

A preliminary molecular phylogeny of *Apogon* and related genera

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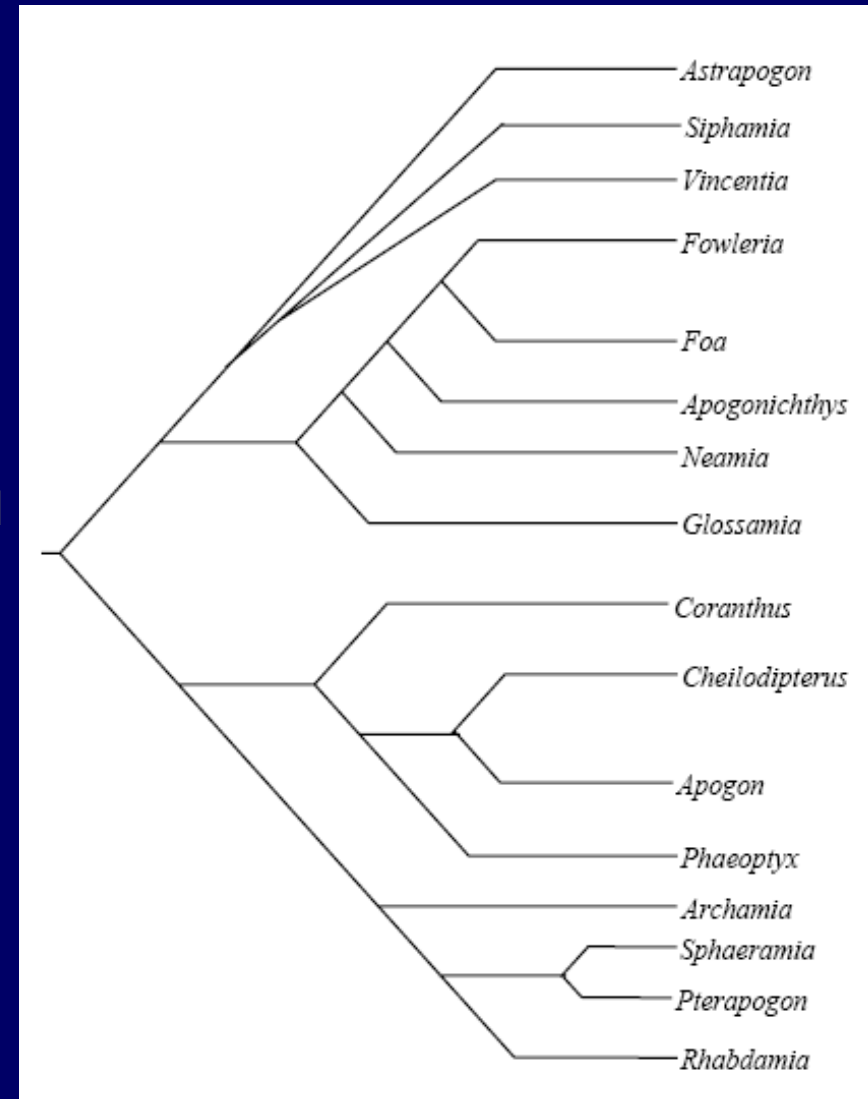
Introduction

- Apogonidae (cardinalfishes) small, carnivorous fish
- Predominantly coral reef
- Deep ocean, estuarine and freshwater species
- Current taxonomy:
 - Two families (Apogoninae and Pseudaminae)
 - 23 Genera
 - > 250 Species
- 8th Most speciose perciform family
- One of the largest coral reef families
- Highest diversity in Indo-Pacific
- Systematic relationships poorly understood
- Little known of evolutionary history of this group



Introduction: Fraser (1972)

- First comprehensive study Apogonidae
- Osteology and morphology
- Families, genera and subgenera
- Generic level relationships in *Apogon*
- Two clusters or groups
- Progression from primitive to advanced



(Fraser, 1972; as reconstructed by Rodman Bergman, 2004)

Rodman Bergman (2004)

