

Where did he come from?
Origin of the Maungatautari *H.*
duvaucelii specimen

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G. bl...

Duvaucel's gecko

- Largest extant New Zealand gecko

Pre-human

- Abundant New Zealand-wide

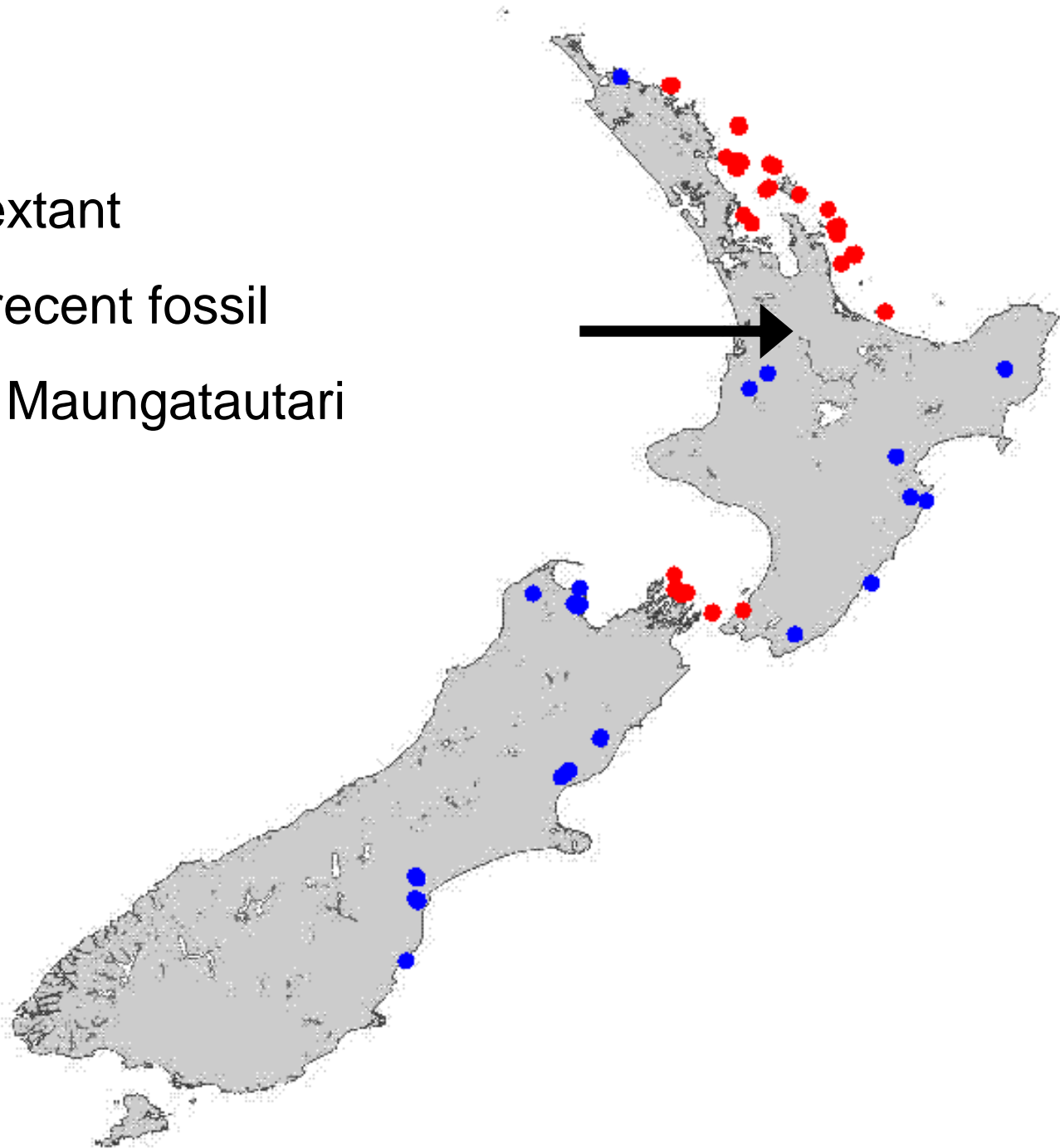
Post-human

- Abundant on offshore islands with no introduced mammals
- Low population density and reduced habitat range on kiore only islands – behaviourally cryptic
- Extremely rare on mainland at European settlement
- Last mainland specimens >60 years old

