma llimonae	1784	1784	93%	0.0	99.19%	999	ON042455.1
✓	Entoloma cetratum strain G1148 large subunit ribosomal RNA gene, partial sequence	Entoloma cetratum	1768	1768	92%	0.0	99.18%	1220	MK277976.1

- Récoltes JMHA 2023 -

2) XC23-096 : *Gyroflexus* ?

→ BLAST séquence *ITS*



	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Phloeomana speirea voucher MushroomObserver.org/307099 internal transcribed spacer 1, partial sequence; 5.8S...	Phloeomana spei...	1122	1122	95%	0.0	99.67%	1040	MH100738.1
✓	Phloeomana speirea voucher AMB 18773 small subunit ribosomal RNA gene, partial sequence; internal transcribed...	Phloeomana spei...	880	880	75%	0.0	99.58%	496	OL839158.1
✓	Phloeomana speirea voucher S.D. Russell iNaturalist # 8590065 internal transcribed spacer 1, partial sequence; 5.8...	Phloeomana spei...	1171	1171	100%	0.0	99.53%	653	MN906057.1
✓	Phloeomana speirea voucher 218n 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA ge...	Phloeomana spei...	1171	1171	100%	0.0	99.53%	798	JF908396.1
✓	Mycena speirea genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gen...	Phloeomana spei...	1171	1171	100%	0.0	99.53%	1067	LT671446.1
✓	Phloeomana speirea isolate MO542250 small subunit ribosomal RNA gene, partial sequence; internal transcribed s...	Phloeomana spei...	1171	1171	100%	0.0	99.53%	691	PP849905.1
✓	Phloeomana speirea isolate iNaturalist # 167068968 small subunit ribosomal RNA gene, partial sequence; internal t...	Phloeomana spei...	1162	1162	99%	0.0	99.53%	666	OR853434.1
✓	Phloeomana speirea isolate CA FUNDIS iNaturalist # 184215987 small subunit ribosomal RNA gene, partial sequen...	Phloeomana spei...	1162	1162	99%	0.0	99.53%	666	PP849864.1
✓	Phloeomana speirea isolate OMDL K. Canan iNaturalist # 169173422 small subunit ribosomal RNA gene, partial se...	Phloeomana spei...	1157	1157	98%	0.0	99.53%	661	OR987384.1
✓	Phloeomana speirea isolate CA FUNDIS iNat147684225 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Phloeomana spei...	1153	1153	98%	0.0	99.52%	630	OR879834.1
✓	Phloeomana speirea isolate iNat65719557 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gen...	Phloeomana spei...	1153	1153	98%	0.0	99.52%	630	OP651132.1
✓	Phloeomana speirea voucher H6039066 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Phloeomana spei...	1099	1099	93%	0.0	99.50%	601	MW540707.
✓	Porothelium omphaliiforme voucher WU 17815 small subunit ribosomal RNA gene, partial sequence; internal trans...	Marasmiellomyce...	1092	1092	93%	0.0	99.50%	632	OM422778.1
✓	Phloeomana speirea voucher WU 17815 small subunit ribosomal RNA gene, partial sequence; internal transcribed ...	Phloeomana spei...	1074	1074	91%	0.0	99.49%	622	OL990024.1
✓	Phloeomana speirea voucher 449 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gen...	Phloeomana spei...	1166	1166	100%	0.0	99.38%	704	JF908438.1
✓	Phloeomana speirea isolate MO190446 small subunit ribosomal RNA gene, partial sequence; internal transcribed s...	Phloeomana spei...	1166	1166	100%	0.0	99.38%	699	PP849896.1
✓	Mycena speirea genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gen...	Phloeomana spei...	1166	1166	100%	0.0	99.38%	1090	LT671445.1

- Récoltes JMHA 2023 -

2) XC23-096 : *Gyroflexus* ?

