



Manaaki Whenua
Landcare Research

10 Years of Barcoding NZ Basidios

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With substantial sequencing support from Duckchul Park

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The need to know our species

- We need an inventory of what species we have – for many reasons
- We need scientifically robust protocols for identifying (fungal) species - for many reasons
 - biosecurity, conservation, human health, environmental health, public understanding ...
- Biosecurity Act 1993: (44) *“Every person is under a duty to inform the Ministry, as soon as practicable in the circumstances, of the presence of what appears to be an organism not normally seen or otherwise detected in New Zealand”.*
- ... but how do we know what is *not normally seen or otherwise detected* if we don't know what we already have?



'Species' & the sequencing revolution – starting 90's/00's

- We saw a shift from fungal species definitions based on morphology alone, to those underpinned by phylogenetic data – with dramatic consequences
- Phylogenetic species have narrow natural regional distributions – rarely global
- Biogeographic patterns of morphologically cryptic taxa – species complexes
- Old morphological 'species' hiding unrelated cryptic phylogenetic species
- Old guesses at evolutionary relationships sometimes right, often wildly wrong
- The revolution continues



We have several unrelated purple pouches

Cortinarius porphyroides



C. violaceovolvatus



C. diaphorus



C. Sp. (PDD 70825)



C. minorisporus



C. violaceocystidiatus



C. purpureocapitatus



Thaxterogaster coneae



- Most of these historically called *Cortinarius porphyroideus*
- Some new species indistinguishable in the field
- All are unrelated to each other



'Coprionellus disseminatus' Species Complex (section disseminati)



New Zealand
Asia

S. America,
Asia

Europe

North America

C. sp. 'Mt Lyford'



Indigenous

C. sp. 'Huntsbury'



Introduced

C. sp.



Indigenous

C. disseminatus!



Introduced

C. disseminatus aff.



Introduced



The new 'species' paradigm – advantages

- Species discovery through sequencing is efficient, does not require extreme taxonomic expertise, and can be 'scaled up' to include contributions from many people
- Species definitions underpinned by phylogenetic data are much more robust & scientifically supportable than those based only on morphology
- They deliver the scientific precision needed to support biosecurity, conservation and biodiversity management policies
- They support new eDNA approaches to fungal ecology, surveys, surveillance & monitoring
- But ...



The new 'species' paradigm – disadvantages

- But ...
- Scientifically robust, phylogenetically-based species definitions often make it difficult/impossible for non-experts to identify species
 - It is not helpful to continually say "*you can't use that name anymore because it's not really in NZ*", or "*There are multiple species involved and you can't use that name without ... a microscope ... a sequencer ...*"
 - Without significant public/naturalists engagement in collecting/identifying fungi we can never hope to know what we have, or understand, appreciate, and protect our fungal diversity
 - We need to find new incentives for engagement and new ways of communicating benefits



The new paradigm - consequences for taxonomic research

- Old names need to be linked unequivocally to modern sequenced collections
- Old collections need reviewing & confirming
 - older collections have limited value for phylogenetics
 - significant new investment needed to unlock their potential
- We need multiple, recent, well documented, photographed collections with sequence data
 - we need you (with a collecting permit)!
- Not sensible to survey/revise one group at a time and then move to the next
 - That is not an efficient use of time or collecting opportunities
- The biggest and most popular fungi are often the poorest known
- The Agaricales ... is by far the largest NZ fungal order – 1500 species



10 years of strategic barcoding – and what have we found?

The Agaricales

- Barcoding allows to 'test' if we got identifications correct & find undescribed species
- It allows us to assess (roughly) if something is indigenous or introduced

Species named/detected so far in NZ	1507	
Indigenous/endemic	1123	75%
Exotic	187	12%
Not sure	197	13%



10 years of strategic barcoding – and what have we learnt?

- Relatively recent collections were targeted for sequencing:
 - Type collections for the 'gold standard' species barcode
 - Collections identified by experienced mycologists for 'silver standard' barcodes
 - Remaining missing species regardless of identifier
 - Interesting looking collections not identified to species

# PDD colls sequenced	1464	
# Types sequenced	193	
Undetermined colls named to species	276	
Existing identification incorrect	446 of 995	47%!



10 years of strategic barcoding – and what have we learnt?