Red – extant

Blue – recent fossil

Arrow - Maungatautari



Maungatautari

- Fenced mainland sanctuary south of Hamilton
- 3363 hectares
- Eroded volcanic cone (797 m) with lowland podocarp/broadleaf forest
- Mammalian pests eradicated 2004-07 except for mice and a few rabbits and hares

Morphology of Maungatautari specimen

- **Size** (37 g) – northern animals considerably larger (to 118 g) than Cook Strait ones (to 49 g) – **matches Cook Strait**
- **Colour and pattern** – brighter and more boldly marked in Cook Strait – **matches Cook Strait?**
- **Lower labial scales** – decrease gradually in size in northern pops; abruptly smaller after fourth in Cook Strait pops – **matches northern**







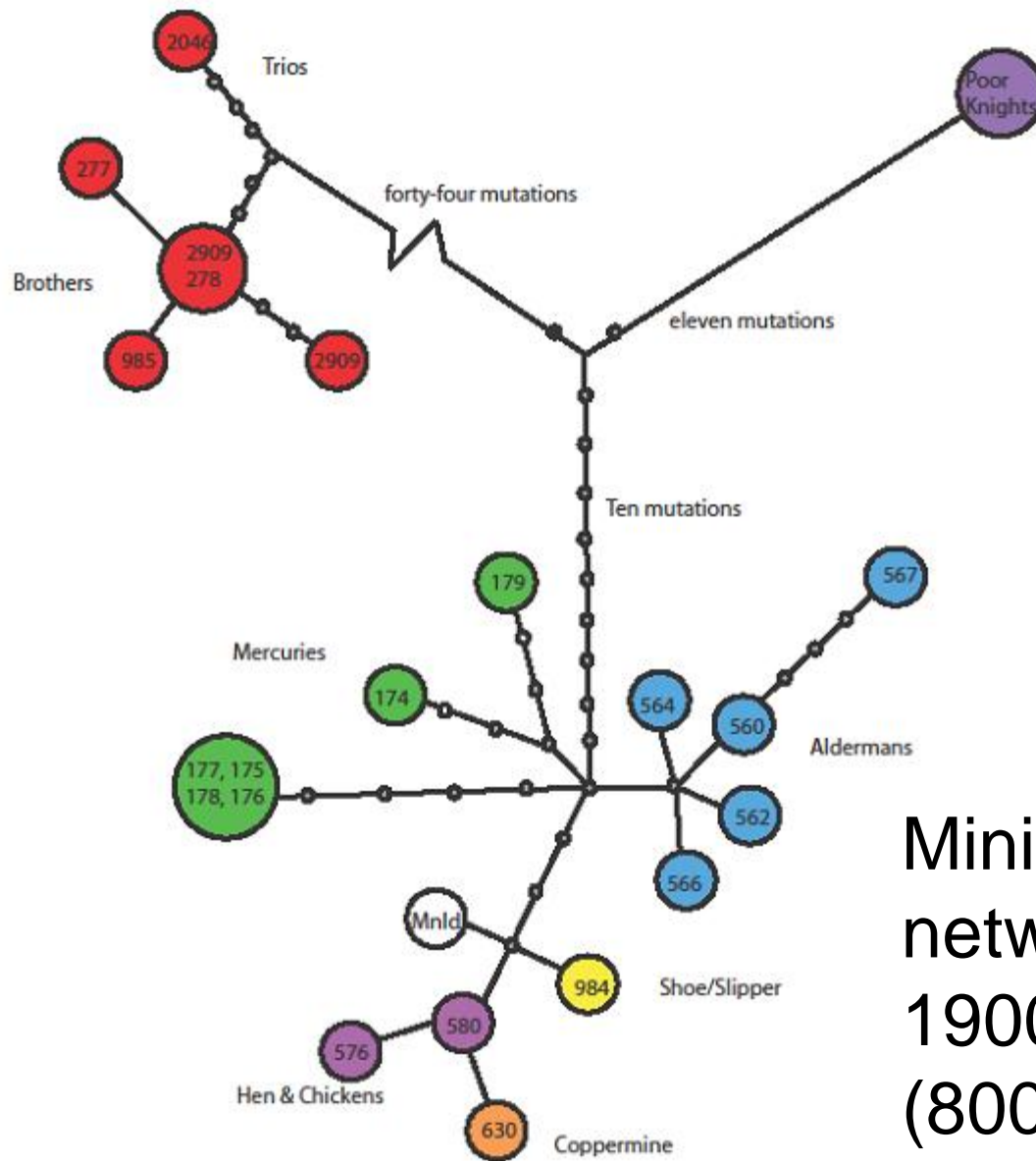
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DNA - Island groups sampled