→ BLAST séquence *ITS*



Score	Expect	Identities	Gaps	Strand
1122 bits(607)	0.0	609/611(99%)	0/611(0%)	Plus/Plus
Query 30	TGTTGTAGCTGGCTCTTCGGAGCATGTGCACGCACTTCAAATTCATCTTTACCACCTGTG	89		
Sbjct 1	TGTTGTAGCTGGCTCTTCGGAGCATGTGCACGCACTTCAAATTCATCTTTACCACCTGTG	60		
Query 90	CACCTTTGTAGACTGTGATAACTCTCAATGGTTTACTCCGTTGGATTGAAGGACATGCGT	149		
Sbjct 61	CACCTTTGTAGACTGTGATAACTCTCAATGGTTTACTCCGTTGGATTGAAGGACATGCGT	120		
Query 150	CTTAGCTGTCTTTGACTTCACAGTCTATGTCTCATCTACTATAAAAAGTCTAGAATGTA	209		
Sbjct 121	CTTAGCTGTCTTTGACTTCACAGTCTATGTCTCATCTACTATAAAAAGTCTAGAATGTA	180		
Query 210	ACTTGTGGGTCTTTGACCTATAAAA(TW)ATACAACCTTCAACAACGGATCTCTTGGCT	269		
Sbjct 181	ACTTGTGGGTCTTTGACCTATAAAA(TT)ATACAACCTTCAACAACGGATCTCTTGGCT	240		
Query 270	CTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTG	329		
Sbjct 241	CTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTG	300		
Query 330	AATCATCGAATCTTTGAACGCACCTTGCACTCCTTGGTATTCCGAGGAGTATGCCTGTTT	389		
Sbjct 301	AATCATCGAATCTTTGAACGCACCTTGCACTCCTTGGTATTCCGAGGAGTATGCCTGTTT	360		
Query 390	GAGTGTCAATTAATCTCAAACCTCTTTGACTTTATTGACAAAGAGGCTTTGGATGTGGG	449		
Sbjct 361	GAGTGTCAATTAATCTCAAACCTCTTTGACTTTATTGACAAAGAGGCTTTGGATGTGGG	420		
Query 450	GGTTGCTGGCTTTACGAGTCAGCTCTCCTTAAATAY)TAGTGGTTACTGTTCTCCACT	509		
Sbjct 421	GGTTGCTGGCTTTACGAGTCAGCTCTCCTTAAATAC)TAGTGGTTACTGTTCTCCACT	480		
Query 510	TCCTGGTGTGATAATATCTACGCCTAGTGGAGATGTTAAGTGTAGCTGCTCTTAACCGT	569		
Sbjct 481	TCCTGGTGTGATAATATCTACGCCTAGTGGAGATGTTAAGTGTAGCTGCTCTTAACCGT	540		
Query 570	CCATGCAATGTGGACAACCTTGAACCTTTGACCTCAAATCAGGTAGGACTACCCGCTGAA	629		
Sbjct 541	CCATGCAATGTGGACAACCTTGAACCTTTGACCTCAAATCAGGTAGGACTACCCGCTGAA	600		
Querv 630	CTTAAGCATAT 640			

- Récoltes JMHA 2023 -

2) XC23-096 : *Gyroflexus* ?

→ BLAST séquence *LSU*



	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	Hemimycena sp. 1 TM02_65 25S large subunit ribosomal RNA gene, partial sequence	Hemimycena sp...	1443	1443	60%	0.0	99.37%	793	EU522786.1
☒	Hemimycena sp. NOFQB15_Q23 gene for large subunit ribosomal RNA	Hemimycena sp.	1439	1439	63%	0.0	98.30%	850	LC757565.1
☒	Hemimycena sp. NOFFB11_F19 gene for large subunit ribosomal RNA	Hemimycena sp.	1435	1435	62%	0.0	98.29%	844	LC757632.1
☒	Phloeomana minutula strain G0202 large subunit ribosomal RNA gene, partial sequence	Phloeomana min...	1504	1558	69%	0.0	97.71%	1281	MK278398.1
☒	Pluteus thomsonii culture CBS:213.46 strain CBS 213.46 large subunit ribosomal RNA gene, partial sequence	Pluteus thomsonii	1504	1504	67%	0.0	97.61%	938	MH867690.1
☒	Mycena olida strain G0813 large subunit ribosomal RNA gene, partial sequence	Mycena olida	1500	1555	69%	0.0	97.60%	1282	MK278135.1
☒	Hemimycena sp. strain G0059 large subunit ribosomal RNA gene, partial sequence	Hemimycena sp.	1496	1551	69%	0.0	97.49%	1290	MK278137.1
☒	Pleurotopsis longinqua isolate RV95/473 25S large subunit ribosomal RNA gene, partial sequence	Pleurotopsis long...	1459	1514	69%	0.0	96.69%	1034	AF042604.1
☒	Panellus longinquus isolate PDD_72536 large subunit ribosomal RNA gene, partial sequence	Panellus longing...	1447	1447	67%	0.0	96.57%	918	PP956783.1
☒	Gerronema viridilucens voucher DED 7822 large subunit ribosomal RNA gene, partial sequence	Gerronema viridil...	1448	1503	69%	0.0	96.47%	976	OR449361.1
☒	Panellus violaceofulvus culture CBS:391.50 strain CBS 391.50 large subunit ribosomal RNA gene, partial sequence	Panellus violace...	1448	1448	67%	0.0	96.47%	947	MH868193.1
☒	Pleurotopsis longinqua strain G0873 large subunit ribosomal RNA gene, partial sequence	Pleurotopsis long...	1443	1498	69%	0.0	96.46%	1282	MK278472.1
☒	Panellus violaceofulvus large subunit ribosomal RNA gene, partial sequence	Panellus violace...	1317	1317	61%	0.0	96.26%	834	AF325361.1
☒	Pleurotopsis longinqua large subunit ribosomal RNA ribosomal RNA gene, partial sequence	Pleurotopsis long...	1315	1315	61%	0.0	96.26%	833	AY014289.1
☒	Lepista panaeola strain G0177 large subunit ribosomal RNA gene, partial sequence	Lepista panaeola	1435	1490	69%	0.0	96.24%	1289	MK278277.1
☒	Hemimycena sp. isolate TMEF17 large subunit ribosomal RNA gene, partial sequence	Hemimycena sp.	1434	1434	67%	0.0	96.24%	965	OL614822.1
☒	Hemimycena ignobilis strain DAOM214662 25S large subunit ribosomal RNA gene, partial sequence	Hemimycena ign...	1430	1485	69%	0.0	96.24%	1104	AF261359.1

