

Comparisons of Papionini genomes

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E&EB 723



The players



Mandrillus



Rungwecebus

Theropithecus



Papio



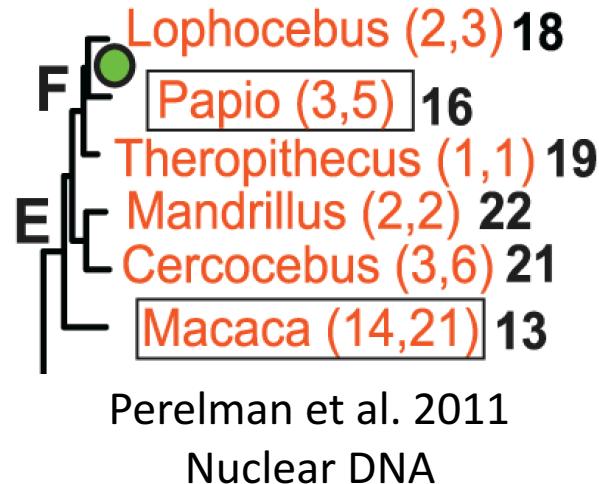
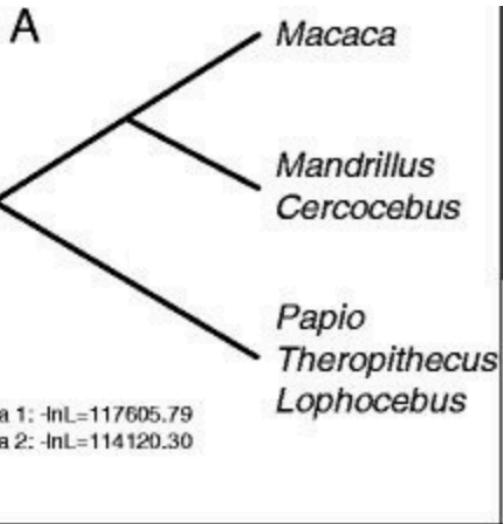
Lophocebus



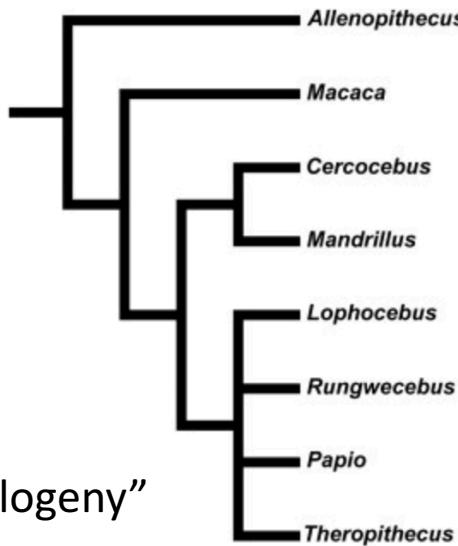
Cercocebus

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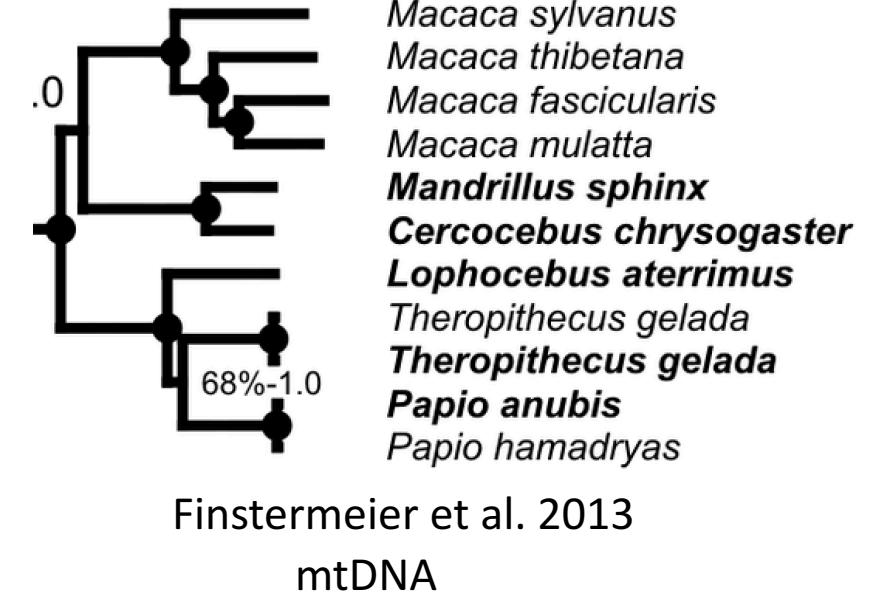
An unresolved phylogeny