- Poor Knights
- Hen & Chickens
- Mercuries
- Shoe group
- Aldermen
- Brothers
- Trios

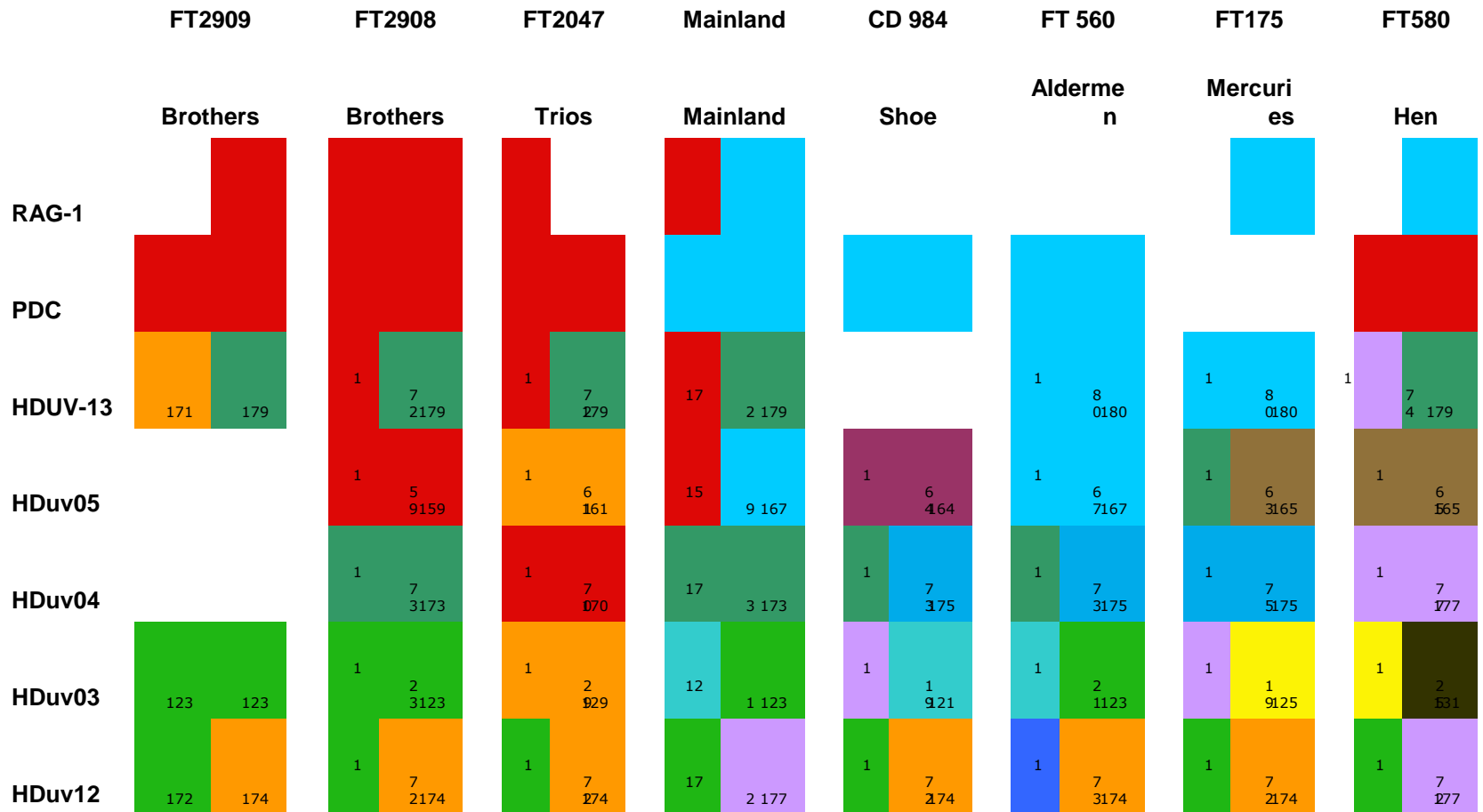
Island groups not sampled

- **Cavallis**
- Bream Islands
- **Mokohinaus**
- Great & Little Barrier
- Cuvier
- Ohinaus
- Motukahakaha Island (BOP)



Minimum spanning network
 1900 bp mtDNA
 (800 16S, 1100 ND2)

Nuclear alleles



Nuclear alleles in Maungatautari specimen

RAG-1	Brothers + Trios	Mercuries + Hen
PDC	Shoe + Aldermen	Shoe + Aldermen
HDUV-13	Brothers	Brothers + Trios + Hen
HDuv05	Brothers	Aldermen
HDuv04	Brothers	Shoe + Aldermen
HDuv03	Brothers	Shoe + Aldermen
HDuv12	Everywhere	Hen

Stats

Small samples, so underestimation of:

- allele sharing between samples
- allelic diversity within samples

Maungatautari specimen has:

- no private nuclear alleles
- highest allelic diversity and heterozygosity of any sampled individual

Preliminary conclusions

- Two scenarios consistent with data at this point
- We disagree on 'best guess' conclusion
- Ex captive of mixed island origin? (RAH)
- Mainland survivor? (MM-R)

Ex captive of mixed island origin?

- High allelic diversity and polymorphism but absence of private alleles consistent with recent between-population hybridisation
- Genetic profile mostly consistent with father from North Brother and mother from eastern Coromandel island
- Genotype consistent with a multi generation cross involving a Hen (or nearby) island ancestor
- Known captive founders from Brothers, Shoe/Slipper group, probably Bream Islands

Mainland survivor?

A natural mainland population would also perhaps:

- combine northern and Cook Strait alleles
- have higher allelic diversity and polymorphism than island populations

H. duvaucelii are very long-lived, and genetic signature of population bottlenecking is not necessarily evident during a decline – shows up after the bottleneck

Another *H. duvaucelii* in a rat trap on Great Barrier Island, January 2011 – but records there until at least 1970s

What evidence would suggest one or other of these alternative conclusions?

Mainland, expect:

- divergence in mt-DNA haplotypes?
- private alleles not seen in island populations?
- **but** island populations of lizards large, not necessarily bottlenecked, so maybe not

North/South balance of alleles too close for northern population?