- Récoltes JMHA 2023 -

3) XC23-131 : *Inocybe* sp.

→ BLAST séquence *ITS*



	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Inocybe tabacina voucher HFRG_PC230723_1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal R...	Inocybe tabacina	1206	1206	97%	0.0	100.00%	653	OR896143.1
✓	Inocybe tabacina voucher HFRG_PC221006_3 small subunit ribosomal RNA gene, partial sequence; internal tra...	Inocybe tabacina	1146	1146	92%	0.0	100.00%	663	OR896123.1
✓	Inocybe tabacina voucher FR-0246016 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Inocybe tabacina	1027	1027	82%	0.0	100.00%	556	MK929272.1
✓	Inocybe tabacina voucher FR-0246017 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Inocybe tabacina	1027	1027	82%	0.0	100.00%	556	MK929260.1
✓	Inocybe tabacina voucher M68 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer ...	Inocybe tabacina	1232	1232	100%	0.0	99.85%	696	MW354989.1
✓	Inocybe tabacina voucher HFRG_PC221006_1 small subunit ribosomal RNA gene, partial sequence; internal tra...	Inocybe tabacina	1166	1166	94%	0.0	99.84%	675	OR896110.1
✓	Inocybe tabacina voucher PAM05071302 (LIP) small subunit ribosomal RNA gene, partial sequence; internal tran...	Inocybe tabacina	1227	1227	100%	0.0	99.70%	711	HQ586865.1
✓	Inocybe tabacina voucher KR-M-0044743 small subunit ribosomal RNA gene, partial sequence; internal transcrib...	Inocybe tabacina	1142	1142	93%	0.0	99.68%	659	MT006020.1
✓	Inocybe tabacina voucher HFRG_PC220927_1 small subunit ribosomal RNA gene, partial sequence; internal tra...	Inocybe tabacina	1123	1123	91%	0.0	99.67%	659	OR896130.1
✓	Inocybe tabacina voucher HFRG_PC211012_1 small subunit ribosomal RNA gene, partial sequence; internal tran...	Inocybe tabacina	1221	1221	100%	0.0	99.55%	702	OQ133559.1
✓	Inocybe cf. tabacina voucher KR-M-0044690 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA...	Inocybe cf. tabac...	1057	1057	87%	0.0	99.31%	582	MT005875.1
✓	Inocybe bombina FR 0246007 ITS region; from TYPE material	Inocybe bombina	889	889	82%	0.0	95.70%	550	NR_173842.1
✓	Inocybe bombina voucher KR-M-0043212 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA g...	Inocybe bombina	889	889	82%	0.0	95.70%	550	MK929261.1
✓	Inocybe bombina voucher FR-0246007 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Inocybe bombina	889	889	82%	0.0	95.70%	550	MK929267.1
✓	Inocybe vulpinella voucher IK-00033 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5...	Inocybe vulpinella	741	741	100%	0.0	87.30%	684	KX602283.1
✓	Uncultured Inocybe clone 12223_B_vivipara 18S ribosomal RNA gene, partial sequence; internal transcribed spa...	uncultured Inocybe	743	743	100%	0.0	87.26%	703	KF000619.1
✓	Uncultured Inocybe clone 12224_B_vivipara 18S ribosomal RNA gene, partial sequence; internal transcribed spa...	uncultured Inocybe	743	743	100%	0.0	87.26%	700	KF000618.1
✓	Uncultured Inocybe clone 12221_B_vivipara 18S ribosomal RNA gene, partial sequence; internal transcribed spa...	uncultured Inocybe	743	743	100%	0.0	87.26%	701	KF000620.1