Liedigk et al. 2014
mtDNA



Gilbert et al. 2011
Morphology



Project goals

- Explain why the molecular phylogeny is inconclusive
 - Quantify the genetic differences between the genera
 - Estimate evolutionary rates from divergence times
- Gain an understanding of genomic analysis software

Methods

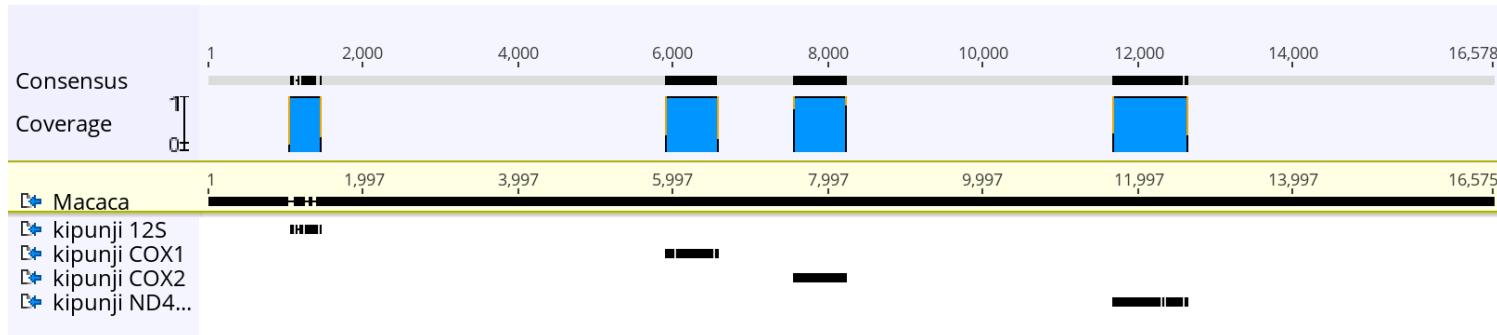
- GenBank complete mitochondrial genomes (6)
 - Rungwecebus select mitochondrial sequences (4)
- Geneious software for analysis
 - Alignment
 - Comparisons
 - Tree building
- Calculate rates with divergence time estimates from literature



