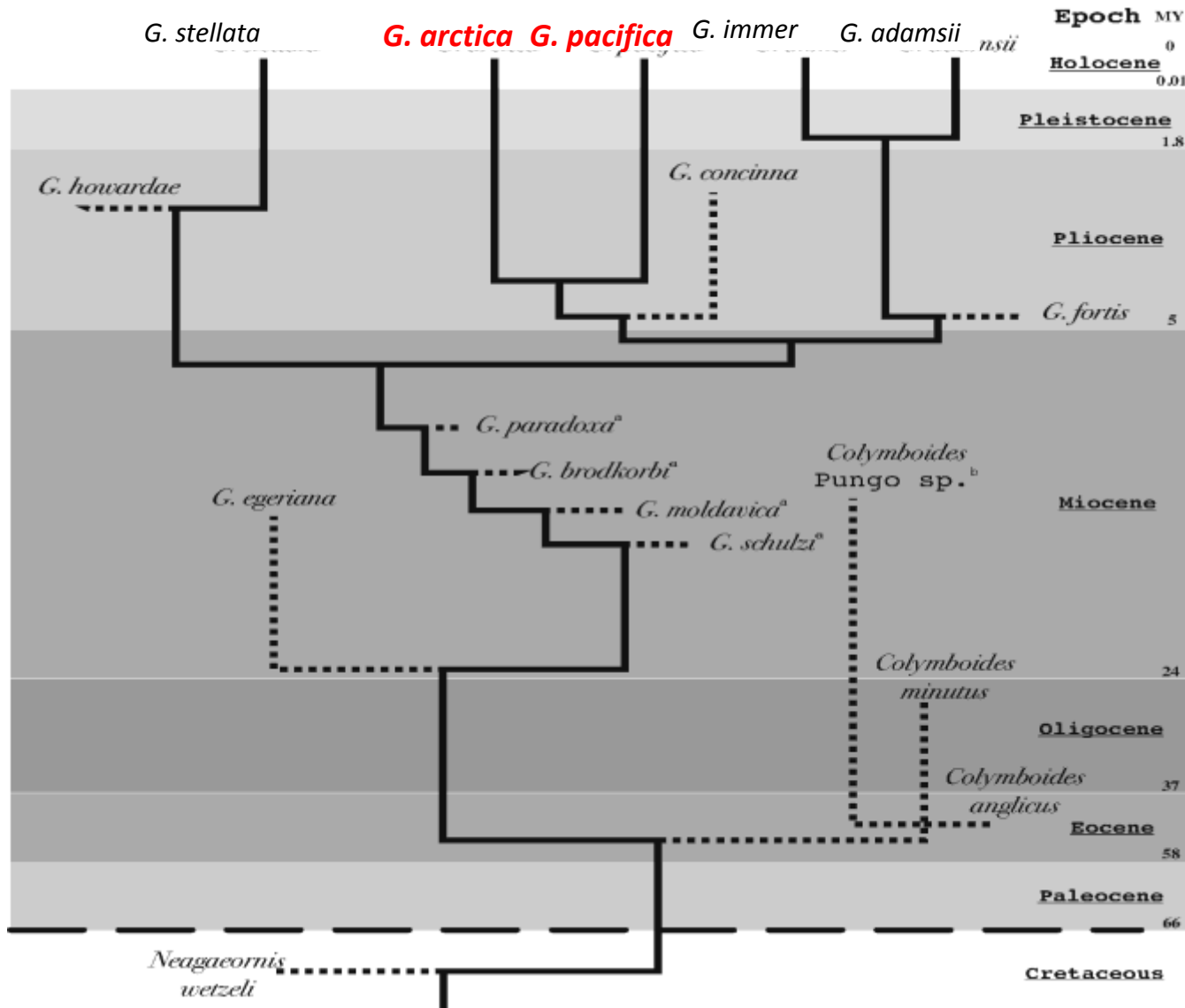


Revising the phylogeny of *Gavia* with second-generation sequencing data

Quentin Sprengelmeyer
Dr. Alec Lindsay







G. arctica



G. pacifica





Red-throated



Arctic



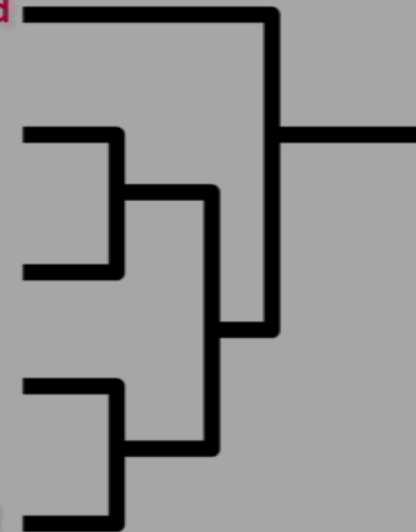
Pacific



Common



Yellow-billed



Morphology

Traditional hypothesis based on morphology and overall similarity (Storer 1978, Boertmann 1990)