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3) XC23-131 : *Inocybe* sp.

→ BLAST séquence *LSU*



	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Inocybe tabacina voucher HMUT M1287 large subunit ribosomal RNA gene, partial sequence	Inocybe tabacina	1869	1869	97%	0.0	100.00%	1012	ON430593.1
✓	Inocybe tabacina voucher PAM05071302 (LIP) large subunit ribosomal RNA gene, partial sequence	Inocybe tabacina	1916	1916	100%	0.0	99.90%	1424	HQ641106.1
✓	Inocybe fibrosoides isolate 14296 voucher EL51-14 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe fibrosoides	1786	1786	100%	0.0	97.61%	1954	KY033846.1
✓	Inocybe fibrosoides voucher PAM01100301 (LIP) large subunit ribosomal RNA gene, partial sequence	Inocybe fibrosoides	1781	1781	100%	0.0	97.51%	1428	HQ641098.1
✓	Inocybe fibrosoides 18S (partial), ITS1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe fibrosoides	1781	1781	100%	0.0	97.51%	1841	AM882827.2
✓	Inocybe phaeosticta voucher PAM05091310 (LIP) large subunit ribosomal RNA gene, partial sequence	Inocybe phaeosti...	1779	1779	100%	0.0	97.51%	1434	HQ641102.1
✓	Inocybe fibrosoides voucher PAM05100801 (LIP) large subunit ribosomal RNA gene, partial sequence	Inocybe fibrosoides	1781	1781	100%	0.0	97.42%	1428	HQ641107.1
✓	Inocybe favrei isolate 6057 voucher EL78-06 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe favrei	1772	1772	100%	0.0	97.33%	1964	KY033800.1
✓	Inocybe arctica isolate 13203 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe arctica	1772	1772	100%	0.0	97.33%	2005	KY033833.1
✓	Inocybe arctica isolate 7115 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe arctica	1772	1772	100%	0.0	97.33%	1789	KY033839.1
✓	Inocybe arctica isolate 8219 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe arctica	1772	1772	100%	0.0	97.33%	2007	KY033843.1
✓	Inocybe baltica isolate 6054 voucher EL71-06 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe baltica	1772	1772	100%	0.0	97.33%	1955	KY033842.1
✓	Inocybe favrei isolate 11258 voucher EL105-11 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe favrei	1772	1772	100%	0.0	97.33%	2000	KY033796.1
✓	Inocybe arctica isolate 11140 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe arctica	1772	1772	100%	0.0	97.33%	2004	KY033832.1
✓	Inocybe rivularis isolate 13286 voucher JRJV30172 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe rivularis	1772	1772	100%	0.0	97.33%	1997	KY033820.1
✓	Inocybe rivularis isolate 12258 voucher EL178-12 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S rRNA gene, ITS2 and 25S rRNA (partial), specimen voucher SS2990	Inocybe rivularis	1772	1772	100%	0.0	97.33%	2002	KY033823.1

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4) XC23-153 : *Pluteus fenzlii*

