Comparisons between two butterflyfish hybrid groups at Christmas Island, within the Indian and Pacific Ocean suture zone

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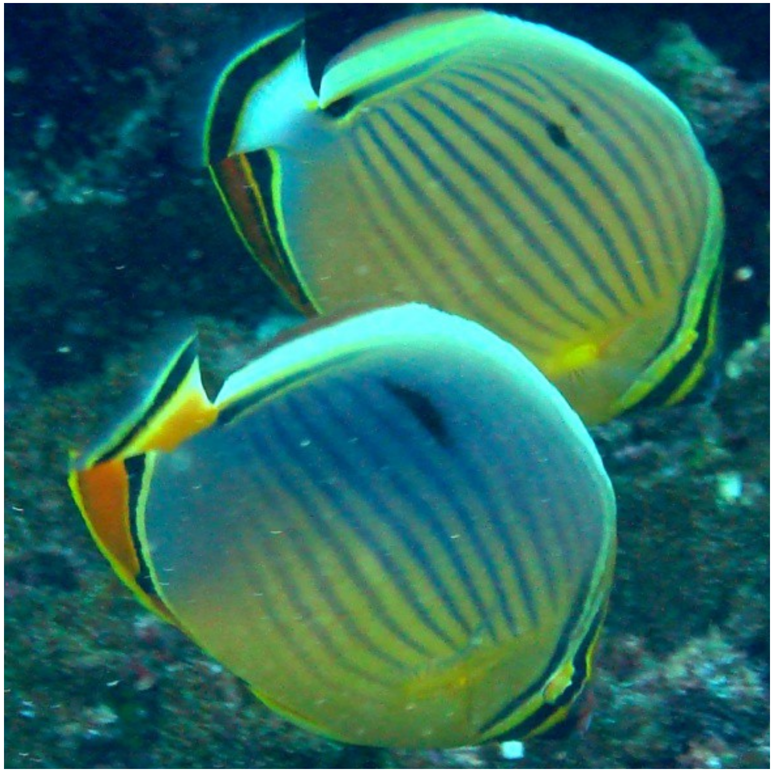

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ARC Centre of Excellence
Coral Reef Studies

Australian Government

Department of Sustainability, Environment, Water, Population and Communities

Christmas Island
Parks Australia

Centre for
Sustainable
Tropical Fisheries
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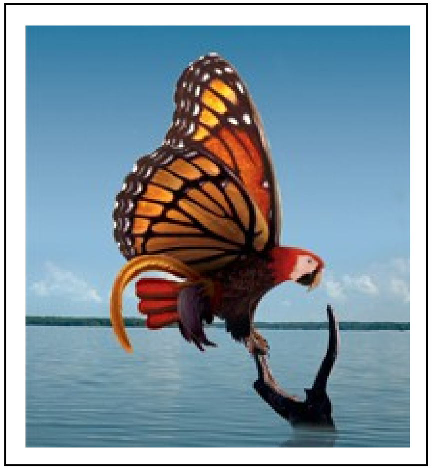
Natural hybridisation

- crossing of genetically distinct clusters, production of viable hybrids
- > 25% of plants, > 10% animals
- important for evolution



- occurs clustered in narrow geographic locations: suture zones (Avise 2000)
- common in corals and reef fishes (Gardner 1997, Willis et al 2006)

Natural hybridisation in reef fishes

over 80 species of reef fishes hybridise

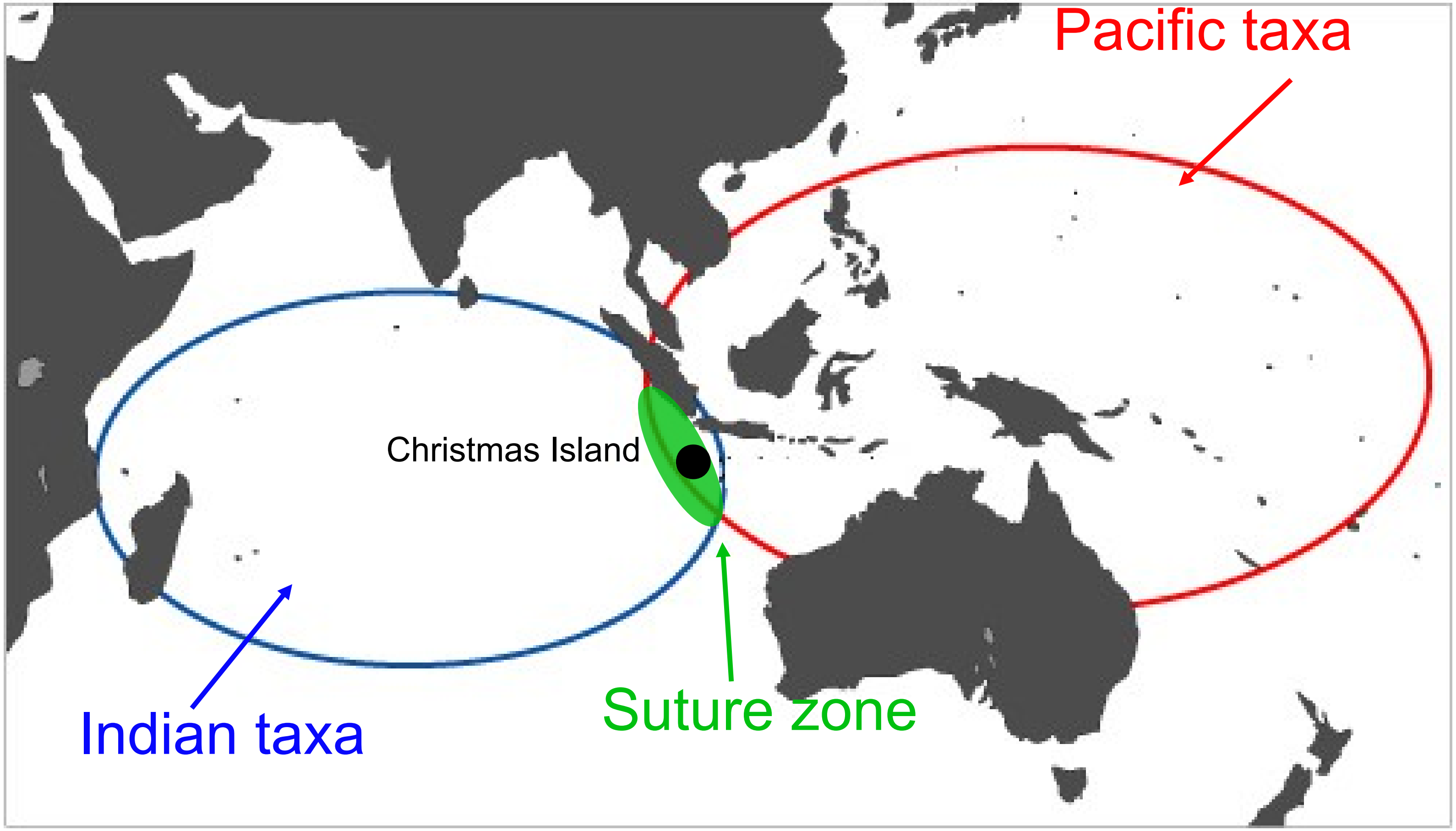
- causes and consequences unknown

terrestrial- and freshwater-derived theory:

- overlapping ecology; rarity of parental species (Grant and Grant 2002, Mallet 2005)
- genetic distance influences outcomes (Smith et al. 2003, Taylor et al. 2006)

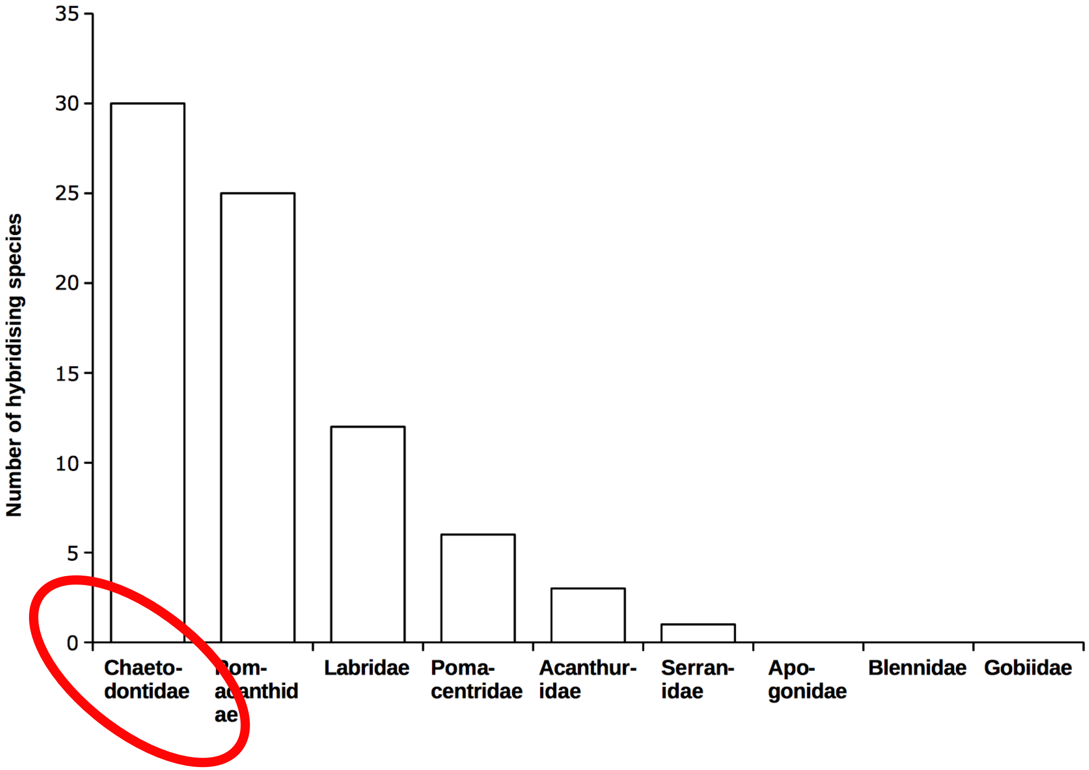
Indo-Pacific biogeographic border: reef fish suture zone

- recently identified as reef fish suture zone
- 16 hybrids reported, involving 25 species across 7 families (Hobbs et al. 2009)
- comparative hybridisation studies in reef fishes



Study species: butterflyfishes

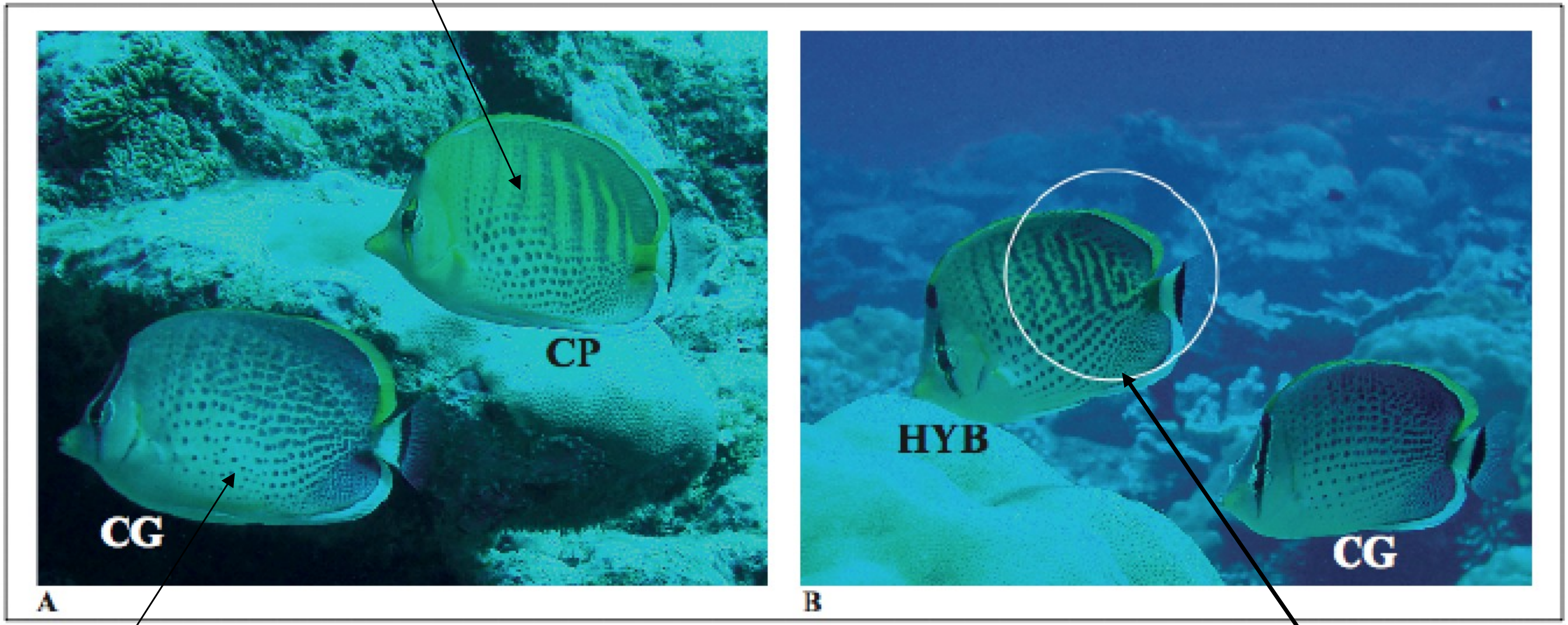
- most reported hybrids than any other reef fish family
- over 40/120 species found to hybridise, >30% (cf other taxa)
- hybrids intermediate colouration, easy to identify