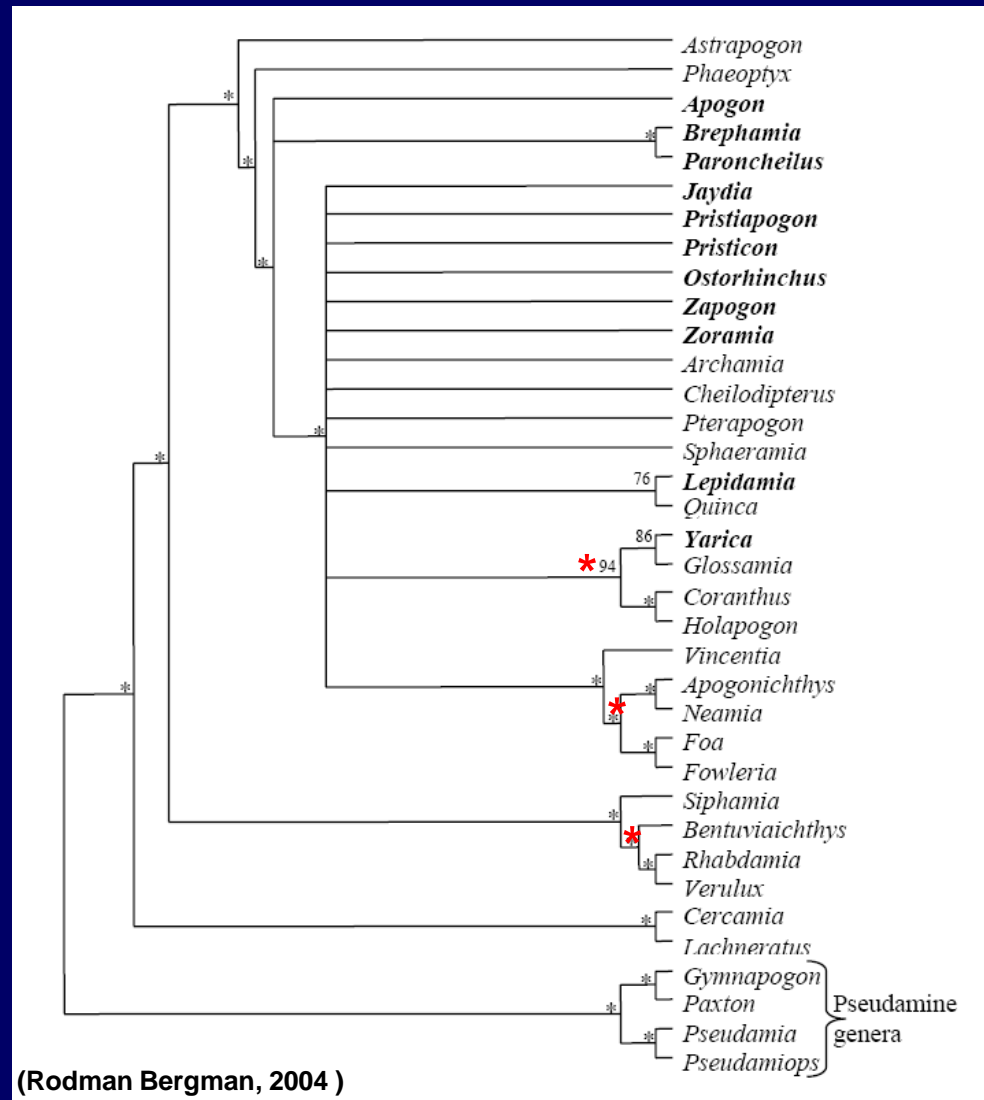
- Shortcomings of Fraser's (1972) work
- Phenetic, rather than cladistic: resulting in unnatural groupings
- Did not define synapomorphies
- Inconsistently used characters of beryciform and lower percoid fishes
- Did not determine polarity of character states, intrafamilial level

- Mosaic
- Subgenera of *Apogon* do not comply with the criteria of genus
- Defined using same (plesiomorphic) characters defining other genera

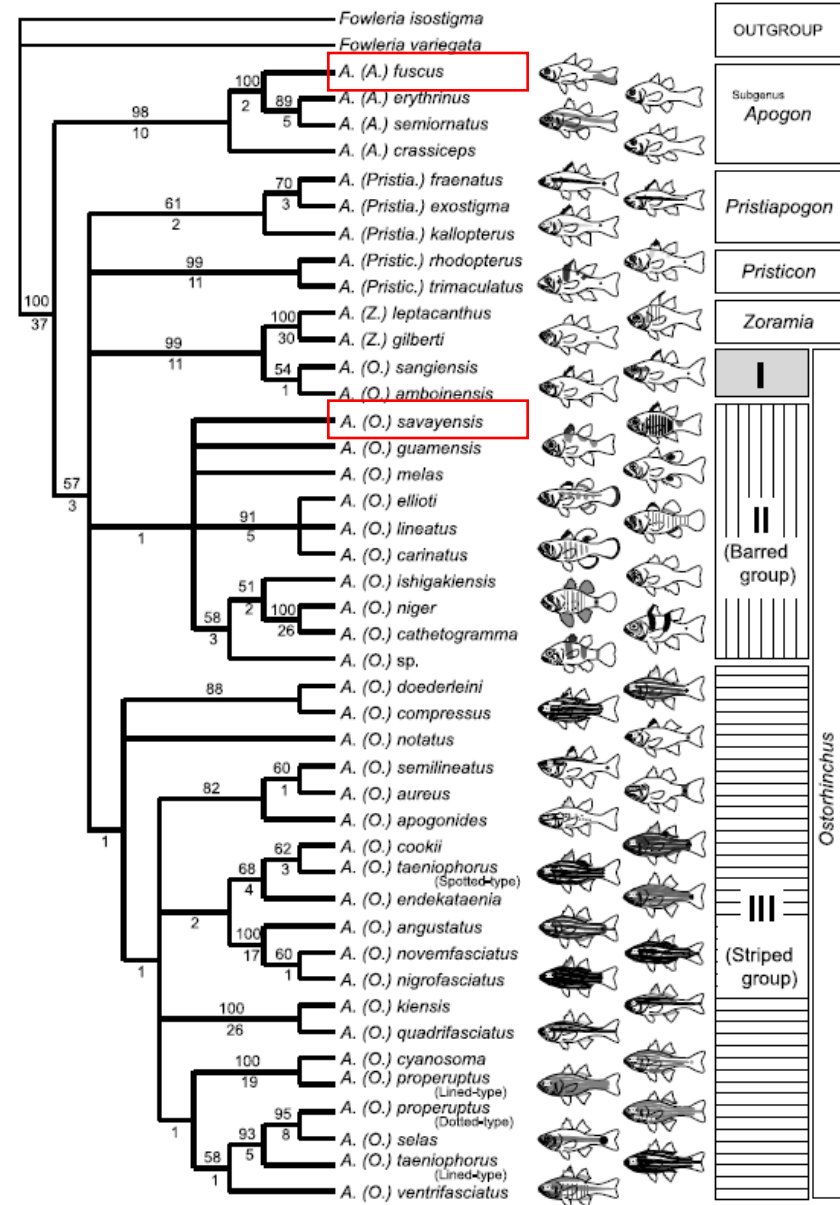
- Reanalysed Fraser's (1972) data set in a cladistic context
- *Cephalic lateralis* system addressed taxonomy and systematics
- Combined analysis to understand systematics and evolution of the group