→ BLAST séquence *ITS*



✓	Pluteus fenzlii voucher LE 303661 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and i...	Pluteus fenzlii	1210	1210	100%	0.0	99.85%	727	KX216339.1
✓	Pluteus fenzlii voucher TNSF12376 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8...	Pluteus fenzlii	1206	1206	100%	0.0	99.85%	695	HM562091.1
✓	Pluteus fenzlii voucher F1020647 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, comp...	Pluteus fenzlii	1138	1138	94%	0.0	99.84%	619	HM562111.1
✓	Pluteus fenzlii voucher BRNM:766999 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 a...	Pluteus fenzlii	867	867	71%	0.0	99.79%	483	MF356571.1
✓	Pluteus fenzlii voucher LIP:GC 03091403 18S ribosomal RNA gene, partial sequence; internal transcribed spacer ...	Pluteus fenzlii	1201	1201	100%	0.0	99.70%	688	MF356566.1
✓	Pluteus fenzlii voucher BRNM:767000 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5...	Pluteus fenzlii	1201	1201	100%	0.0	99.70%	688	MF356560.1
✓	Pluteus fenzlii voucher L.Albert AL 15/133 18S ribosomal RNA gene, partial sequence; internal transcribed spacer ...	Pluteus fenzlii	1201	1201	100%	0.0	99.70%	688	MF356559.1
✓	Pluteus fenzlii voucher LE 246083 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S...	Pluteus fenzlii	1201	1201	100%	0.0	99.70%	840	FJ774082.1
✓	Pluteus fenzlii voucher PRM:888602 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8...	Pluteus fenzlii	1201	1201	100%	0.0	99.70%	688	MF356563.1
✓	Pluteus fenzlii voucher PSG 587 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ri...	Pluteus fenzlii	1201	1201	100%	0.0	99.70%	688	MF356564.1
✓	Pluteus fenzlii voucher BRNM:788131 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5...	Pluteus fenzlii	1201	1201	100%	0.0	99.70%	688	MF356561.1

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4) XC23-153 : *Pluteus fenzlii*

→ BLAST séquence *LSU*



☒ Pluteus fenzlii strain PL29 large subunit ribosomal RNA gene, partial sequence	Pluteus fenzlii	1929	1929	99%	0.0	99.90%	1286	MK278498.1
☒ Pluteus mammillatus ASM 7916 large subunit ribosomal RNA gene, partial sequence	Pluteus mammill...	1941	1941	100%	0.0	99.81%	1220	DQ451549.1
☒ Pluteus ephebeus strain PL36 large subunit ribosomal RNA gene, partial sequence	Pluteus ephebeus	1829	1829	99%	0.0	98.19%	1286	MK278497.1
☒ Pluteus tomentosulus voucher QHU20130 large subunit ribosomal RNA gene, partial sequence	Pluteus tomentos...	1834	1834	100%	0.0	98.01%	1396	OM942706.1
☒ Pluteus aff. diettrichii strain G0697 large subunit ribosomal RNA gene, partial sequence	Pluteus aff. diettri...	1773	1773	96%	0.0	97.95%	1262	MK278495.1
☒ Pluteus multiformis strain oka109 large subunit ribosomal RNA gene, partial sequence	Pluteus multiformis	1812	1812	99%	0.0	97.90%	1218	MT982429.1
☒ Pluteus cinereofuscus strain PL33 large subunit ribosomal RNA gene, partial sequence	Pluteus cinereofu...	1810	1810	99%	0.0	97.90%	1284	MK278491.1
☒ Pluteus eludens strain PL45 large subunit ribosomal RNA gene, partial sequence	Pluteus eludens	1810	1810	99%	0.0	97.90%	1284	MK278496.1
☒ Pluteus multiformis strain PL40 large subunit ribosomal RNA gene, partial sequence	Pluteus multiformis	1807	1807	98%	0.0	97.90%	1283	MK278503.1
☒ Pluteus multiformis strain oka110 large subunit ribosomal RNA gene, partial sequence	Pluteus multiformis	1805	1805	98%	0.0	97.89%	1159	MT982430.1

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5) XC23-205 : *Clitopilus nevillei*