DNA-based

Lindsay's (2002) hypothesis based on genetic data from ~4500bp of mitochondrial DNA and ~500bp of nuclear intron DNA



- Construct a robust phylogenetic tree of the genus *Gavia*
 - *Good sampling among taxa*
 - *Good selection of characters*
- Understand speciation and geographic events

SAMPLES



G. adamsii (7) – AK

G. immer (7) – NH, ME, AK, NY

G. pacifica (9) -AK

G. arctica (7)-Sweden, Russia

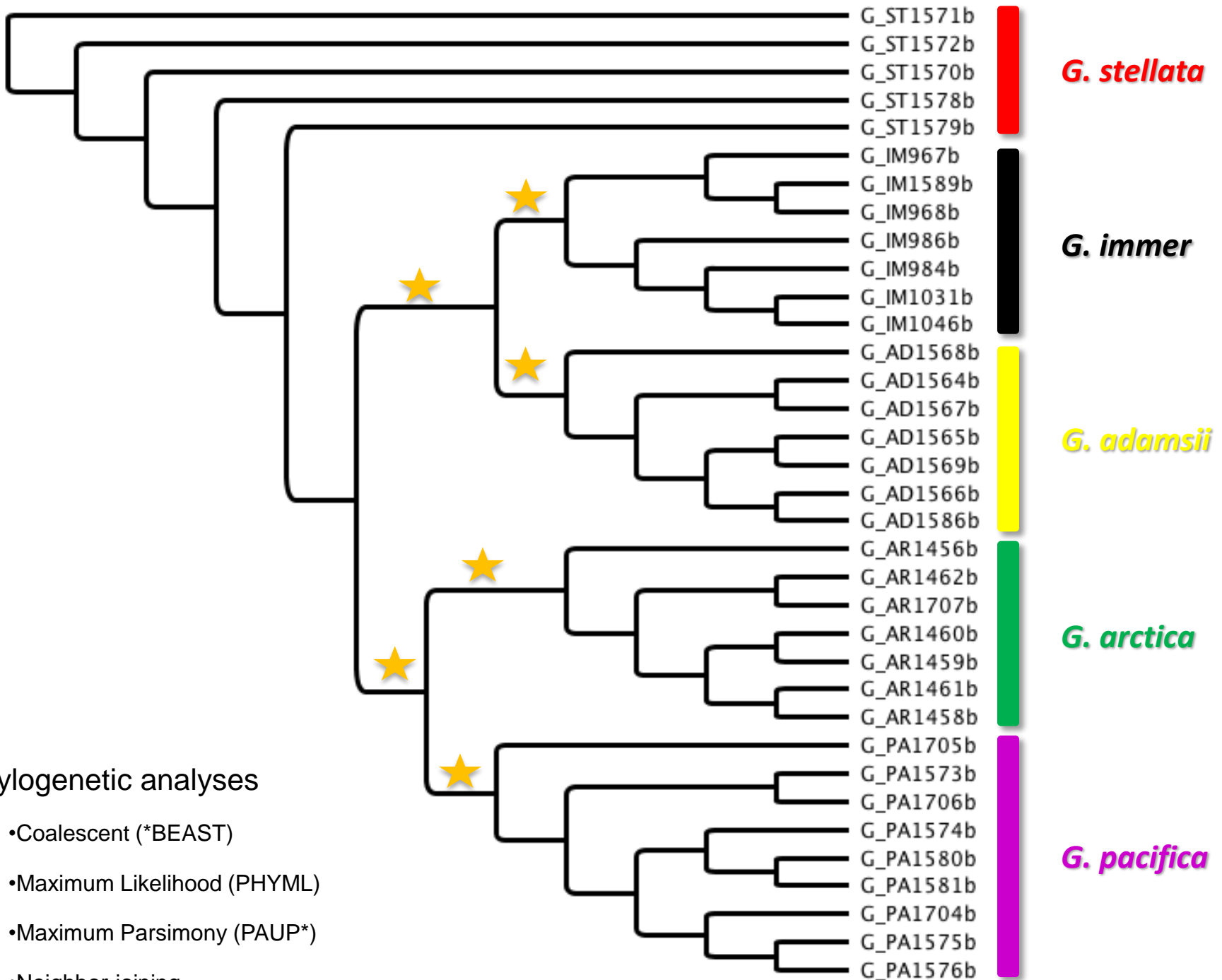
G. stellata (5)-AK

DNA Sequence Data

- Double-digest “RAD-seq” protocol
- For 35 taxa
 - 166,466 bps of data
 - 6323 informative sites, across 1750 loci
- Phylogenetic analyses
 - Coalescent (*BEAST)
 - Maximum Likelihood (PHYML)
 - Maximum Parsimony (PAUP*)
 - Neighbor-joining

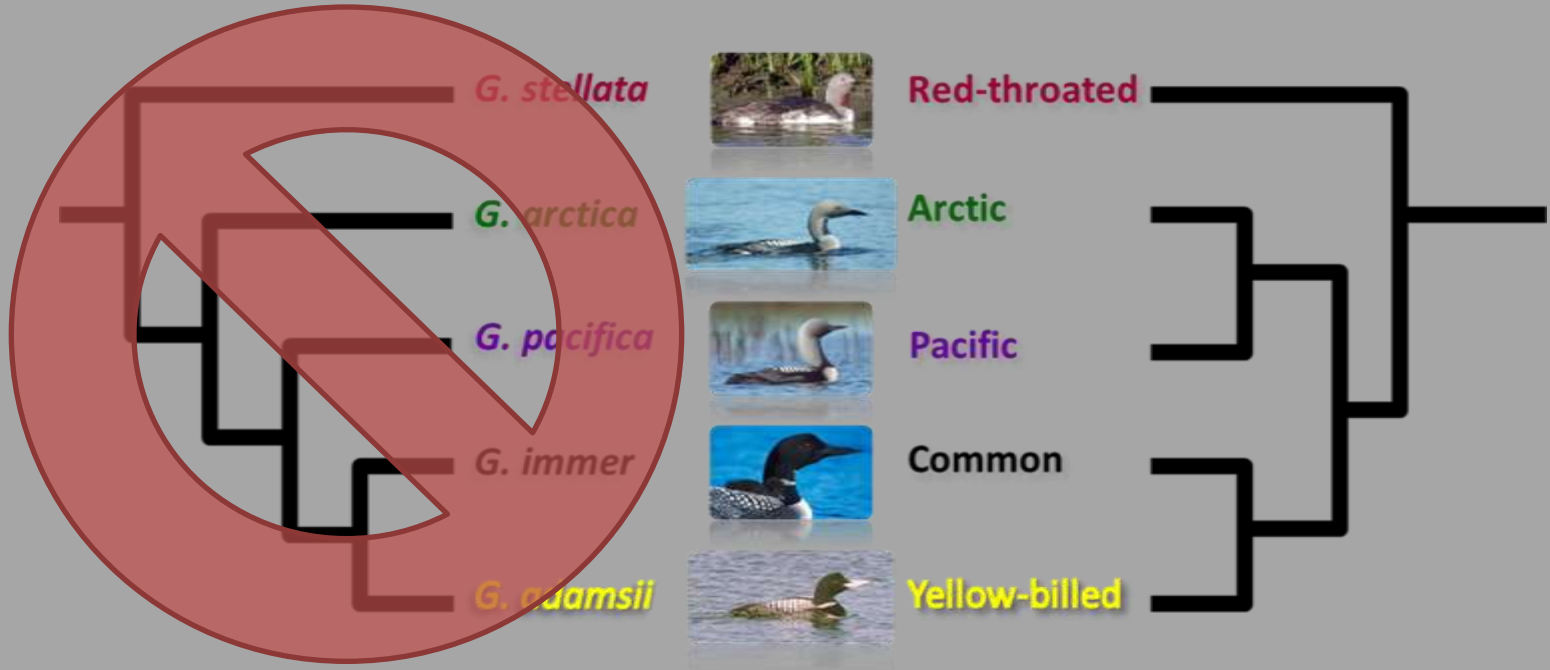
Baird et al. 2008. PLoS One
Peterson et al. 2012. PLoS One
DaCosta & Sorenson. In Review