Addition of *cephalic lateralis* characters

- Cephalic lateralis characters
- High variability
- 8 additional characters



- *Apogon*: 5 of 12 subgenera
- *Fowleria*
- Japan
- 1 500 bp mtDNA (12S – tRNA^{Val} – 16S)
- *Apogon* monophyletic
- Subgenus *Apogon*; 4 of 35 species
- Subgenus *Pristiapogon*
- Subgenus *Pristicon*
- Subgenera *Zoramia* and *Ostorhinchus*
- Two clades in subgenus *Ostorhinchus*
- Clades reflect stripe-pattern
- *Nectamia* nested within
- Clades consistent
- Relationships vary by analysis



Aims & Methodology

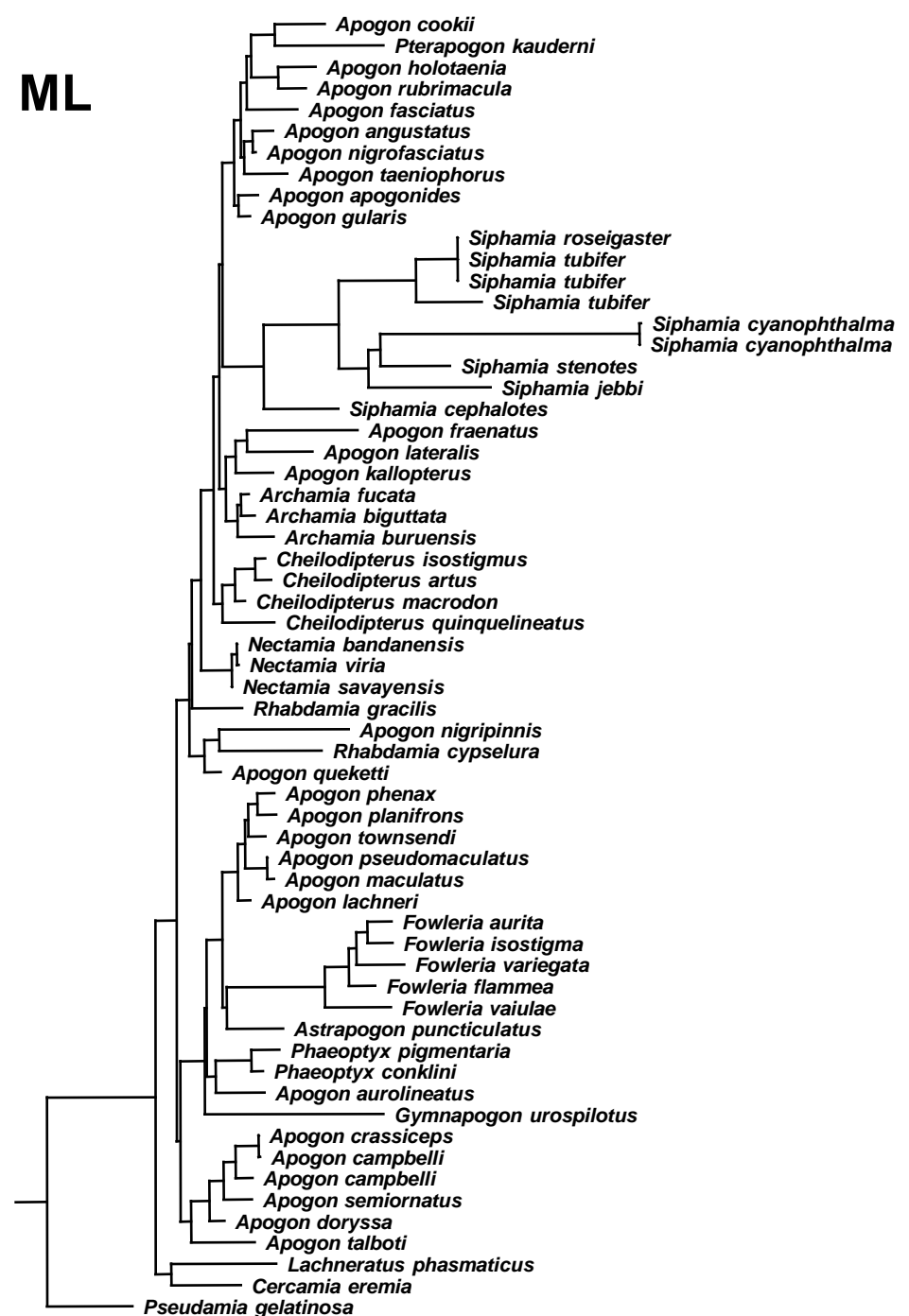
- Global phylogeny
- Relationships at all levels
- 61 Ingroup taxa, 57 species
- Samples sourced from:
 - SAIAB National Fish Collection
 - Australian Museum
 - Kansas University Museum
 - Colleagues and collaborators
- *Epigonus constanciae* (EF120867)
- *Epigonus telescopus* (EU848458)
- Sequenced partial (~ 550 bp) 16S rRNA mtDNA gene fragment