- Many older species concepts (descriptions, keys) do not work under a phylogenetic-based species concept.
 - A substantial level (50%) of historical misidentification using older resources
 - Older resources need reviewing and revising, and sometimes abandoning totally
- We have lots of related and unrelated cryptic species hiding under broadly applied older names
- Heaps of undescribed species
 - If they turn up multiple times from different locations they get a 'tag name'
- Over time we have targeted groups/species with problems
 - And the fungal foray has contributed significantly to that targeted effort



10 years of strategic barcoding – and what have we found?

Species name status	#	%	
Barcoded (described + tagged)	1237	82%	
Undescribed (but given a barcode tag name)	320	21%	Undescribed tagged species are 35% of total
Barcoded exotics	166	89%	of all known exotics
Undescribed sequence singletons (no tag name – just genus/family name)	750		917 described species versus 1070 undescribed species. 54% of collections undescribed!

- More than half of sequenced collections represent undescribed species
- 82% of our 'known/described' Agarics are now barcoded
 - probably more than any country of comparable size & a significant achievement
- But ... we have a residual 262 described species we know are present & with no reference barcode
 - Why not?



18% of described species are without a barcode after 10 years?

- Here's where most unbarcoded species are hiding ...

	# Not barcoded	% Not barcoded	# Spp in family	
Clavariaceae (Petersen)	22	34%	65	
Crepidotaceae (Horak)	11	30%	37	
Entolomataceae (Horak)	34	30%	114	80 Horak, 34 more added subsequently (Au:Gates & Noordeloos + exotics)
Inocybaceae (Horak)	16	23%	69	39 Horak, 30 more added subsequently (Au:Matheney & Bougher + exotics)
Tubariaceae (Horak)	8	35%	23	
Cortinariaceae (Soop et al)	7	3%	243	A modern, sequence-based approach. Minority missing are old Horak names



Why are these old (and not so old) revisions a problem

	Represented by 0 or 1 collection in PDD	
Clavariaceae	12	55%
Crepidotaceae	7	64%
Entolomataceae	10	29%
Inocybaceae	10	63%
Tubariaceae	7	88%

- The remaining gap is dominated by names described from 1 or 2 collections
 - Genuinely rare?
 - They aren't easily identified from existing descriptions
 - They have been so broadly misidentified the real version is 'lost in the crowd'
 - They may have been aberrant collections of other named species
 - Old types (1970s, 1980s) are very difficult/expensive to sequence to resolve issues
- We should probably forget most of them as 'nomen confusum' and move on



Agarics – pretty good – what about the rest?

Order	Total present, or might be	% NZ barcoded	labelled 'indigenous' but type not Australasian
Agaricales	1507	82%	2 species from Raoul Island!
Polyporales	226	31%	58%
Russulales	161	62%	27%
Boletales	95	82%	8%
Cantharellales	56	39%	30%
Gomphales	36	81%	14%

- For the agarics we now know the majority of indigenous species are only found in Australasia
 - Just 2 definite indigenous species were described from elsewhere and both collected on Raoul Island
- Bracket fungi (polypores etc) need much more attention
 - Note that 58% of 'indigenous' brackets were described elsewhere
 - Many will be different, regional cryptic species – but the barcoding/taxonomy needs doing



Barcoding Agarics – the summary

- Basing revisions on collections by one individual will massively underestimate the true fungal diversity
 - It needs all of us, professional and non-professional, and across the country, to contribute
- Basing new species descriptions on morphology alone is error prone
 - And naming species based on 1 or 2 collections is a really bad idea
- Species described outside Australasia are usually not indigenous to New Zealand
 - And many groups of fungi have this legacy of imprecision
- Finally, we have a good basis for revising (some) Agaric groups to include most/all common species
- Currently 54% of sequence detected species are undescribed
 - That will be a significant underestimate
- Phylogenetic species concepts have changed our understanding significantly
 - But they have the potential to disenfranchise an important community who can no longer identify many cryptic species



The (political) message

- Older collections are important, but a lot of expensive work is needed to unlock their potential
 - The real journey has only just begun & it needs modern collections
- Public good research of this kind no longer appears on any official agendas for future funding, and that is alarming and depressing
- 'Applied' taxonomic research should NOT be the only NZ funding priority in this area
 - That view is short-sighted and ultimately counter-productive
- We need to engage the public and take them on the journey of exploration and understanding NZ's unique Biota
- If we don't then government policies around biosecurity, conservation, environmental protection, sustainability all become opaque to the general public, misunderstood, unsupported, unenforceable & irrelevant
 - Environmental attrition will continue. Key ecosystem functions founded on fungal diversity will degrade, and we will lose unique & largely hidden diversity

Thank you!