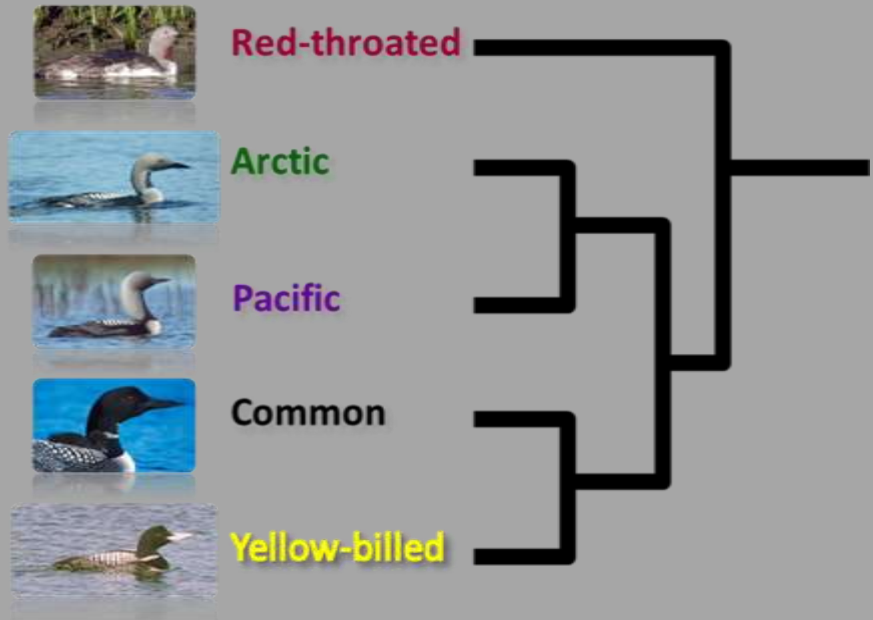


•Phylogenetic analyses

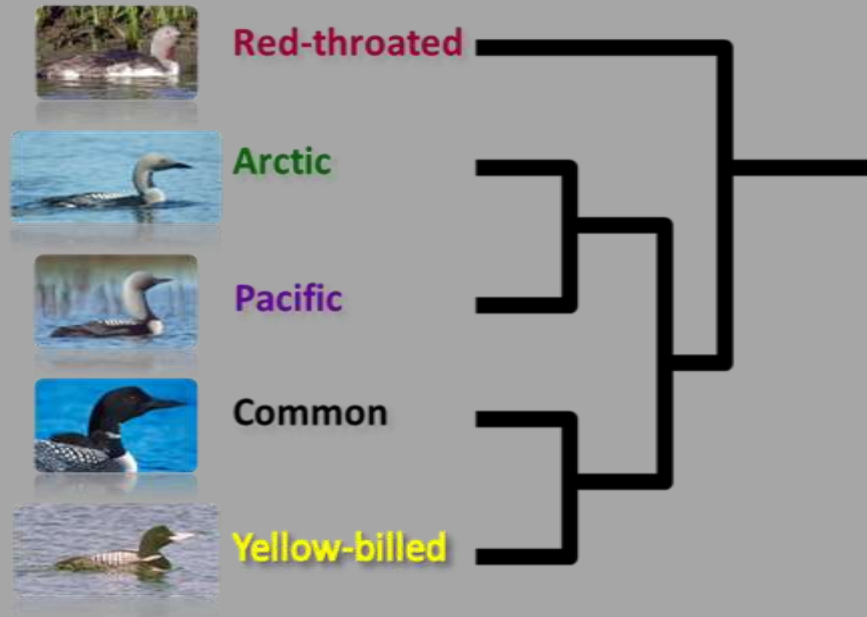
- Coalescent (*BEAST)
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- Neighbor-joining



Sorry, Lindsay 2002!