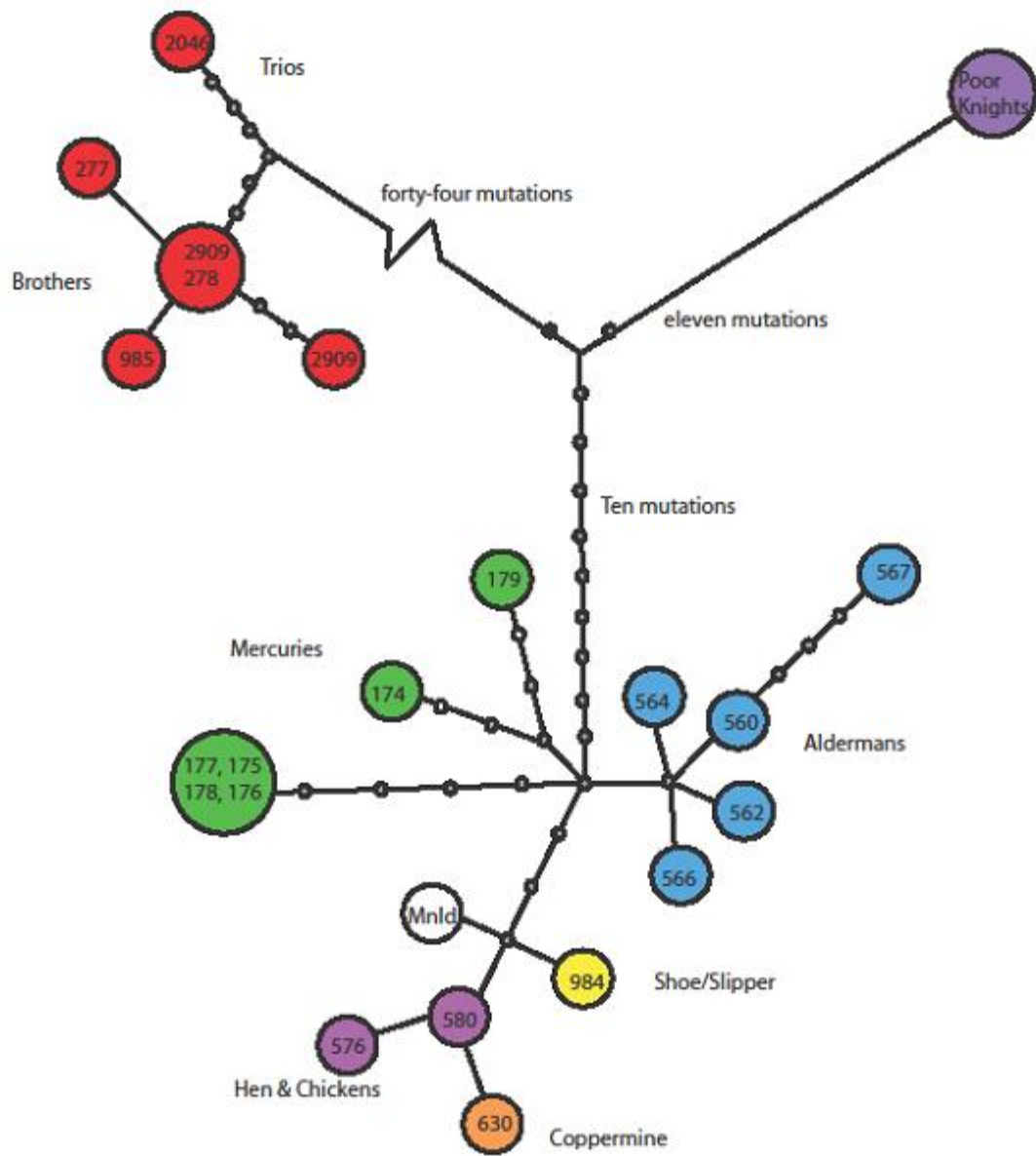
Brothers, not Trios alleles where these differ

What next

- Look for more – under way
- Confirm microsatellite genotypes for all available island samples/all loci – under way
- Genotype captive individuals of known and unknown origin – under way
- Genotype mainland fossil bones?

Mitochondrial tree

- Minimum spanning network of 1900 bp mtDNA (800 16S, 1100 ND2) from *Hoplodactylus duvaucelii*
- c. 3.4% sequence divergence between northern and southern populations
- Poor Knights sample c. 1.4% divergent from other northern populations (land bridge islands)



cf. tuatara (Hay et al. 2010)

Gecko has:

- similar pattern
- much greater mt-DNA sequence divergence north-Cook Strait
- more microsatellite divergence north-Cook Strait – far more private alleles and some loci with no shared alleles (but small sample sizes)