→ BLAST séquence *ITS*



✓	Clitopilus pinsitus culture CBS:401.79 strain CBS 401.79 internal transcribed spacer 1, partial sequence; 5.8S ribo...	Clitopilus pinsitus	1136	1136	100%	0.0	100.00%	642	MH861223.1
✓	Clitopilus pinsitus strain CBS 401.79 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene an...	Clitopilus pinsitus	1086	1086	95%	0.0	100.00%	615	FJ770387.1
✓	Clitopilus hobsonii voucher K (M) 167650 small subunit ribosomal RNA gene, partial sequence; internal transcribe...	Clitopilus hobsonii	1083	1083	95%	0.0	100.00%	629	MN855371.1
✓	Clitopilus hobsonii K(M) 122842 ITS region; from TYPE material	Clitopilus hobsonii	1077	1077	95%	0.0	99.83%	629	NR_182819
✓	Clitopilus hobsonii voucher K (M) 199928 small subunit ribosomal RNA gene, partial sequence; internal transcribe...	Clitopilus hobsonii	1077	1077	95%	0.0	99.83%	629	MN855373.1
✓	Clitopilus hobsonii voucher K(M) 122842 small subunit ribosomal RNA gene, partial sequence; internal transcribed...	Clitopilus hobsonii	1077	1077	95%	0.0	99.83%	629	MN855372.1
✓	Clitopilus hobsonii strain CBS 269.36 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5...	Clitopilus hobsonii	1127	1127	100%	0.0	99.67%	646	FJ770395.1
✓	Clitopilus hobsonii voucher K (M) 189044 small subunit ribosomal RNA gene, partial sequence; internal transcribe...	Clitopilus hobsonii	1072	1072	95%	0.0	99.66%	630	MN855374.1
✓	Clitopilus sp. voucher MushroomObserver.org/395797 internal transcribed spacer 1, partial sequence; 5.8S riboso...	Clitopilus sp.	1055	1055	95%	0.0	98.98%	606	MZ914514.1
✓	Clitopilus sp. 'CA02' voucher HAY-F-005312 small subunit ribosomal RNA gene, partial sequence; internal transcri...	Clitopilus sp. 'CA...	1098	1098	100%	0.0	98.86%	670	OR681900.1
✓	Clitopilus sp. 'CA02' voucher HAY-F-002890 small subunit ribosomal RNA gene, partial sequence; internal transcri...	Clitopilus sp. 'CA...	1098	1098	100%	0.0	98.86%	665	PP407442.1
✓	Clitopilus hobsonii isolate internal transcribed spacer internal transcribed spacer 1, partial sequence; 5.8S ribosom...	Clitopilus hobsonii	1035	1035	94%	0.0	98.80%	595	MT032481.1

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5) XC23-205 : *Clitopilus nevillei*

→ BLAST séquence *LSU*



✓ Clitopilus sp. TB8024 28S ribosomal RNA gene, partial sequence	Clitopilus sp. TB...	1613	1613	87%	0.0	99.11%	917	GU384613.1
✓ Clitopilus hobsonii strain QYL-10 large subunit ribosomal RNA gene, partial sequence	Clitopilus hobsonii	1555	1555	85%	0.0	98.85%	872	OK655769.1
✓ Uncultured Basidiomycota clone C31_D07 18S ribosomal RNA gene, partial sequence; internal transcribed sp...	uncultured Basid...	1520	1520	83%	0.0	98.83%	1681	EU490059.1
✓ Clitopilus prunulus voucher GLM 45889 28S large subunit ribosomal RNA gene, partial sequence	Clitopilus prunulus	1820	1820	99%	0.0	98.82%	1078	AY207161.1
✓ Clitopilus cretoalbus LAH 35709 28S rRNA gene, partial sequence; from TYPE material	Clitopilus cretoa...	1615	1615	88%	0.0	98.79%	924	NG_228950.1
✓ Clitopilus cretoalbus voucher LAH37017 large subunit ribosomal RNA gene, partial sequence	Clitopilus cretoa...	1581	1581	86%	0.0	98.76%	895	OM934826.1
✓ Clitopilus hobsonii strain NL-19 large subunit ribosomal RNA gene, partial sequence	Clitopilus hobsonii	1550	1550	85%	0.0	98.74%	872	OK655770.1
✓ Clitopilus prunulus strain TB8229 28S ribosomal RNA gene, partial sequence	Clitopilus prunulus	1762	1762	96%	0.0	98.69%	1292	GU384615.1
✓ Clitopilus sp. voucher KUN-HKAS 117632 (WXH8007) large subunit ribosomal RNA gene, partial sequence	Clitopilus highla...	1576	1576	86%	0.0	98.65%	955	ON999062.1
✓ Clitopilus abprunulus voucher KUN-HKAS 107042 (JSP665) large subunit ribosomal RNA gene, partial sequen...	Clitopilus abprun...	1565	1565	86%	0.0	98.64%	887	MT345052.1
✓ Clitopilus sp. VHAs07/02 28S ribosomal RNA gene, partial sequence	Clitopilus sp. VH...	1816	1816	100%	0.0	98.64%	1058	EF421092.1

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5) XC23-205 : *Clitopilus nevillei*

→ Séquence de *C. nevillei* sur GenBank?



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clitopilus[All Fields]) AND
nevillei[All Fields]

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clitopilus nevillei (0) Nucleotide

clitopilus nevillei (1569) Nucleotide

Hygrocybe marchii voucher RBG Kew
K(M)14907 small subunit ribosomal Nucleotide

Hygrocybe marchii (4) Nucleotide

Entoloma araneosum (9) Nucleotide