Family	Genus	Subgenus	Species	
Apogoninae	<i>Apogon</i>	<i>Apogon</i>	12	
	-	<i>Jaydia</i>	1	
	-	<i>Ostorhinchus</i>	11	
	-	<i>Pristiapogon</i>	2	
	-	<i>Archamia</i>	3	
	-	<i>Astrapogon</i>	1	
	-	<i>Cercamia</i>	1	
	-	<i>Cheilodipterus</i>	4	
	-	<i>Fowleria</i>	5	
	-	<i>Lachneratus</i>	1	
	-	<i>Nectamia</i>	3	
	-	<i>Phaeoptyx</i>	2	
	-	<i>Pterapogon</i>	<i>Pterapogon</i>	1
	-	<i>Rhabdamia</i>	<i>Rhabdamia</i>	1
-	-	<i>Verulux</i>	1	
Pseudaminae	<i>Siphamia</i>		6	
	<i>Gymnapogon</i>		1	
	<i>Pseudamia</i>		1	

- **Maximum Likelihood (ML)**
 - Optimal model chosen using ModelTest3.7, parameters implemented
 - Heuristic search, TBR-branch swapping, 10 random stepwise taxa additions
- **Bayesian inference (BI)**
 - 4 Simultaneous, independent runs
 - 4 Markov Monte Carlo chains, run for 10^7 generations, every 2 000th sampled
 - “Burn-in” of 10%, leaving 4500 samples of the posterior distribution
- **Maximum parsimony (MP)**
 - Heuristic search, TBR-branch swapping, 1 000 random stepwise taxa additions
 - Bootstrapping (1 000 replicates, each with 10 random taxon addition replicates)