MITOS

Name	Start	Stop	Strand	Length	ovl/nc	Codons	Infos
trnF(gaa)	1	72	+	72	0		svg ps
rrnS	73	1019	+	947	0		svg ps
trnV(tac)	1020	1088	+	69	0		svg ps
rrnL	1089	2650	+	1562	0		svg ps
trnL2(taa)	2651	2725	+	75	2		svg ps
nad1	2728	3684	+	957	-2	ATG/TAG	
trnI(gat)	3683	3751	+	69	-3		svg ps
trnQ(ttg)	3749	3820	-	72	1		svg ps
trnM(cat)	3822	3889	+	68	0		svg ps
nad2	3890	4928	+	1039	9	ATC/T(AA)	
trnW(tca)	4938	5004	+	67	7		svg ps
trnA(tgc)	5012	5080	-	69	1		svg ps
trnN(gtt)	5082	5154	-	73	2		svg ps
OL	5157	5186	+	30	-1		svg ps
trnC(gca)	5186	5254	-	69	-1		svg ps
trnY(gta)	5254	5319	-	66	11		svg ps
cox1	5331	6899	+	1569	-28	ATG/TAA	
trnS2(tga)	6872	6940	-	69	3		svg ps
trnD(gtc)	6944	7011	+	68	1		svg ps
cox2	7013	7696	+	684	22	ATG/TAA	
trnK(ttt)	7719	7783	+	65	1		svg ps
atp8	7785	7991	+	207	-46	ATG/TAG	
atp6	7946	8626	+	681	-1	ATG/TAA	
cox3	8626	9410	+	785	-1	ATG/TA(A)	
trnG(tcc)	9410	9477	+	68	9		svg ps
nad3	9487	9835	+	349	-12	ATA/T(AA)	
trnR(tcg)	9824	9888	+	65	0		svg ps
nad4l	9889	10185	+	297	-7	ATG/TAA	
nad4	10179	11556	+	1378	0	ATG/T(AA)	
trnH(gtg)	11557	11625	+	69	0		svg ps
trnS1(gct)	11626	11684	+	59	0		svg ps
trnL1(tag)	11685	11755	+	71	6		svg ps
nad5	11762	13567	+	1806	0	ATG/TAA	
nad6	13568	14092	-	525	0	ATG/AGG	
trnE(ttc)	14093	14161	-	69	5		svg ps
cob	14167	15307	+	1141	0	ATG/T(AA)	
trnT(tgt)	15308	15371	+	64	1		svg ps
trnP(tgg)	15373	15440	-	68	372		svg ps
OH	15813	16004	+	192	486		

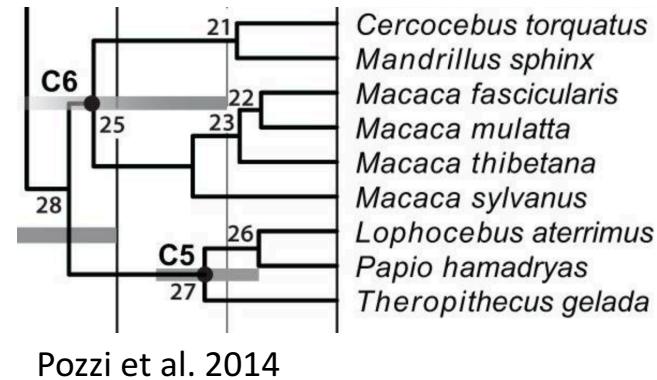
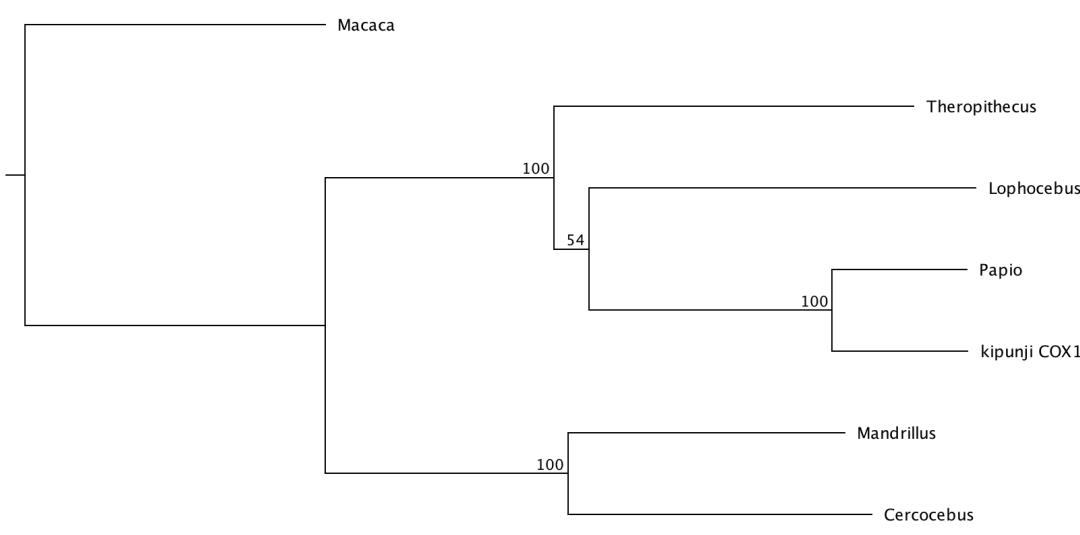
Analysis of difference