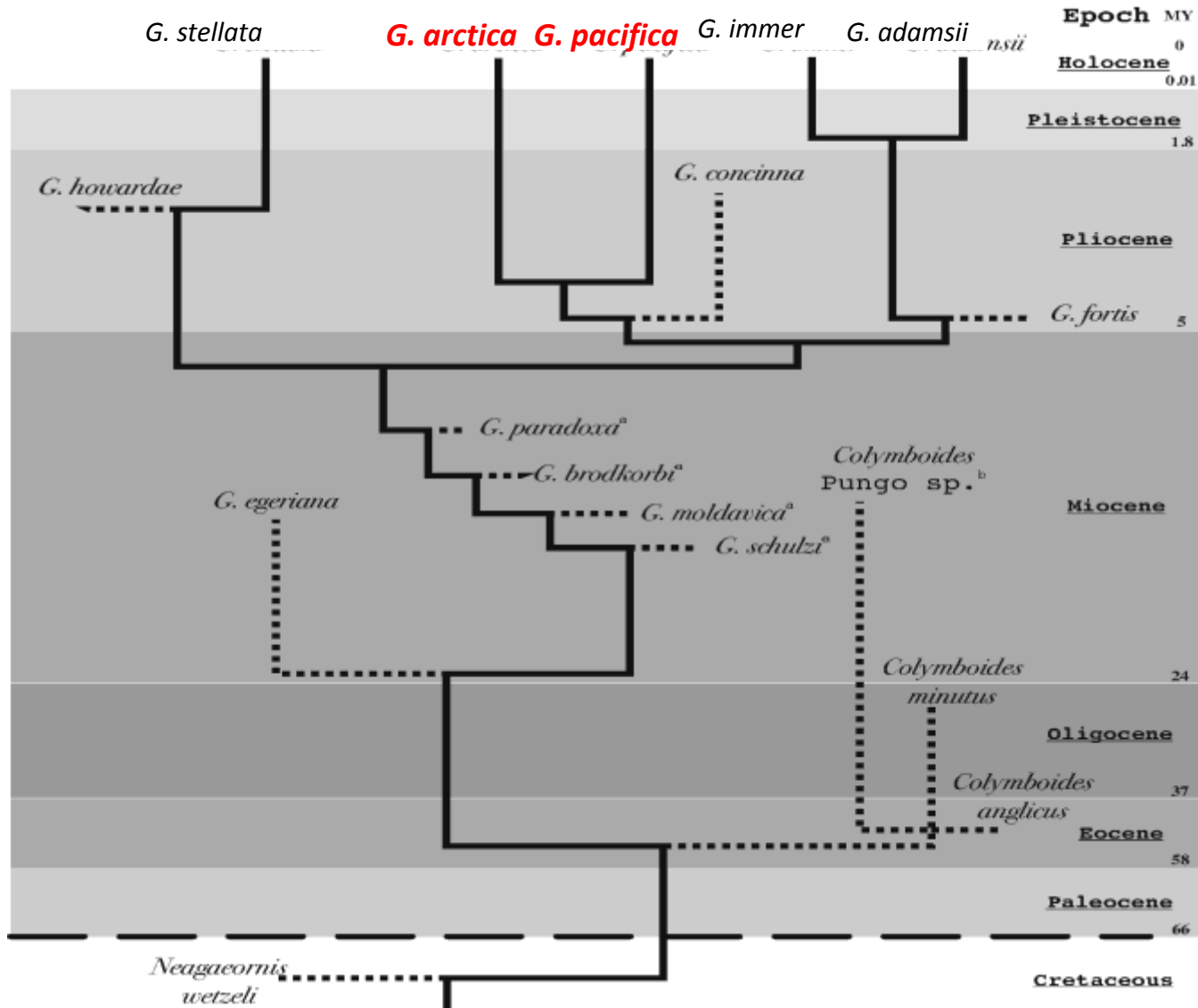


	GAST	GAAR	GAPA	GAIM	GAAD
GAST	0.22%				
GAAR	1.81%	0.35%			
GAPA	1.80%	0.48%	0.37%		
GAIM	1.83%	0.67%	0.69%	0.20%	
GAAD	1.84%	0.68%	0.70%	0.28%	0.04%



Calibrating with *G. concinna* (4.8MY for GAAR-GAPA)

	GAST	GAAR	GAPA	GAIM	GAAD
GAST					
GAAR	18.2				
GAPA	18.2	4.8			
GAIM	18.4	6.8	6.9		
GAAD	18.6	6.9	7.0	2.8	



Lindsay 2002

SUMMARY

- Strong support for traditional tree
- *G. immer* and *G. adamsii* most recent divergence
- Modern loons share a common ancestor from the early Miocene

Acknowledgements



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