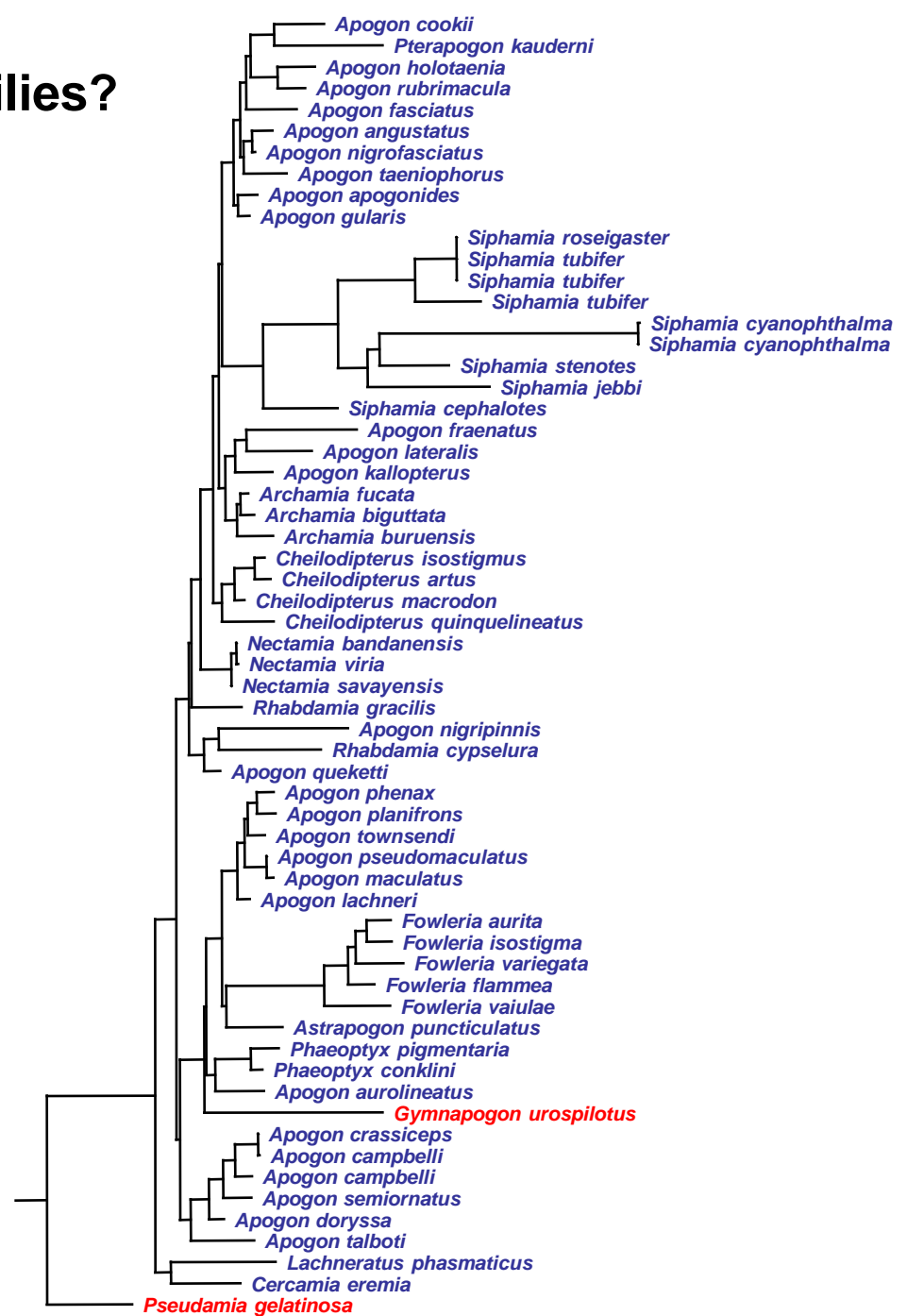
Results: ML

- 61 Ingroup taxa
- 533 bp 16S rRNA
- $-\ln L = 7\,206.150$
- GTR + I + Γ



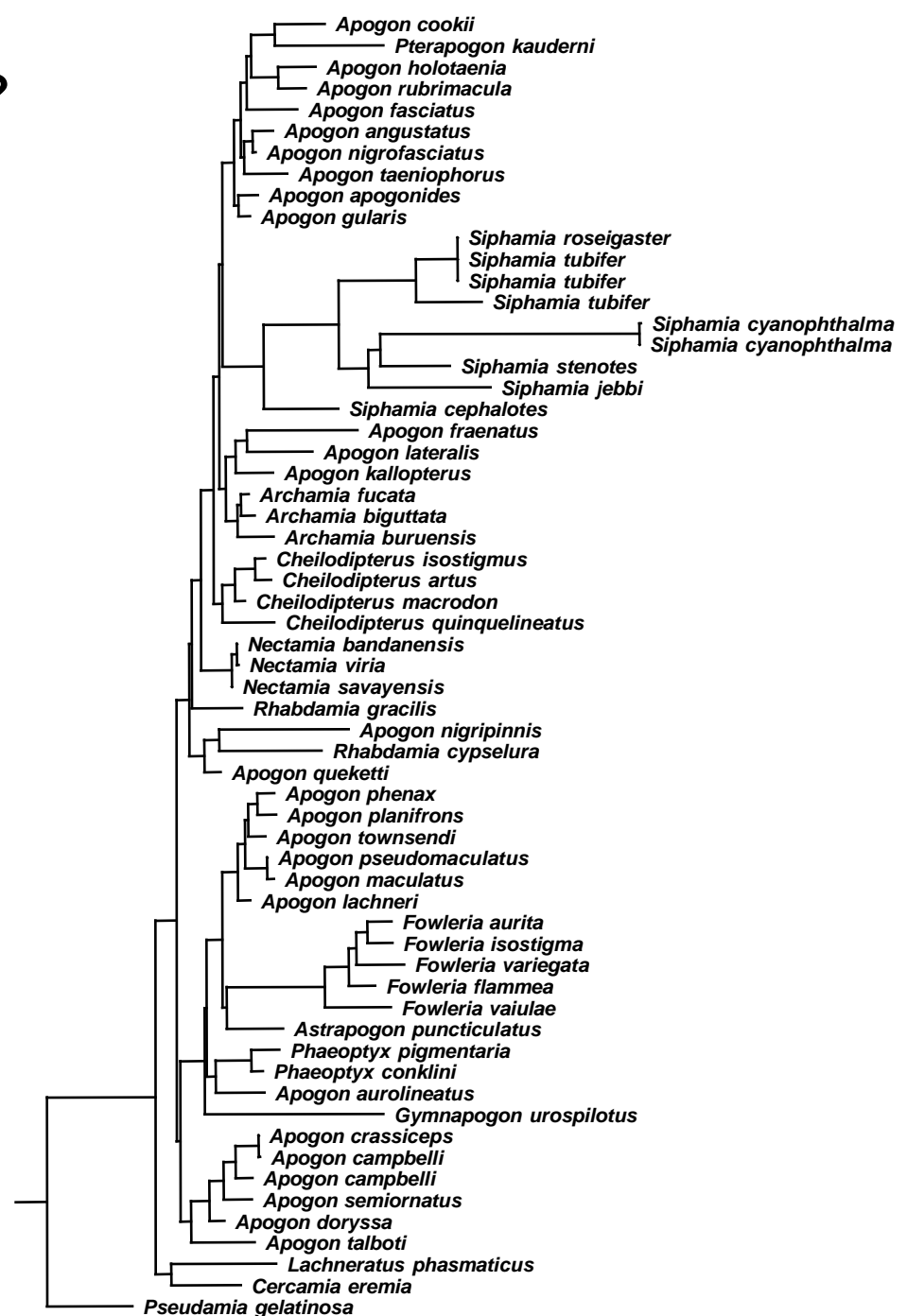
Subfamilies?