	Papio	Mandrillus	Cercocebus	Lophocebus	Theropith...	kipunji CO...	Macaca
Papio	X	2,476	2,587	1,784	1,628	25	2,502
Mandrillus	2,476	X	1,400	2,474	2,387	87	2,245
Cercocebus	2,587	1,400	X	2,615	2,491	89	2,301
Lophocebus	1,784	2,474	2,615	X	1,726	63	2,505
Theropithecus	1,628	2,387	2,491	1,726	X	67	2,419
kipunji COX1	25	87	89	63	67	X	97
Macaca	2,502	2,245	2,301	2,505	2,419	97	X

	Papio	Mandrillus	Cercocebus	Lophocebus	Theropith...	kipunji CO...	Macaca
Papio	X	85.1%	84.4%	89.2%	90.2%	96.2%	84.4%
Mandrillus	85.1%	X	91.6%	85.1%	85.6%	86.8%	86.0%
Cercocebus	84.4%	91.6%	X	84.3%	85.0%	86.5%	85.7%
Lophocebus	89.2%	85.1%	84.3%	X	89.6%	90.4%	84.4%
Theropithecus	90.2%	85.6%	85.0%	89.6%	X	89.8%	85.0%
kipunji COX1	96.2%	86.8%	86.5%	90.4%	89.8%	X	85.3%
Macaca	84.4%	86.0%	85.7%	84.4%	85.0%	85.3%	X

Evolutionary rates



	Divergence ages mtDNA1	Divergence ages mtDNA3
Split		
Cercopithecini - Papionini	14.85 (12.91-16.75)	14.72 (12.82-16.61)
Macaca - Mandrillus+Cercocebus+Lophocebus+Theropithecus+Papio	11.35 (10.15-12.62)	11.13 (9.91-12.32)
Macaca sylvanus - M. thibetana+M. fascicularis+M. mulatta	7.40 (6.21-8.60)	7.00 (5.90-8.12)
Macaca thibetana - M. fascicularis+M. mulatta	5.28 (4.32-6.30)	4.99 (3.98-6.01)
Macaca fascicularis - M. mulatta	3.92 (3.05-4.89)	3.82 (2.86-4.78)
Mandrillus+Cercocebus - Lophocebus+Theropithecus+Papio	10.76 (9.46-12.00)	10.37 (9.13-11.62)
Mandrillus - Cercocebus	3.95 (2.80-5.09)	3.67 (2.62-4.78)
Lophocebus - Theropithecus+Papio	5.39 (4.59-6.16)	5.18 (4.37-5.96)
Theropithecus - Papio	4.43 (3.84-5.05)	4.31 (3.70-4.93)

Finstermeier et al. 2013

Node	Divergence Time (Ma)	Total # bp differences	bp difference / site	Rate (bp/site/Ma)	
Macaca - Papio	11.35	2502	0.152	0.0134	
Mandrillus - Papio	10.76	2476	0.150	0.0139	
Mandrillus - Cercocebus	3.95	1400	0.085	0.0215	
Lophocebus - Papio	5.39	1784	0.108	0.0201	
Theropithecus - Papio	4.43	1628	0.099	0.0223	

Conclusions

- Genomes very similar, especially within smaller clades in Papionina (>90%)
- Rates slower at the base of the clade, then differences accumulate more rapidly towards the tips
- More to learn
 - Complete genome of *Rungwecebus*
 - BEAST for better rate estimates
 - R