Redrawn from Yaakub et al. 2006

Study species: butterflyfishes

Chaetodon puncatofasciatus (CP) – Pacific Ocean

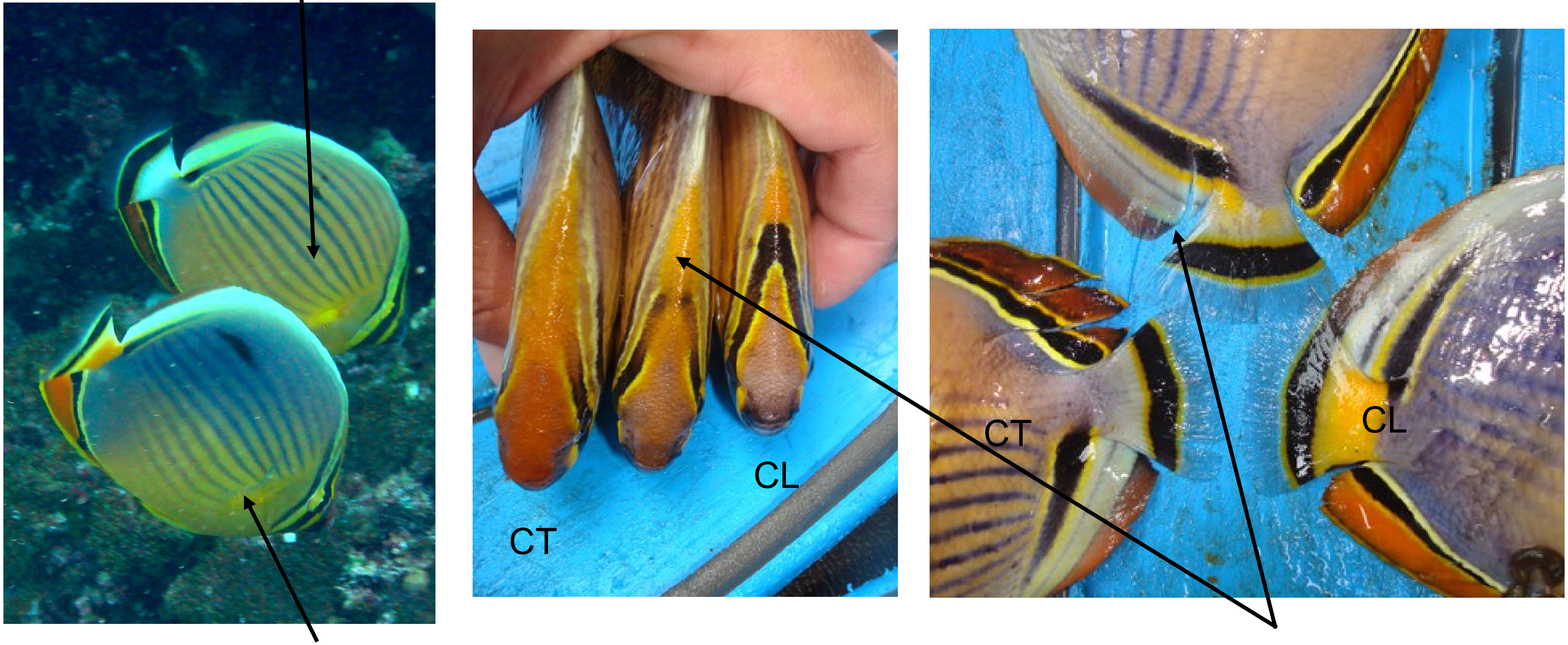


Chaetodon guttatissimus (CG) – Indian Ocean

Hybrid

Study species: butterflyfishes

Chaetodon lunulatus (CL) - Pacific Ocean



Chaetodon trifasciatus (CT) - Indian Ocean

Hybrid

Aims

Compare ecological drivers of hybridisation

- habitat use (Underwater Visual Census- UVC)
- diet (3 minute observations)
- abundance (UVC)
- mate choice (UVC)

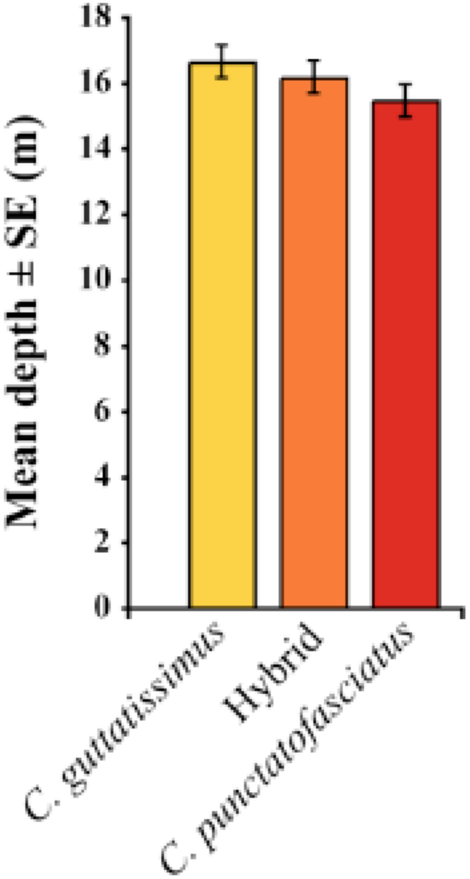
Compare genetics of hybridisation

- hybrid status
- directionality
- introgression

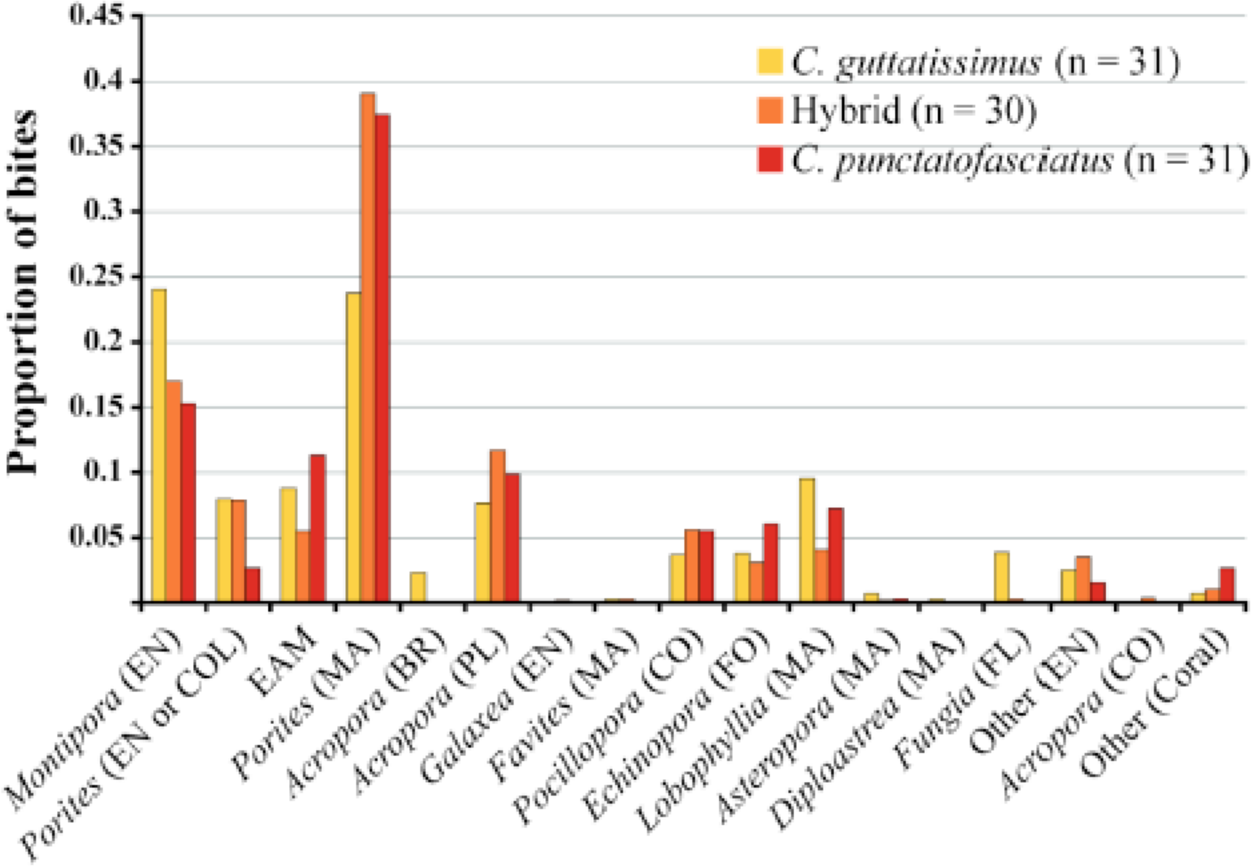
Check theoretical consistency

Depth distribution and diet:

C. guttatissimus x C. punctatofasciatus



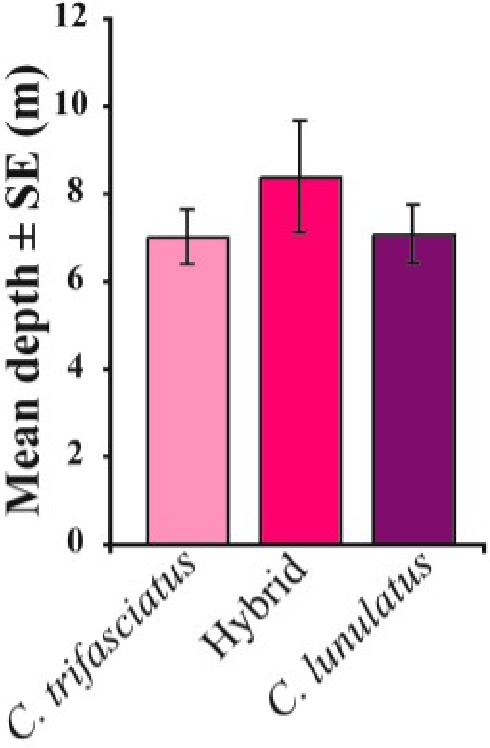
ANOVA, df = 1, F = 3.137, p = 0.08

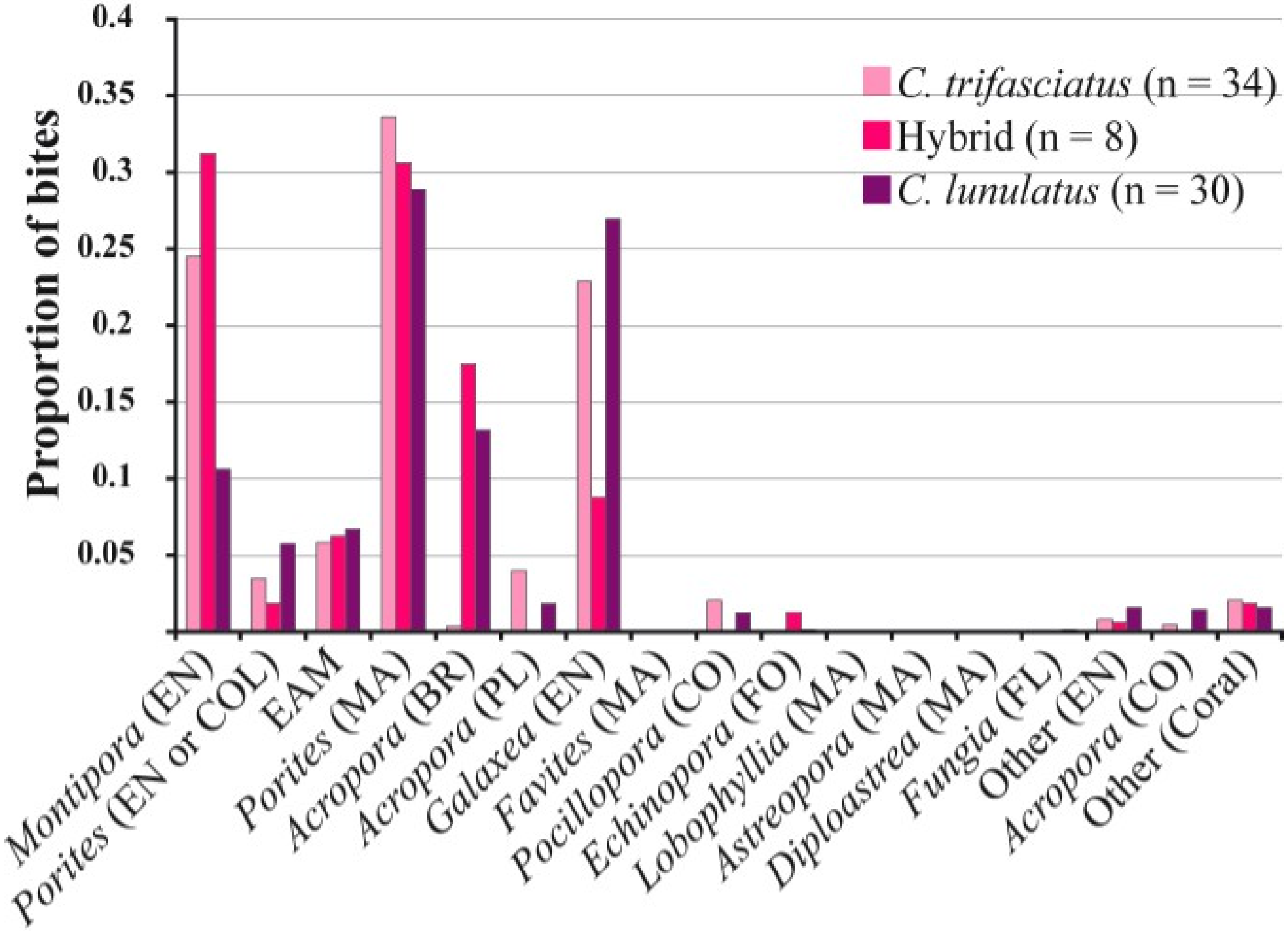


MANOVA, Pillai’s Trace = 0.511, hypothesis df = 34, p = 0.085

Depth distribution and diet:

C. trifasciatus x C. lunulatus



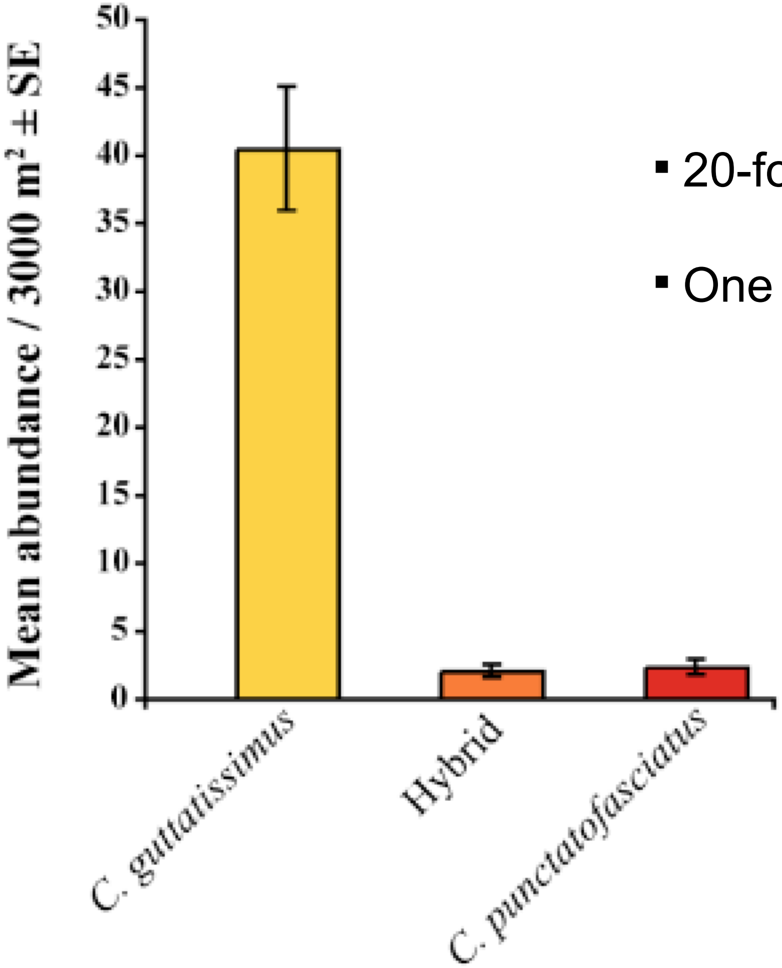


ANOVA, df=2, F=0.489, p=0.615

MANOVA, Pillai's Trace=0.715, hypothesis df=32, p=0.062

Abundance:

C. guttatissimus x C. punctatofasciatus

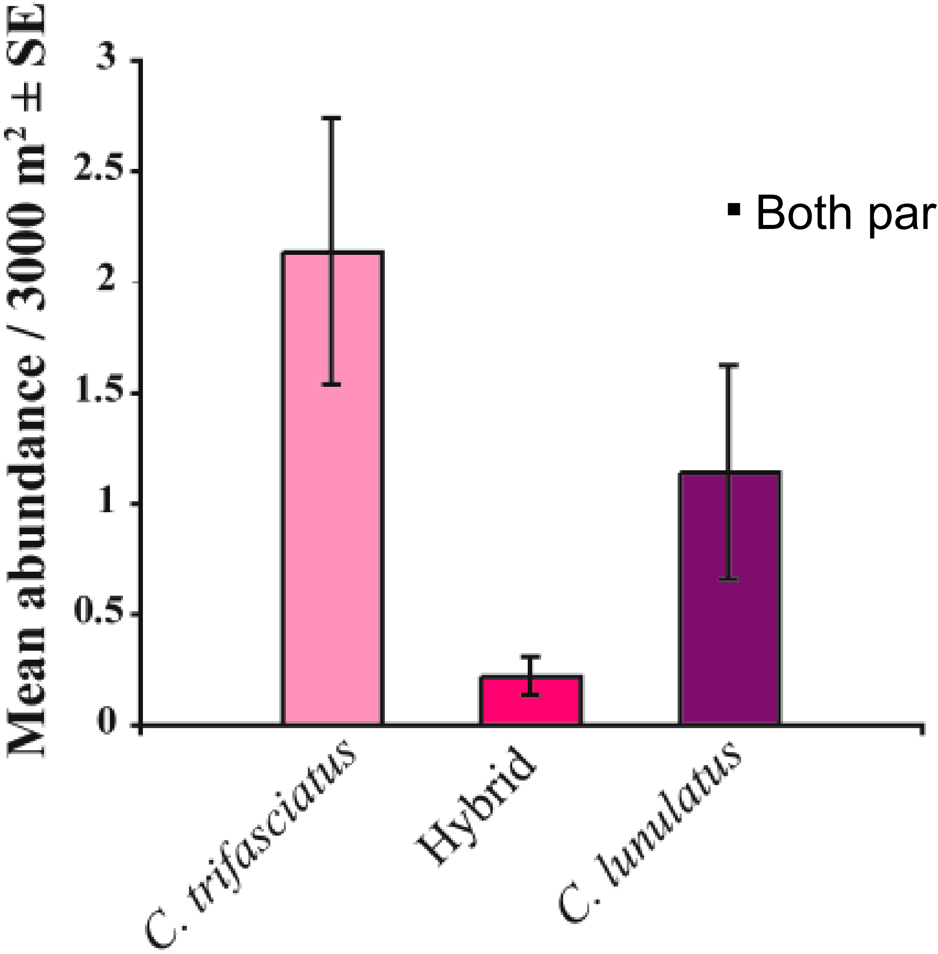


- 20-fold abundance disparity
- One parent rare

t-test, t = 8.325, df = 13, $p < 0.0001$

Abundance:

C. trifasciatus x C. lunulatus

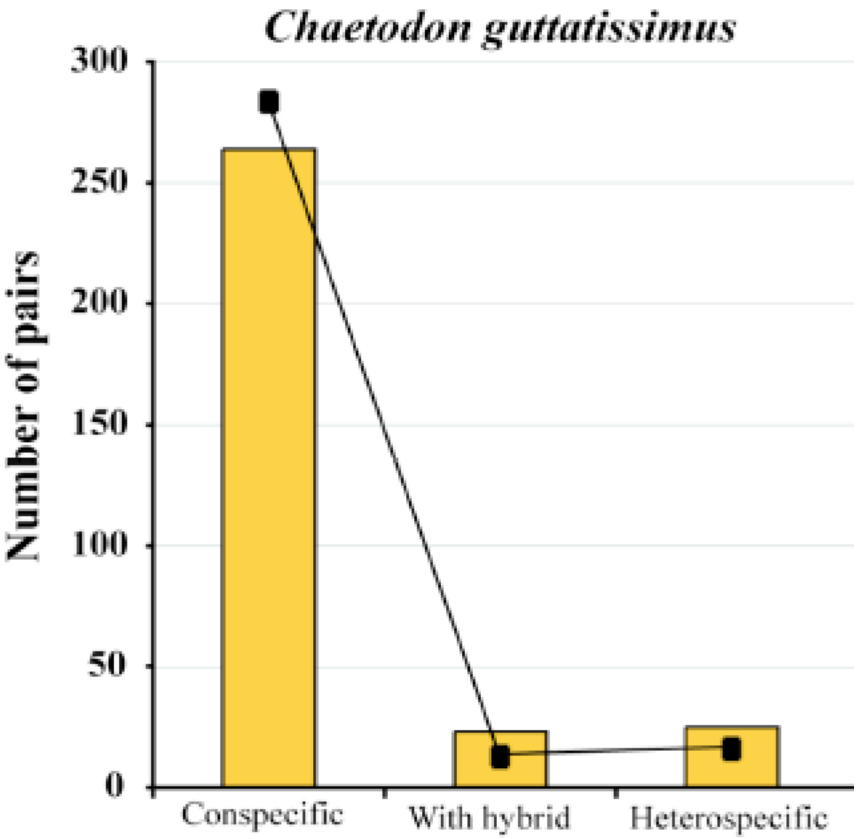


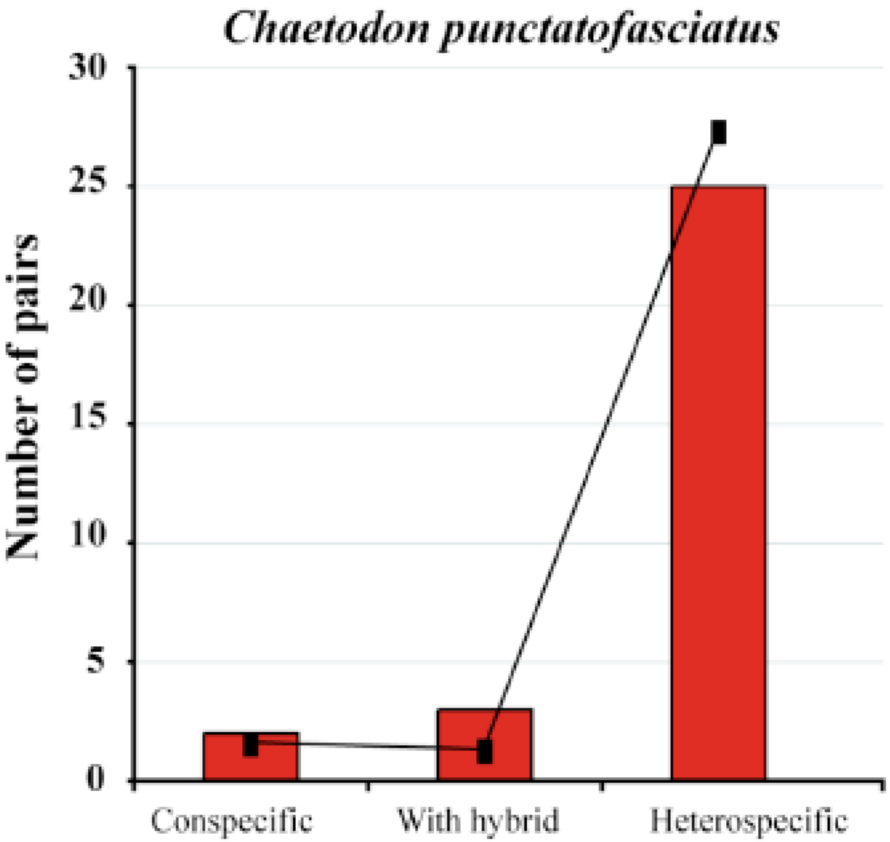
- Both parents rare

t-test, t = 1.285, df = 38, p = 0.207

Pairing behaviour:

C. guttatissimus x C. punctatofasciatus



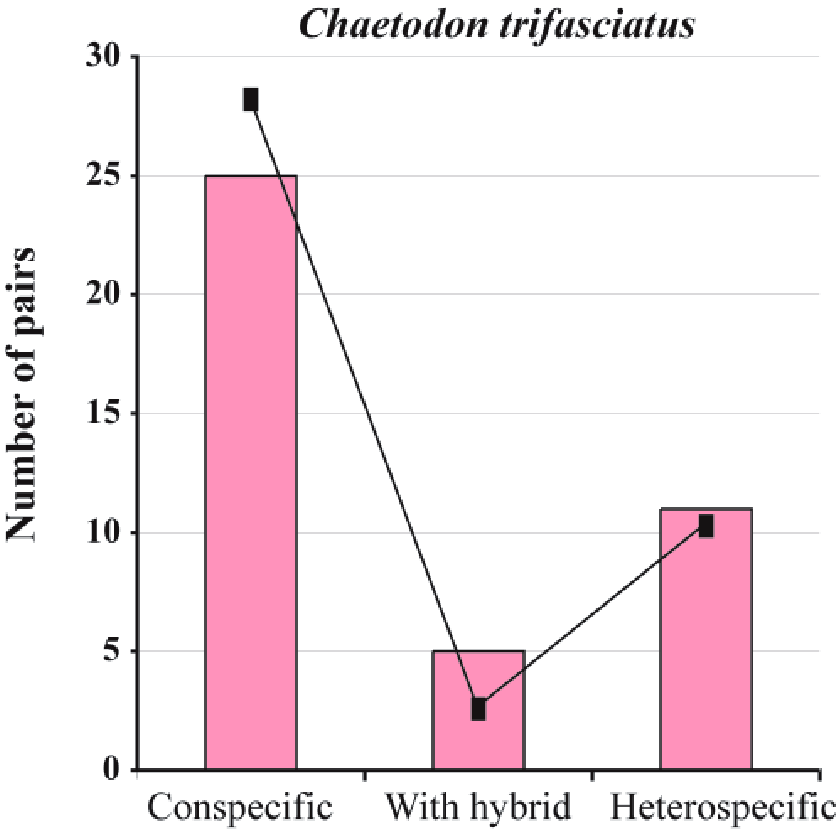


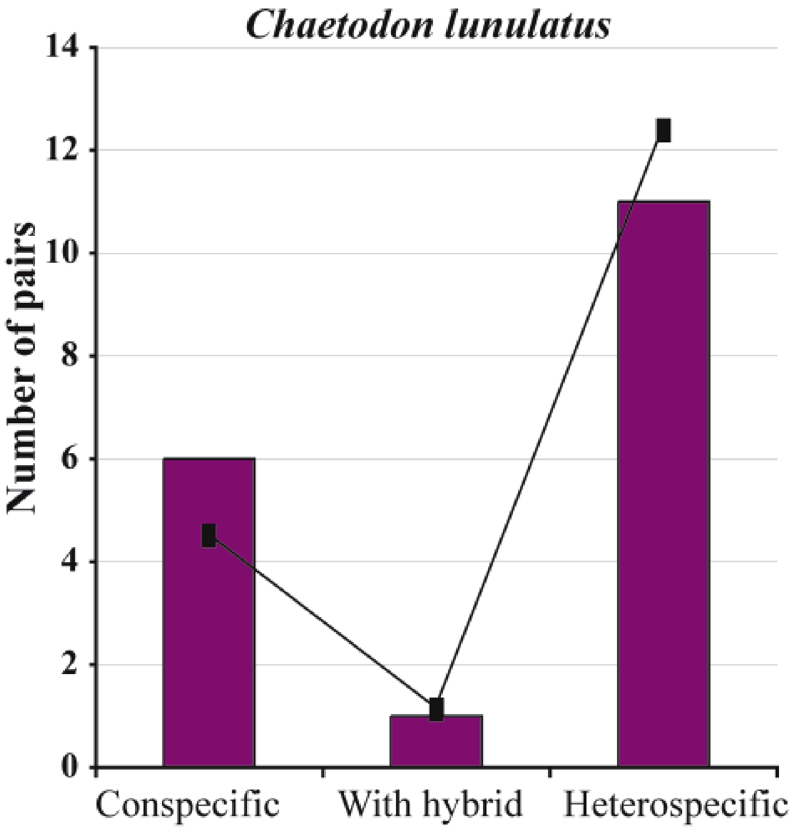
$\chi^2 = 14.91$, df = 2, $p < 0.001$

$\chi^2 = 2.89$, df = 2, $p = 0.24$

Pairing behaviour:

C. trifasciatus x C. lunulatus

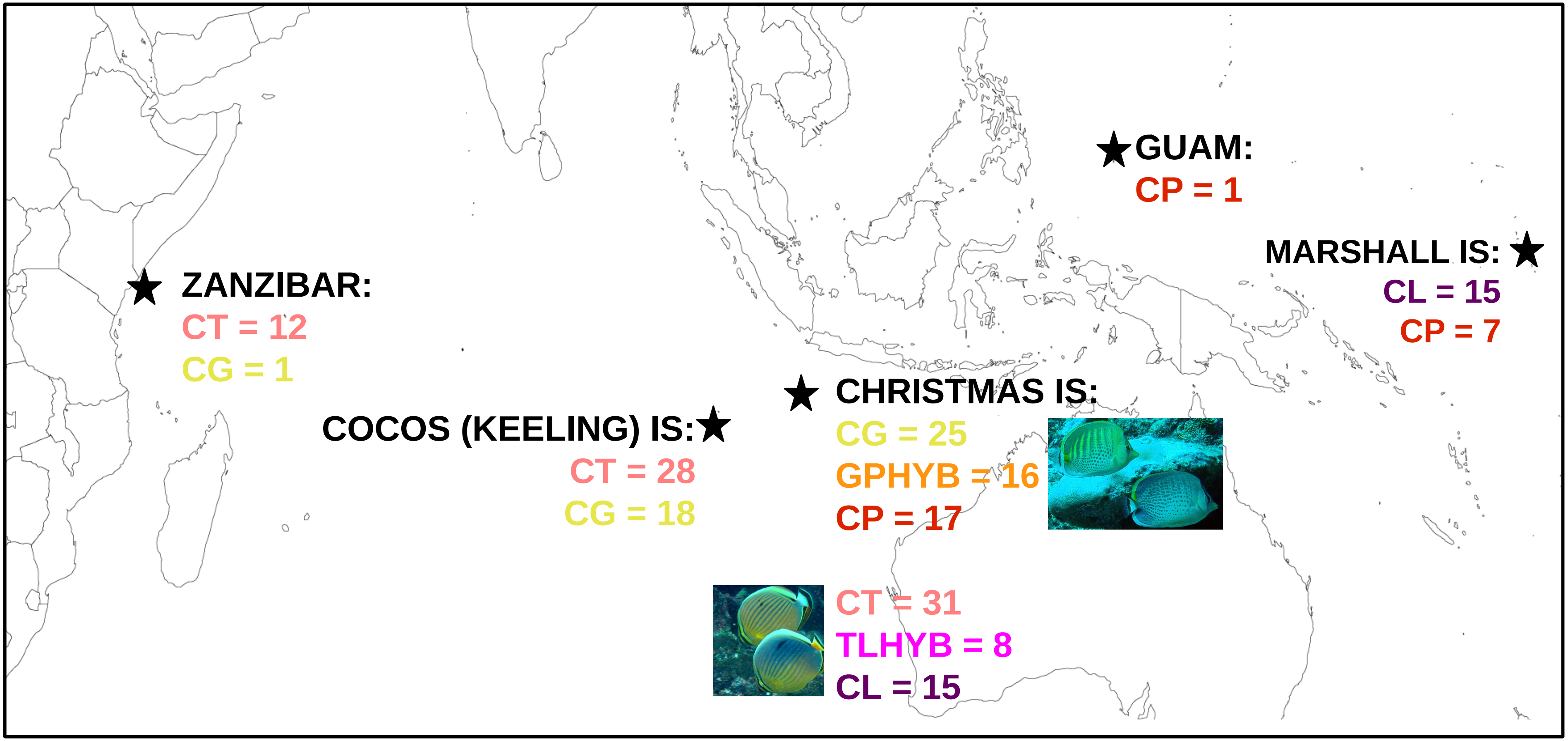




$\chi^2=2.73$, df=2, p = 0.26

$\chi^2=0.67$, df=2, p = 0.71

Molecular genetics: methodology



Mitochondrial DNA:

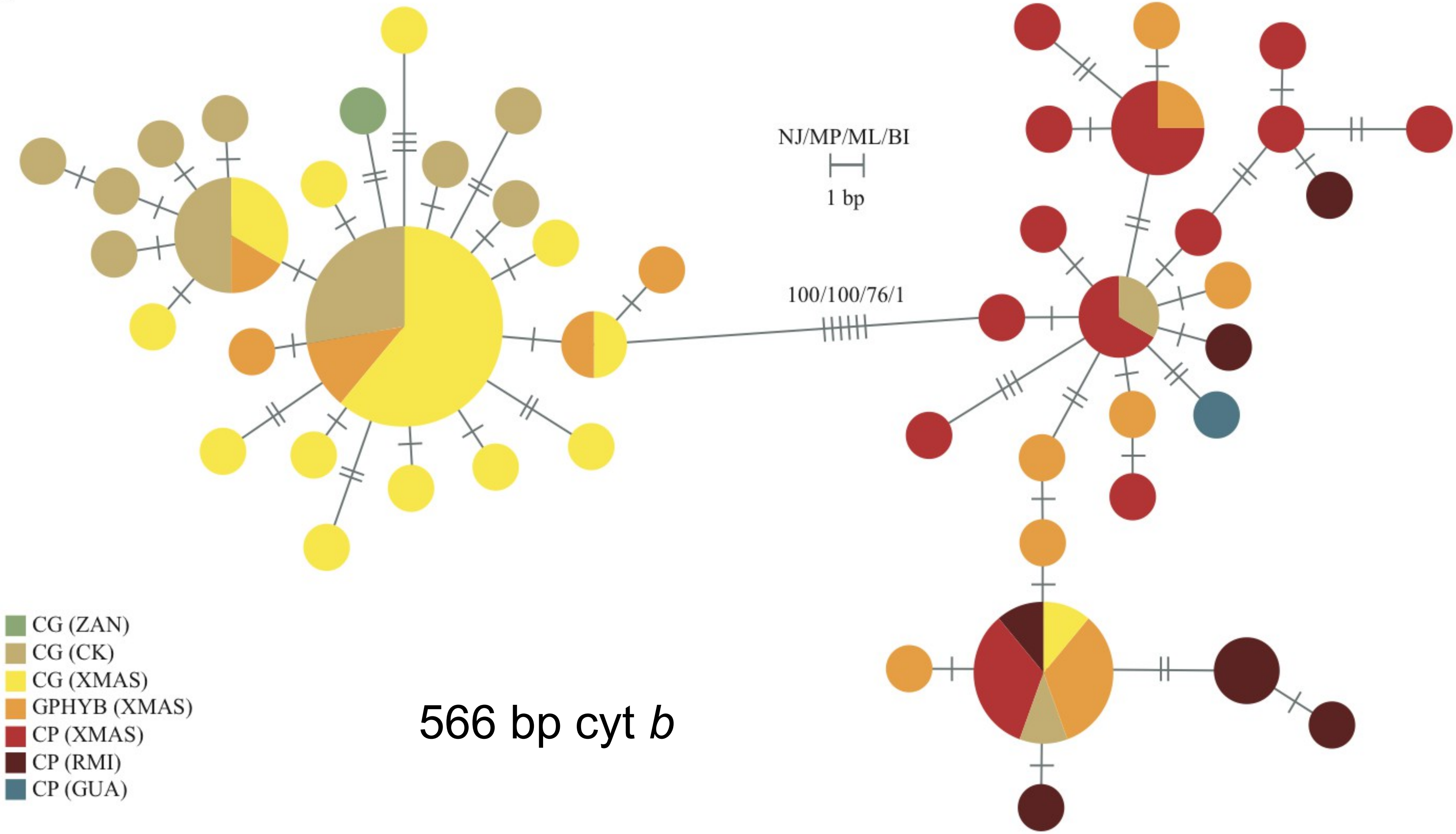
Partial cyt *b* (McMillan and Palumbi 1995)

Nuclear DNA:

12 msat markers for *C. lunulatus*; (Lawton et al. 2009)   20 msat markers for *C. punctatofasciatus* (Montanari et al. 2013)

mtDNA:

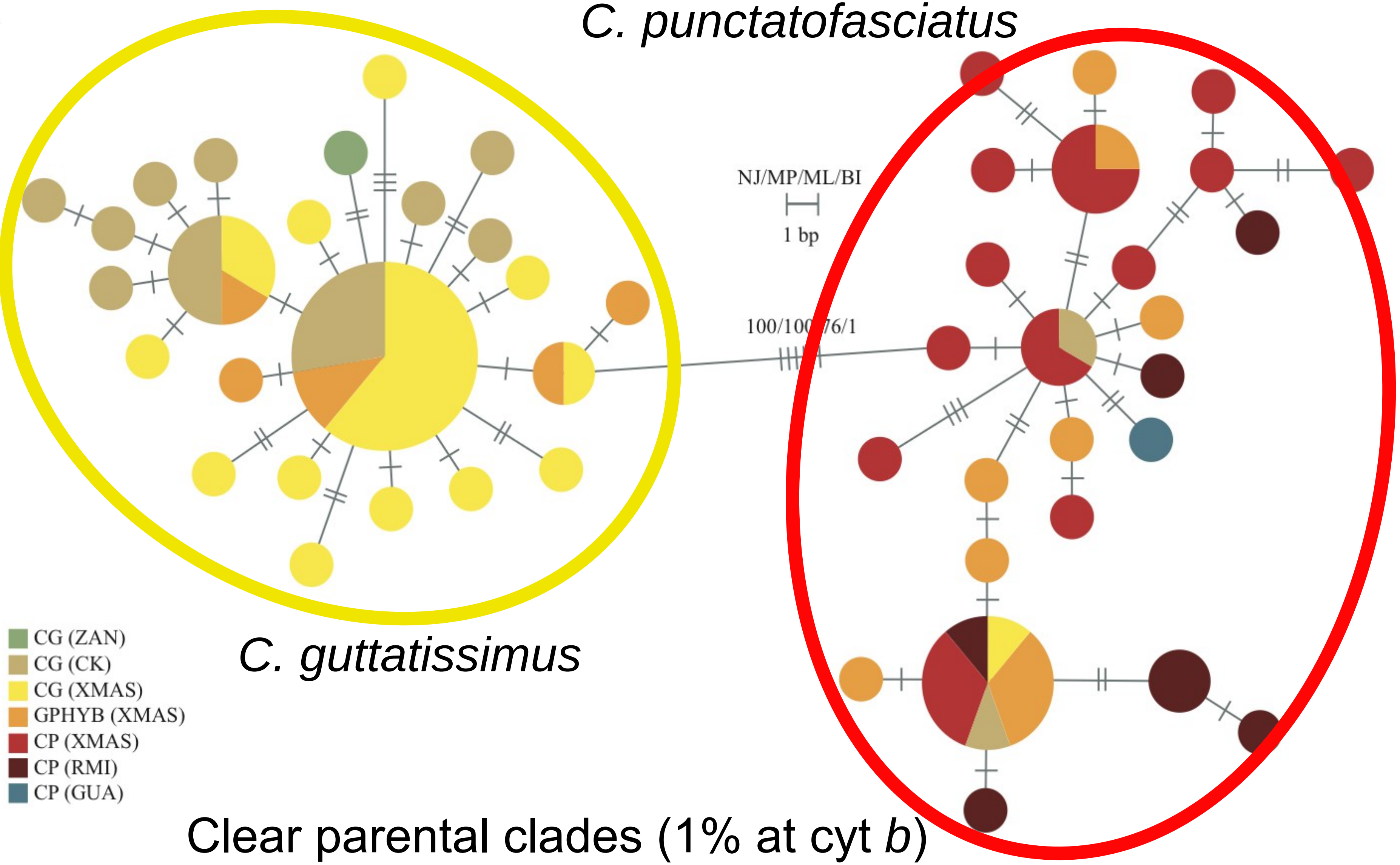
C. guttatissimus x C. punctatofasciatus



566 bp cyt *b*

mtDNA:

C. guttatissimus x C. punctatofasciatus



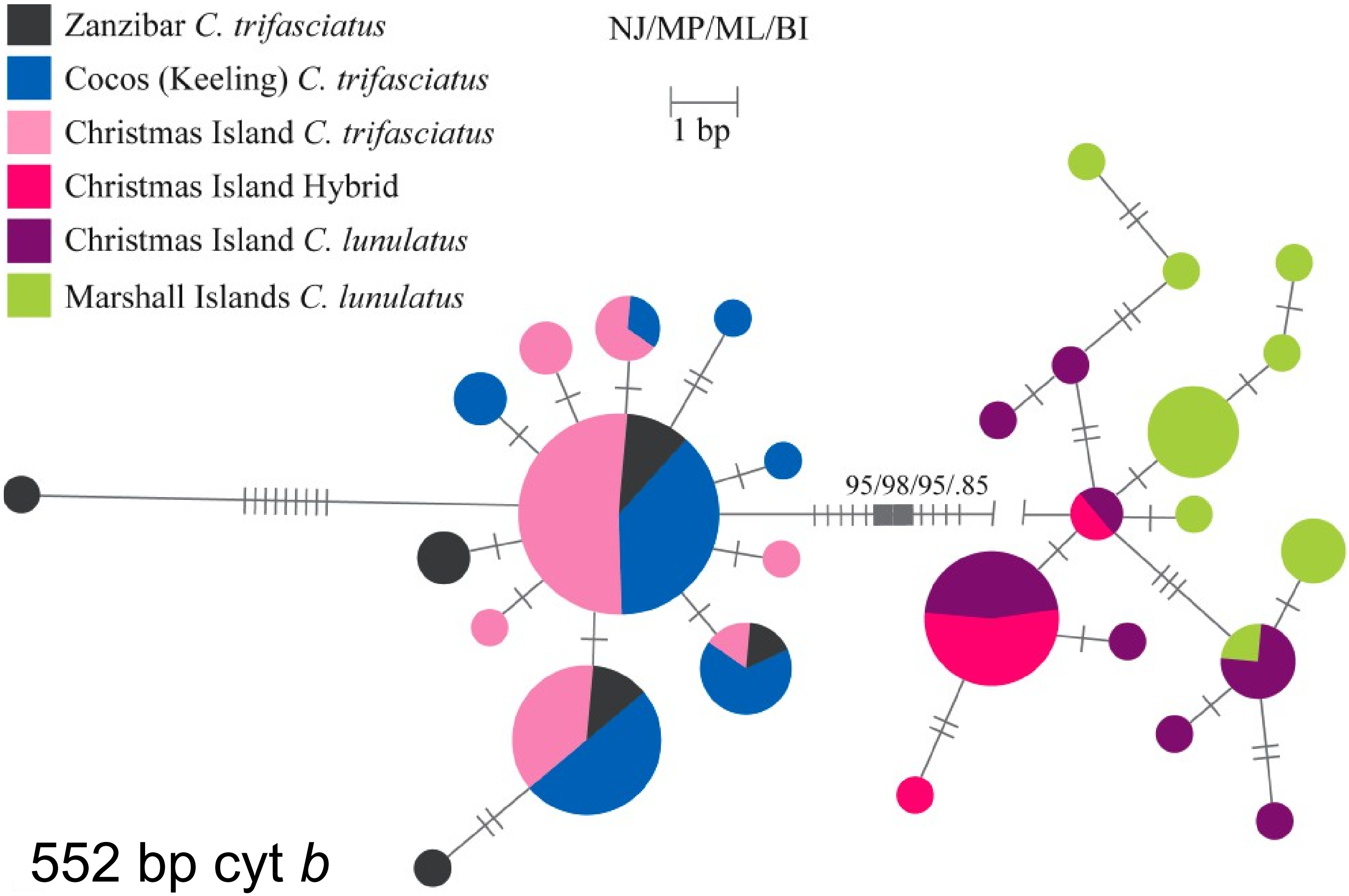
C. punctatofasciatus

C. guttatissimus

Clear parental clades (1% at cyt *b*)

mtDNA:

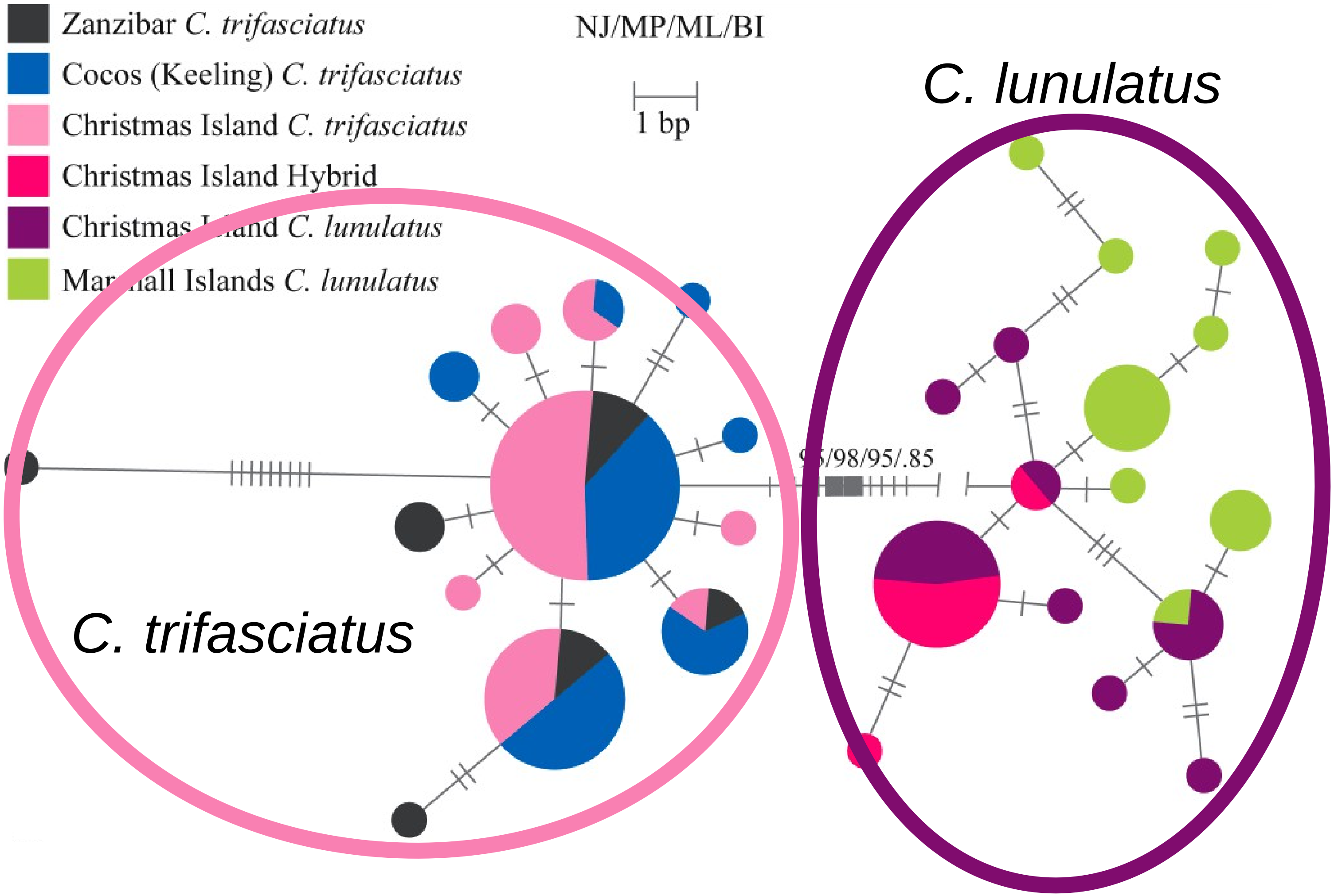
C. trifasciatus x *C. lunulatus*



552 bp cyt *b*

mtDNA:

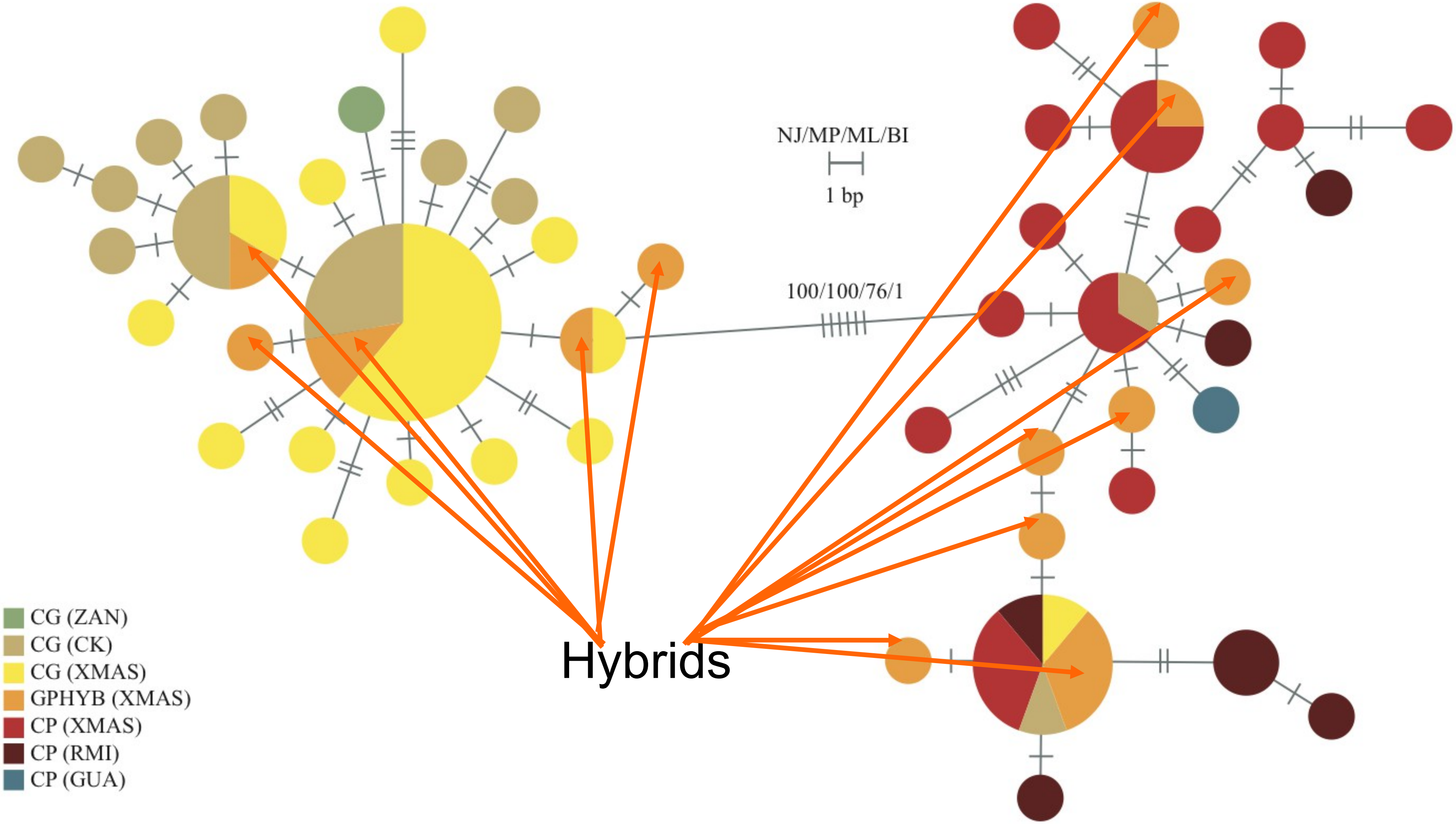
C. trifasciatus x C. lunulatus



Clear parental clades (5% at cyt *b*)

mtDNA:

C. guttatissimus x C. punctatofasciatus

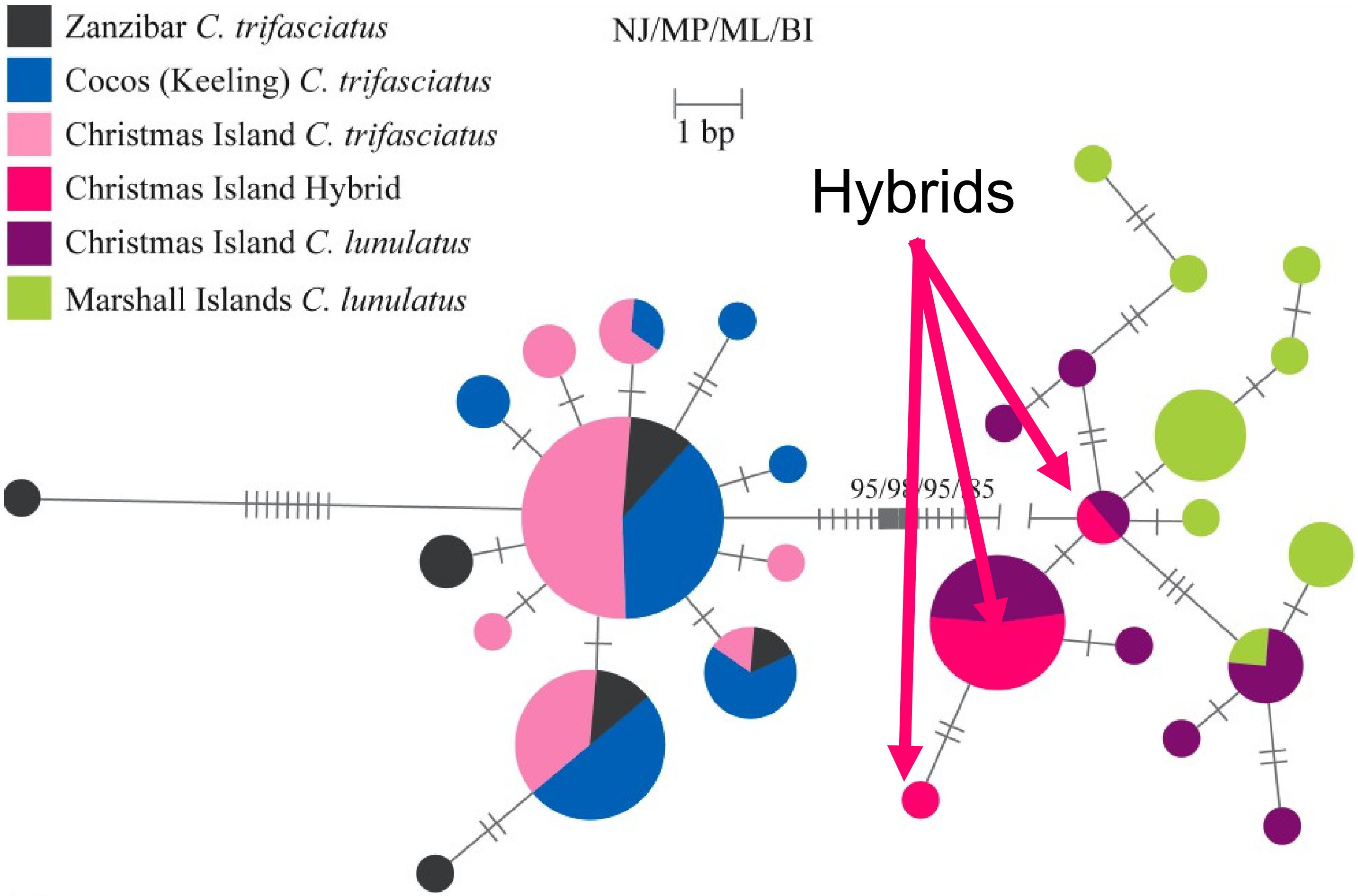


Hybrids

Hybrids in both clades: bidirectional maternity

mtDNA:

C. trifasciatus x C. lunulatus

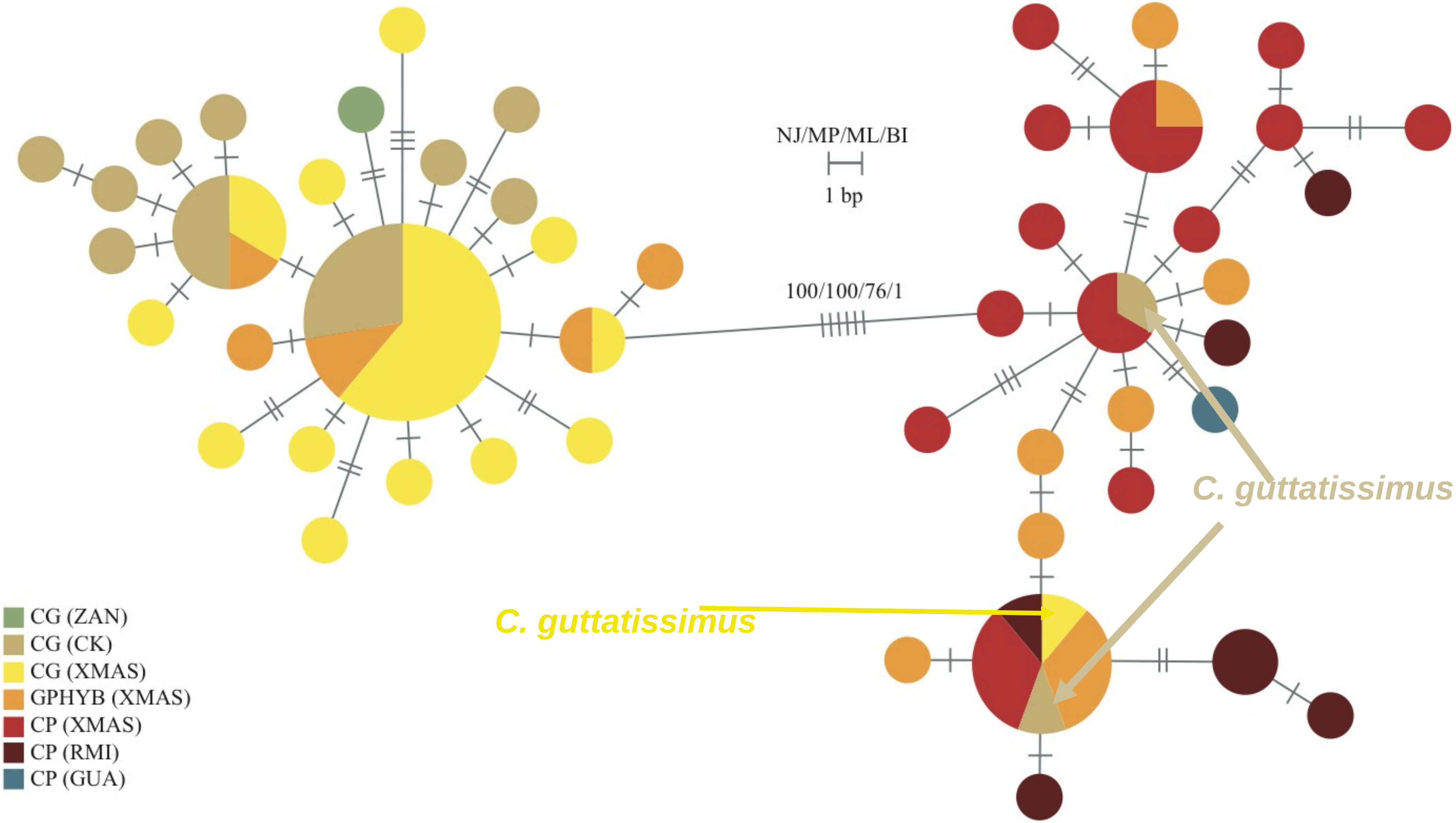


Hybrids

Hybrids in one clade only: unidirectional maternity

mtDNA:

C. guttatissimus x C. punctatofasciatus



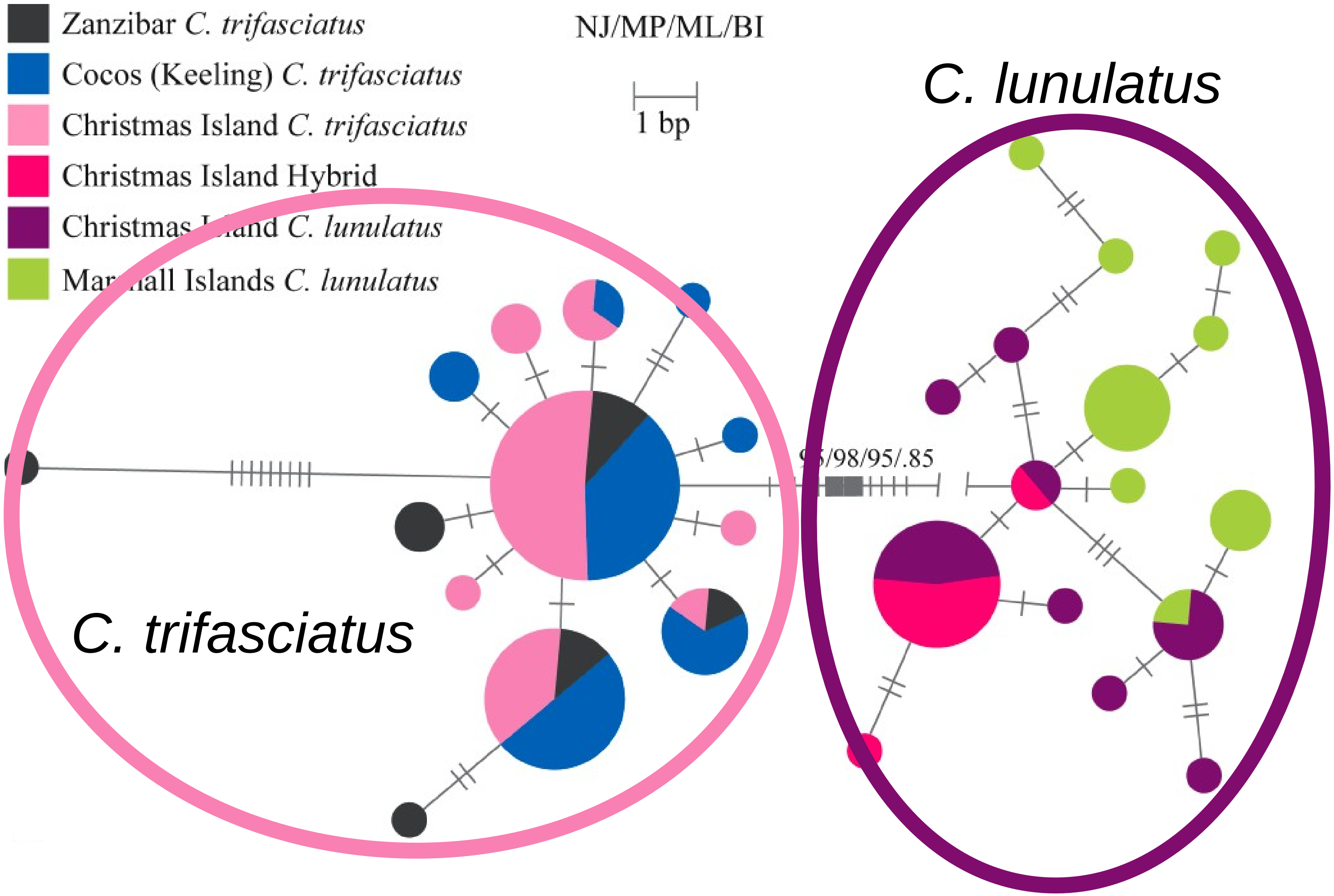
C. guttatissimus

C. guttatissimus

Evidence of introgression: in and out of hybrid zone

mtDNA:

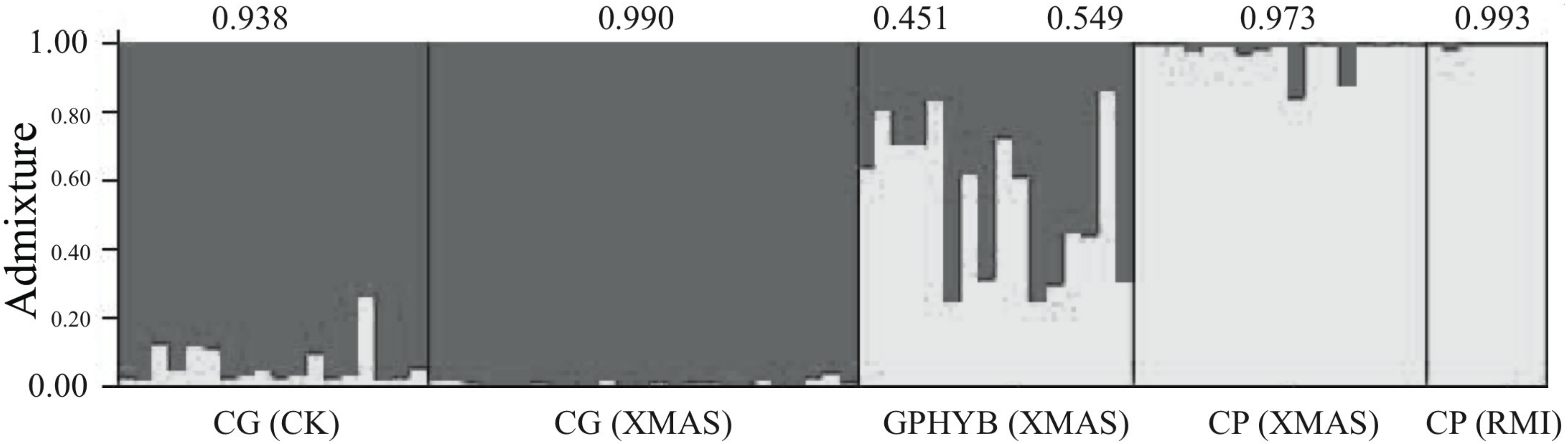
C. trifasciatus x C. lunulatus



No evidence of introgression

Nuclear msatDNA:

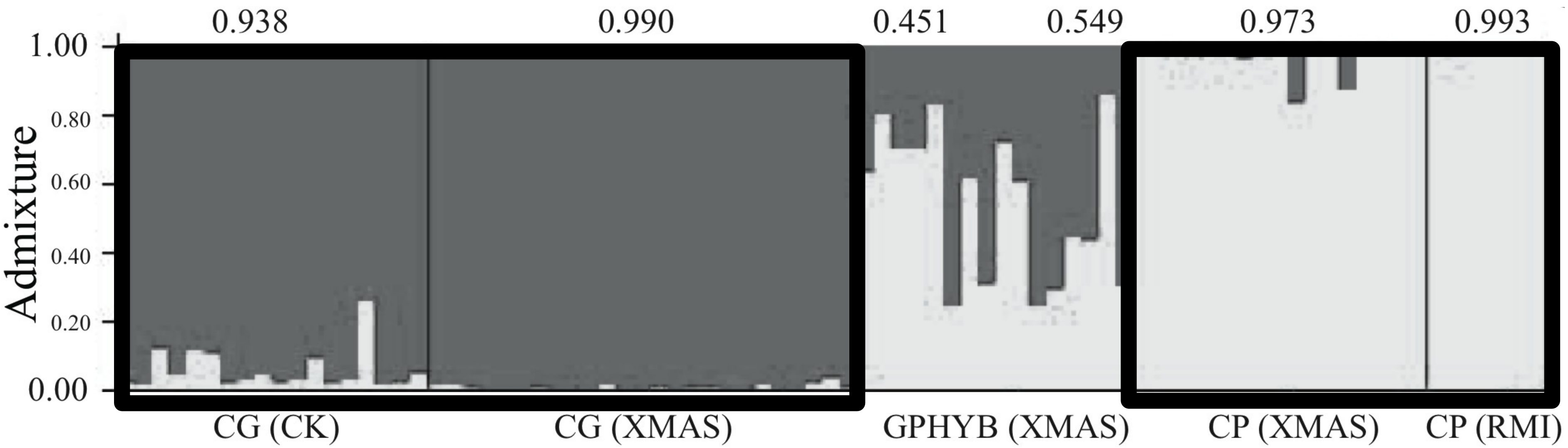
C. guttatissimus x C. punctatofasciatus



- STRUCTURE: (Q plot)
- 20 msat loci
- k = 2 clusters

Nuclear msatDNA:

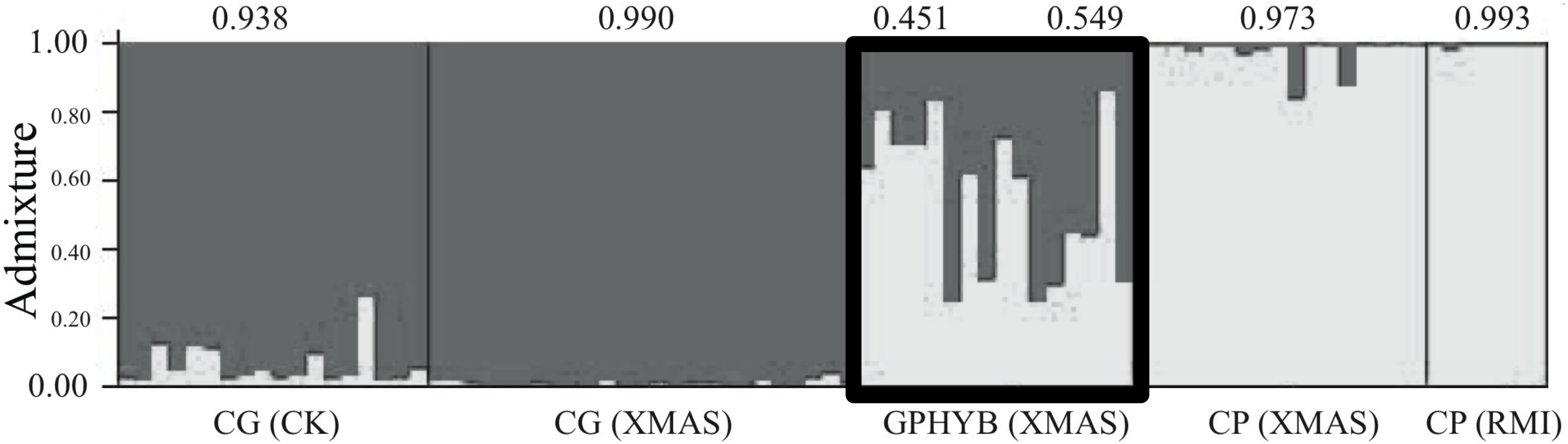
C. guttatissimus x C. punctatofasciatus



- 2 clusters correspond to parental species
- species-level: little admixture (< 6.2%)

Nuclear msatDNA:

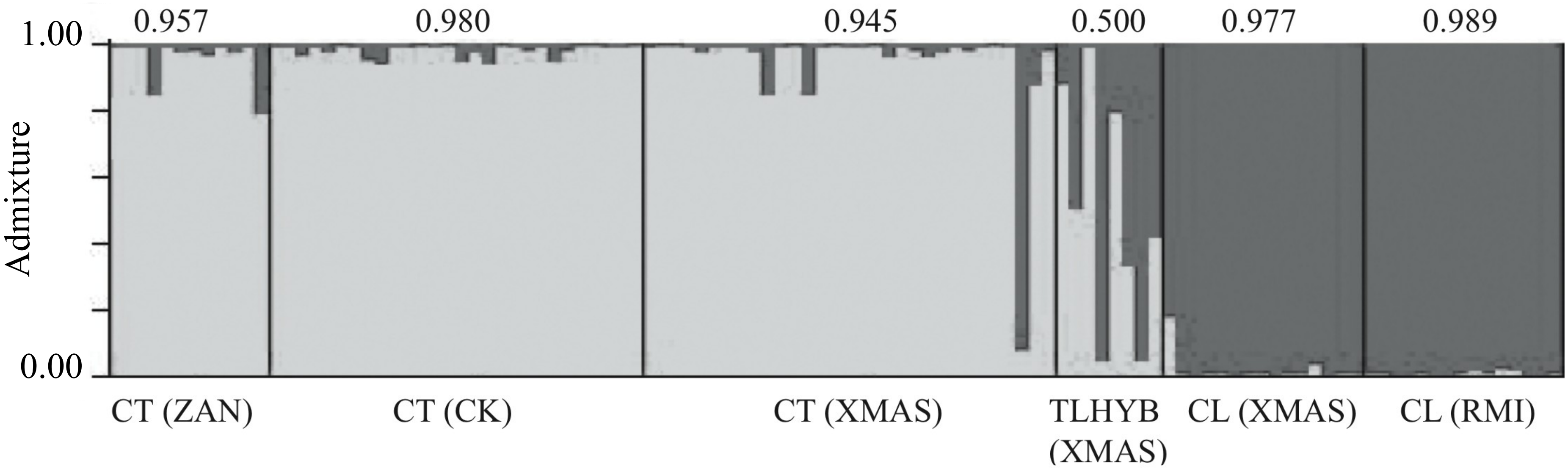
C. guttatissimus x C. punctatofasciatus



- hybrids belong to either cluster
- overall, a mix between parental clusters
- not enough power to discriminate classes

Nuclear msatDNA:

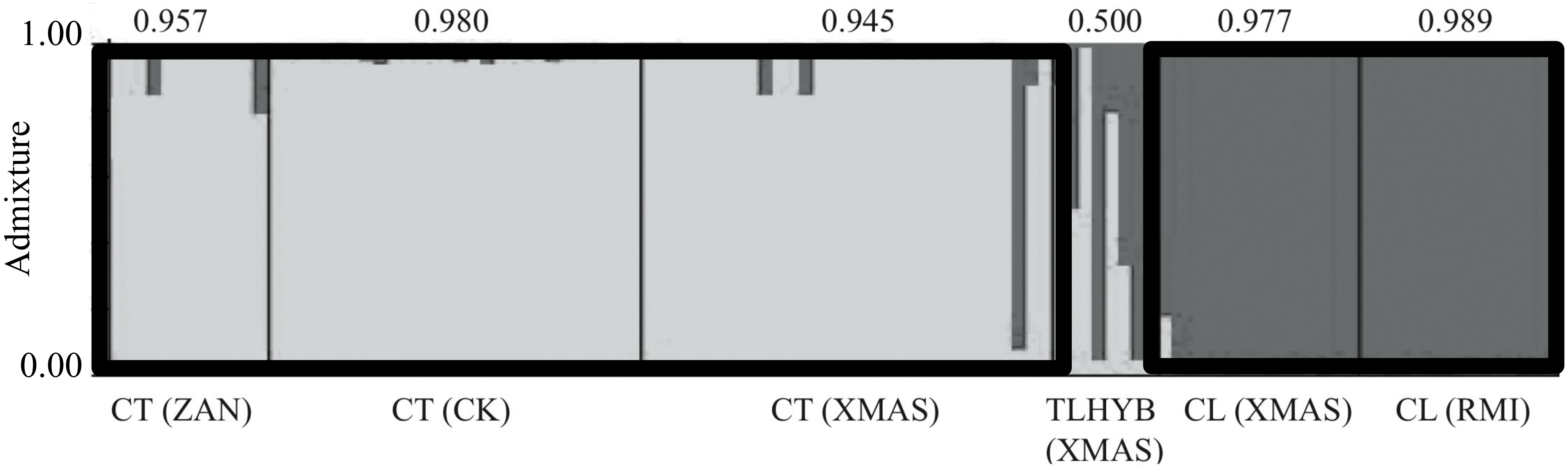
C. trifasciatus x C. lunulatus



- STRUCTURE: (Q plot)
- 12 msat loci
- k = 2 clusters

Nuclear msatDNA:

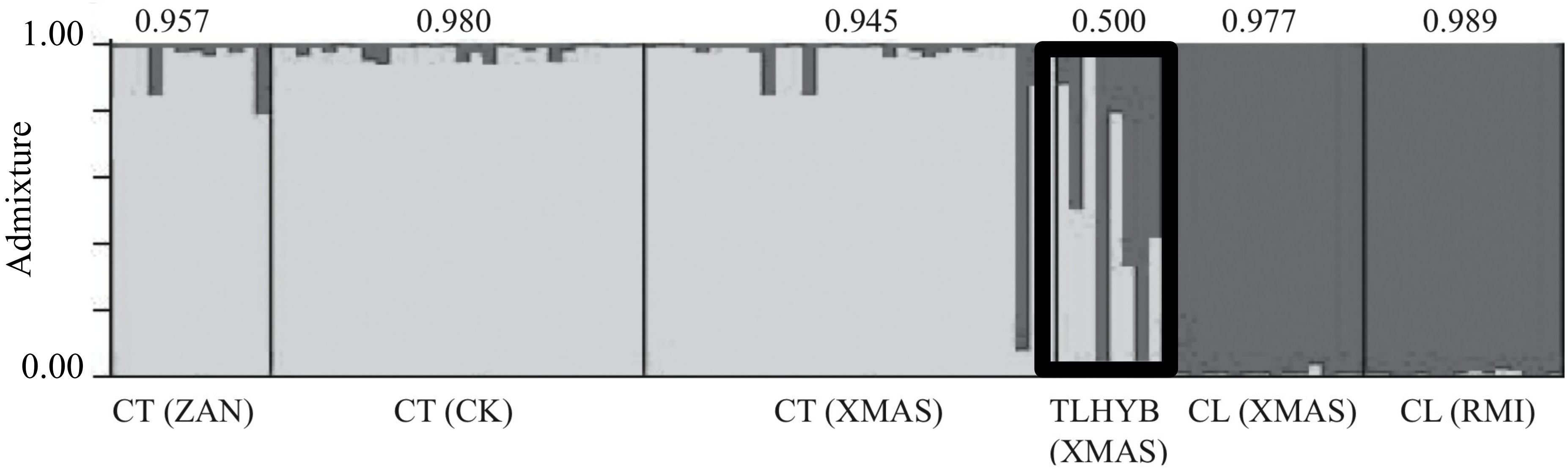
C. trifasciatus x C. lunulatus



- 2 clusters correspond to parental species
- species-level: little admixture (< 5.5%)

Nuclear msatDNA:

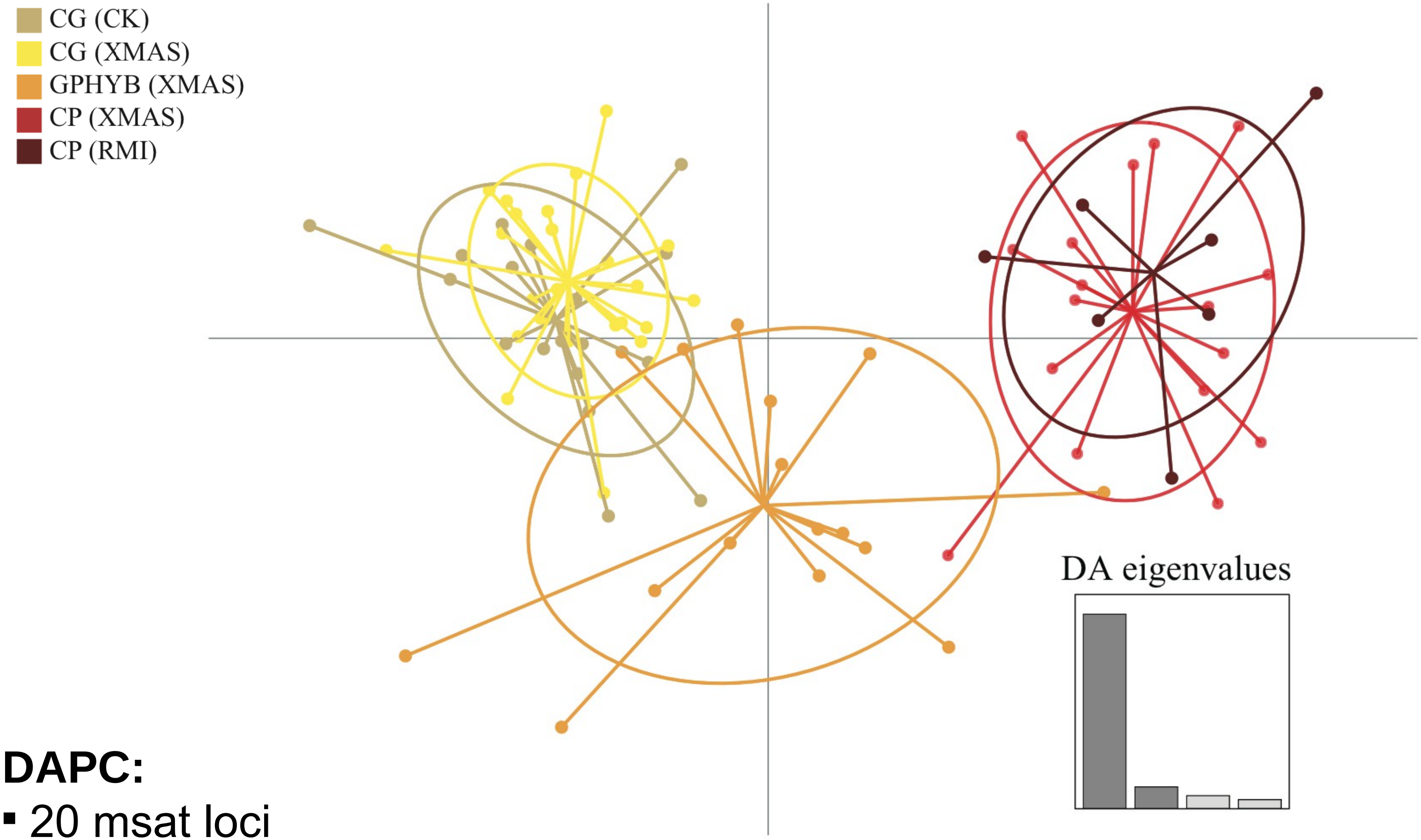
C. trifasciatus x C. lunulatus



- hybrids belong to either cluster
- 50% admixture
- cannot distinguish classes

Nuclear msatDNA:

C. guttatissimus x C. punctatofasciatus

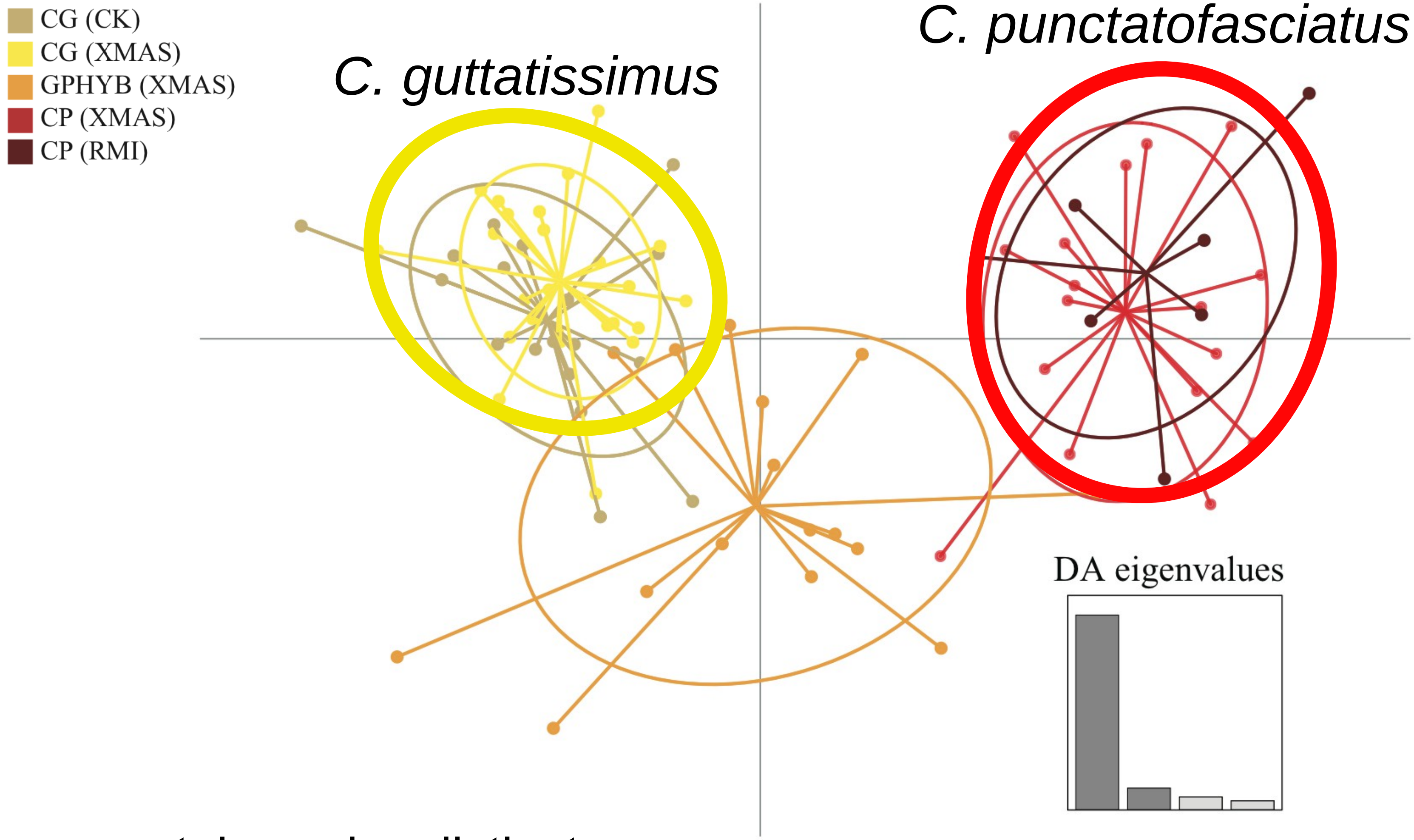


DAPC:

- 20 msat loci
- 27 PCs: 65% genetic variability retained

Nuclear msatDNA:

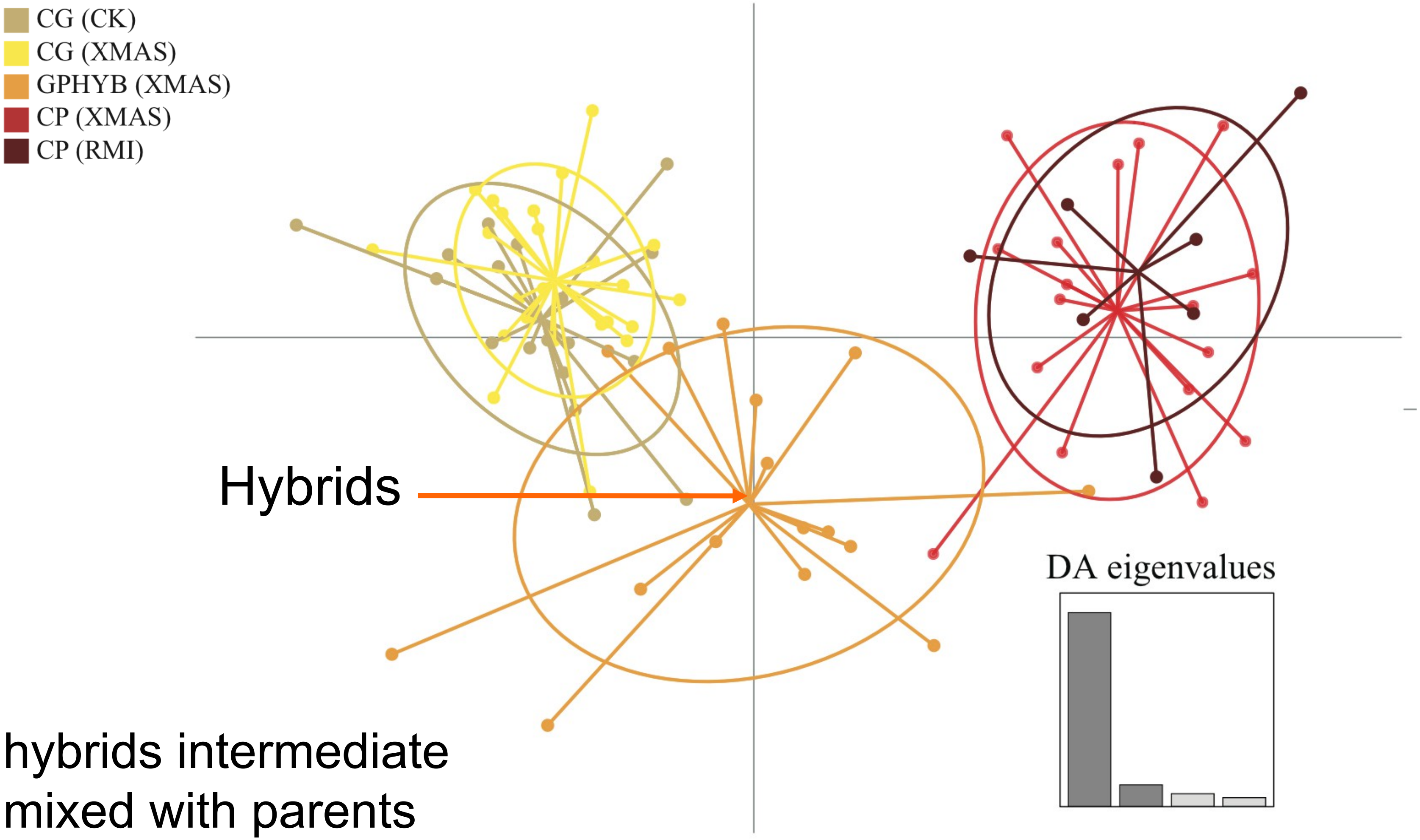
C. guttatissimus x C. punctatofasciatus



- parental species distinct

Nuclear msatDNA:

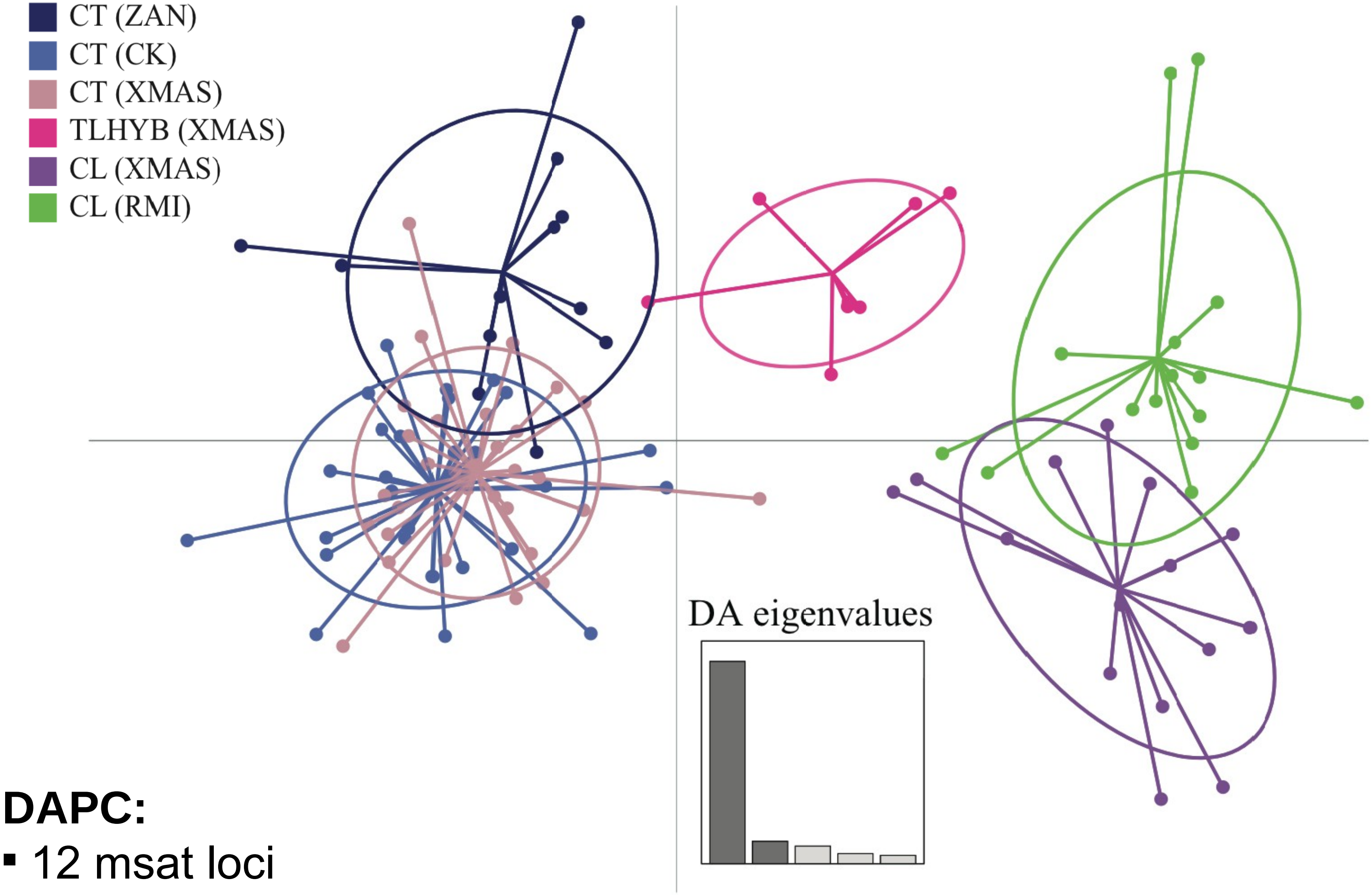
C. guttatissimus x C. punctatofasciatus



- hybrids intermediate
- mixed with parents

Nuclear msatDNA:

C. trifasciatus x C. lunulatus

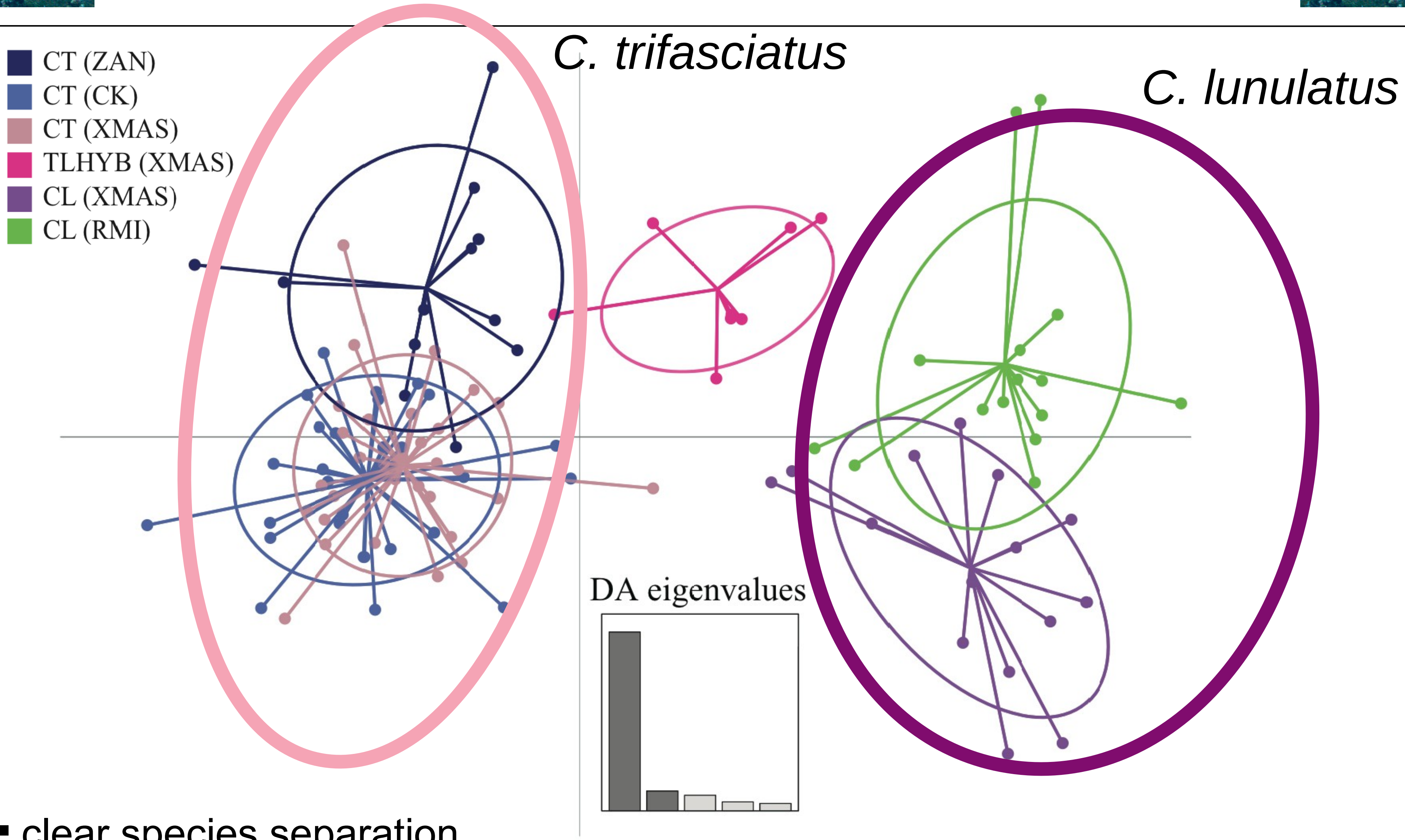


DAPC:

- 12 msat loci
- 36 PCs: 69% genetic variability retained

Nuclear msatDNA:

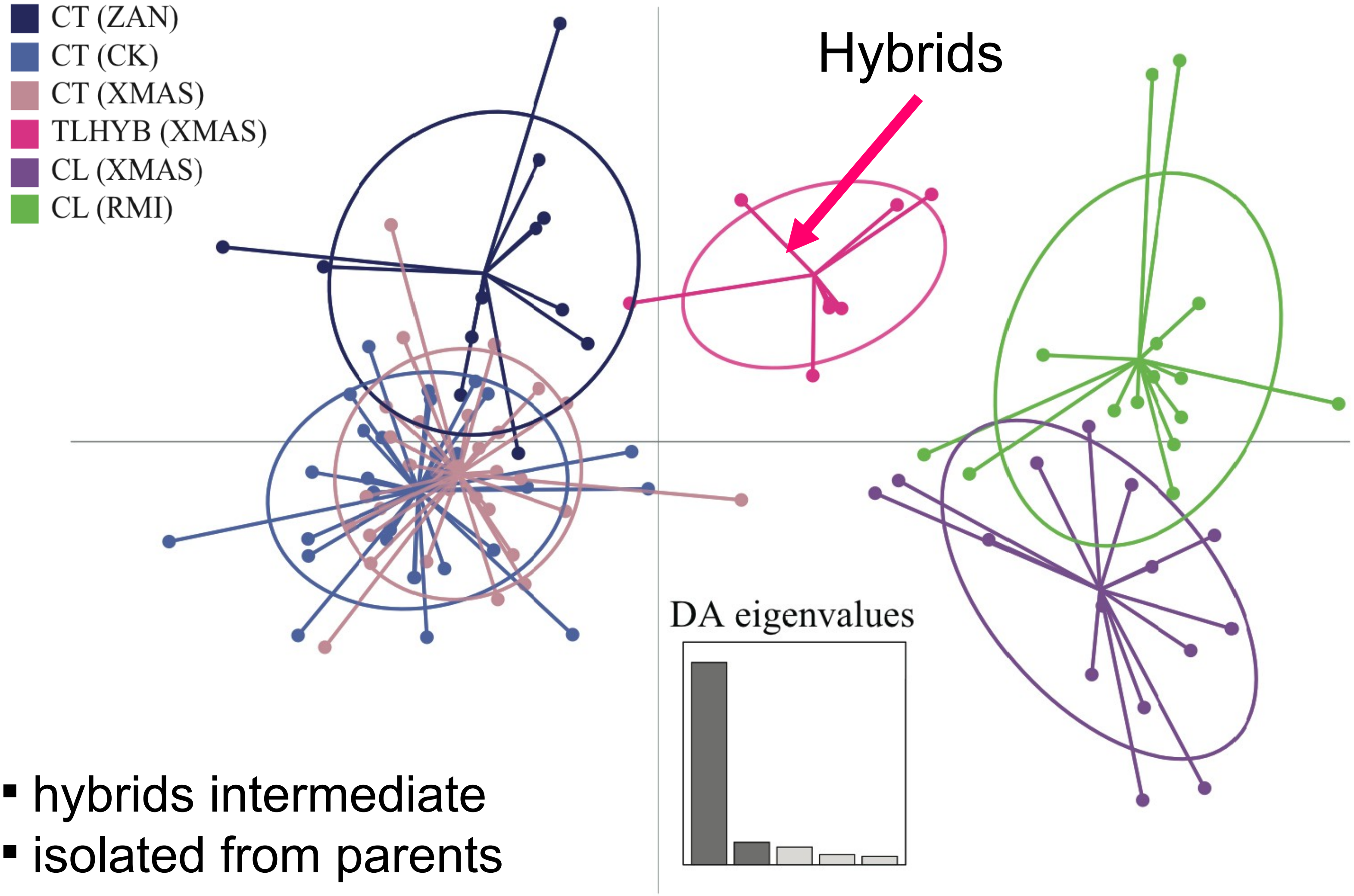
C. trifasciatus x C. lunulatus



- clear species separation

Nuclear msatDNA:

C. trifasciatus x C. lunulatus



Hybrids

- hybrids intermediate
- isolated from parents

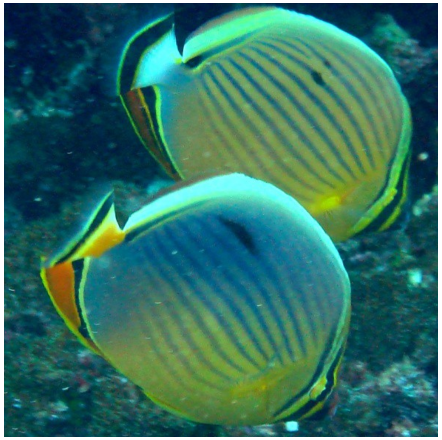
Conclusions

Similar ecological frameworks

- niche overlap
- rarity of parents
- non-assortative mating

Differences in genetics

- maternal inheritance
- introgression
- hybrid classes
- barriers to backcrossing



=> Hybridisation influenced by genetic break

Another mixed pair from Christmas Island?

Population	n	nh	*h*	*π*
Cocos Is. *C. guttatissimus*	18	14	0.95	0.007
Christmas Is. *C. guttatissimus*	25	19	0.93	0.004
Christmas Is. Hybrid	16	15	0.99	0.011
Christmas Is. *C. punctatofasciatus*	18	14	0.97	0.006
Marshall Is. *C. punctatofasciatus*	7	7	1	0.008

Population	n	nh	*h*	*π*
Zanzibar *C. trifasciatus*	10	6	0.89	0.007
Cocos Is. *C. trifasciatus*	28	10	0.82	0.002
Christmas Is. *C. trifasciatus*	28	8	0.71	0.001
Christmas Is. Hybrid	9	4	0.58	0.001
Christmas Is. *C. lunulatus*	15	8	0.83	0.005

Diversity metrics comparable between 2 hybridising groups