- Apogoninae
- Pseudaminae



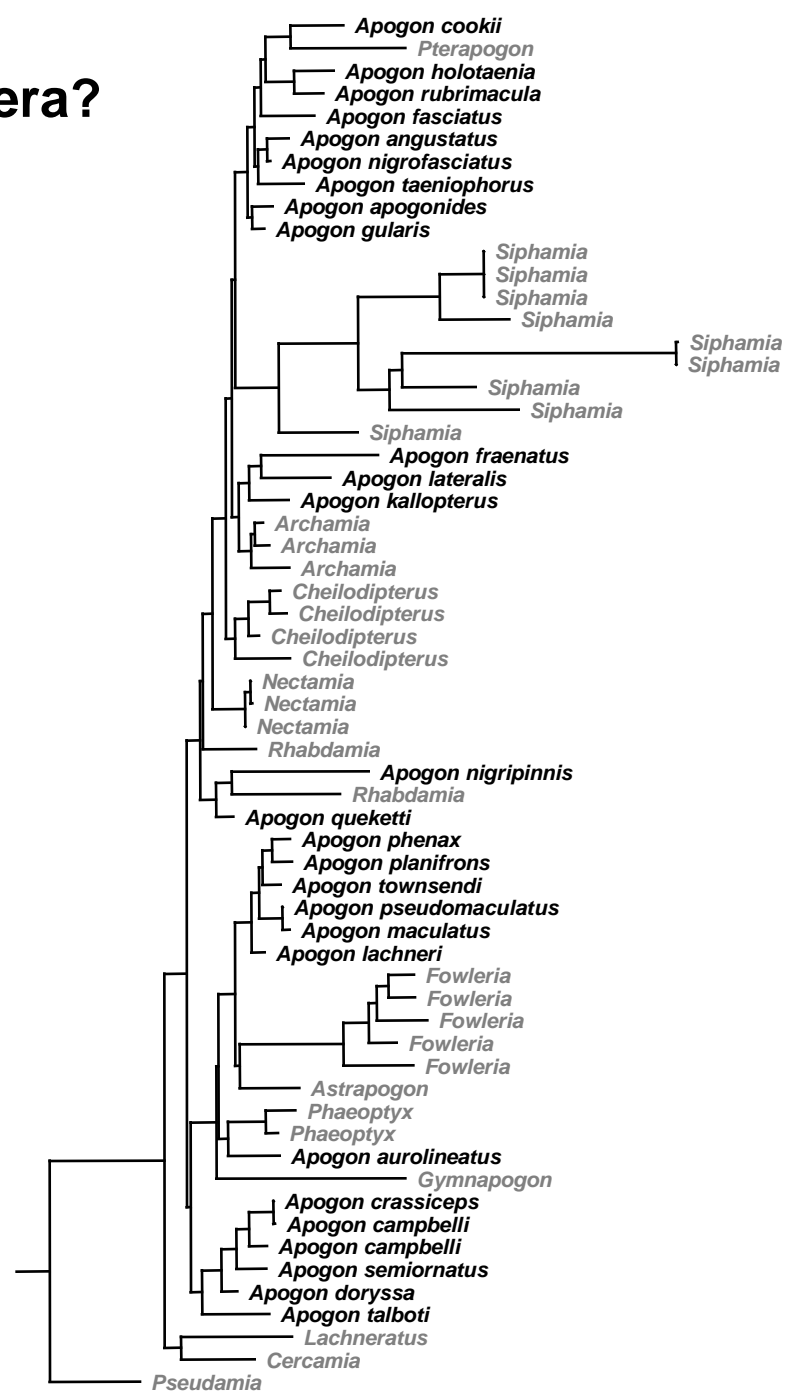
Genera?

- Monophyletic genera
- *Siphamia*
- *Archamia*
- *Cheilodipterus*
- *Nectamia*
- *Fowleria*
- *Phaeoptyx*
- Polyphyletic genera
- *Apogon*
- *Rhabdamia*



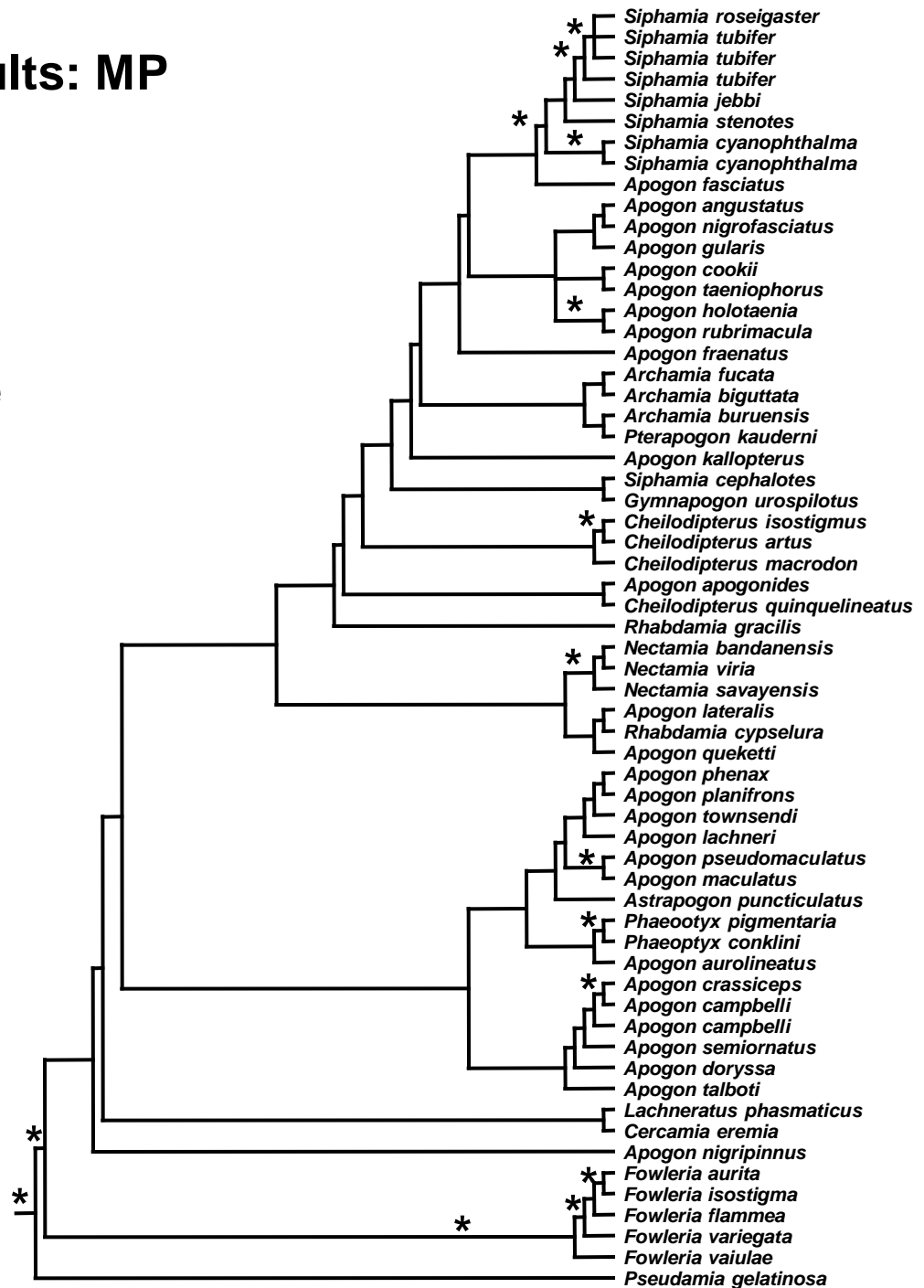
Subgenera?

- *Jaydia*
- *Ostorhinchus*
- *Pristiapogon*
- *Apogon*



Results: MP

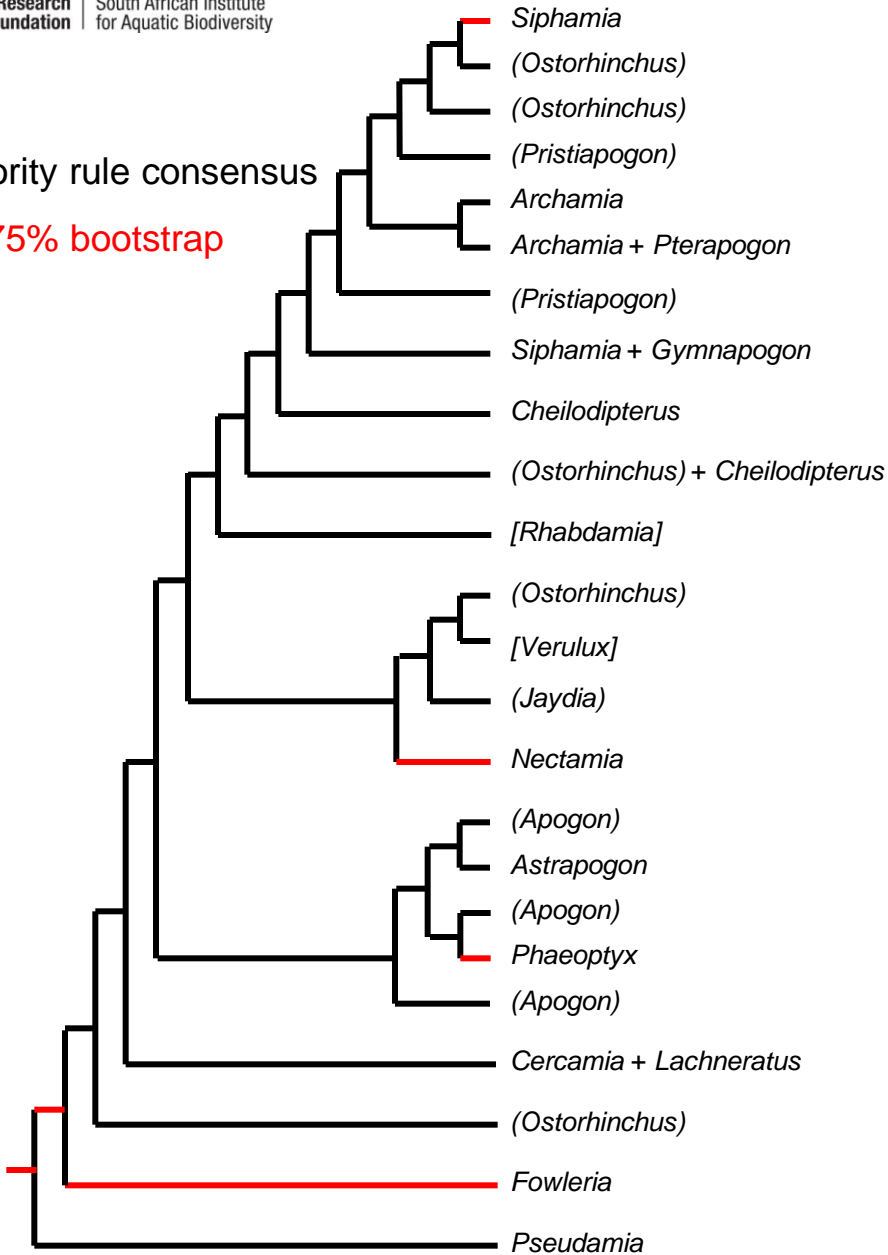
- 440 characters
- 207 variable
- 172 parsimony informative
- 66 trees of 1 026 steps
- **CI = 0.272**
- **RI = 0.592**
- Rescaled CI = 0.161
- * Bootstrap support > 75%



MP:

Majority rule consensus

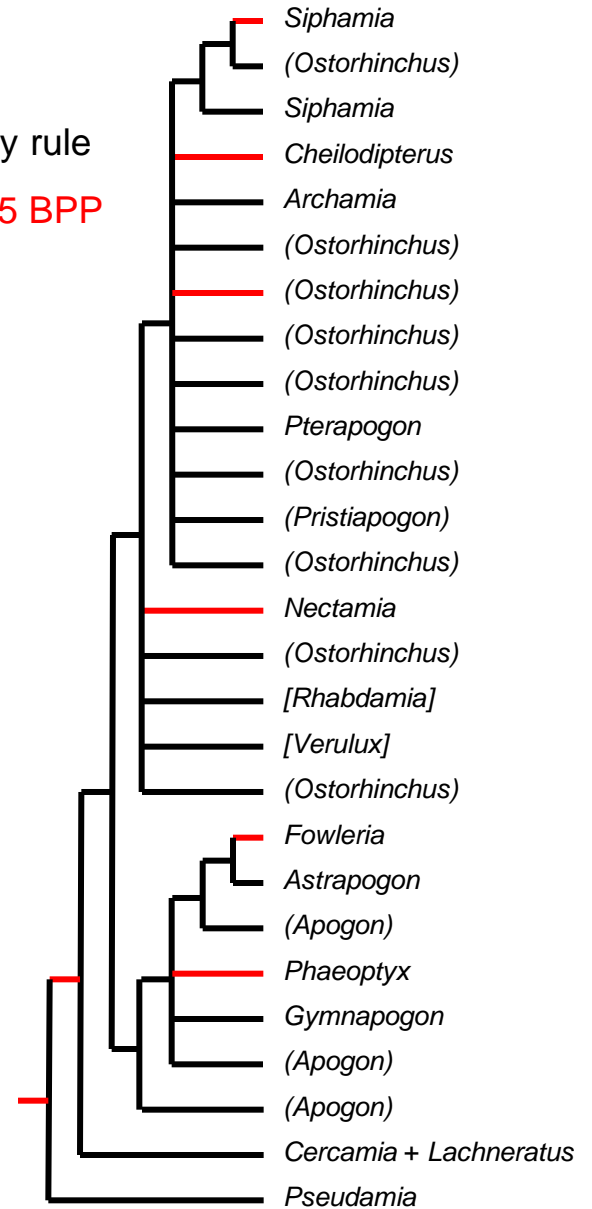
* > 75% bootstrap



BI:

Majority rule

* > 0.95 BPP



Summary

	Fraser (1972)*	Rodman Bergman (2004)	16S rRNA
Apogoninae	Monophyletic	Monophyletic	Paraphyletic
Pseudaminae	Monophyletic	Monophyletic	Polyphyletic
<i>Apogon</i> *	Polyphyletic	Polyphyletic	Polyphyletic
<i>Archamia</i>	-	-	Monophyletic
<i>Cheilodipterus</i>	-	-	Monophyletic
<i>Folweria</i>	-	-	Monophyletic
<i>Nectamia</i>	-	-	Monophyletic
<i>Phaeoptyx</i>	-	-	Monophyletic
<i>Pterapogon</i> *	Polyphyletic	Polyphyletic	-
<i>Rhabdamia</i> *	Monophyletic	Monophyletic	Paraphyletic
<i>Siphamia</i>	-	-	Monophyletic

Summary & Conclusions

- *Apogon* subgenera
 - *Apogon*: 2 or 3 lineages/groups
 1. West Atlantic clade, *Phaeoptyx* and *Astrapogon*
 2. Widespread Indo-Pacific clade
 - *Ostorhinchus*: 3 lineages
 - *Pristiapogon*: not monophyletic, 2 lineages
- Taxonomic and systematic re-evaluation at nearly all levels
- Subgenera may not be of lesser taxonomic rank than genera
- Many of the subgenera may be regarded as genera
- Subgenera themselves are not monophyletic or natural groupings
- More supraspecific units recognised
- Groups in large genera (*Cheilodipterus*, *Siphamia?*, *Fowleria?*)

- **Preliminary!**
- Alignment homologies, direct optimization (e.g., POY)
- Include additional gene regions (COI analysis underway and others)
- Missing taxa
- Pseudamine genera: *Paxton*, *Pseudamiops*
- Apogonine genera: *Apogonichthys*, *Coranthus*, *Foa*, *Glossamia*, *Holapogon*, *Neamia*, *Sphaeramia*, *Vincentia*
- Subgenera in *Apogon*: *Brephamia*, *Lepidamia*, *Paroncheilus*, *Pristicon*, *Yarica*, *Zapogon*, *Zoramia*
- Subgenus in *Pterapogon*: *Quinca*
- Subgenus in *Rhabdamia*: *Bentuviaichthys*

- Incorporate sequence alignment of Mabuchi *et al.* (2006)
- Incorporate osteological and *cephalic lateralis* system data matrices of Fraser (1972) and Rodman Bergman (2004)

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