A nana-rama? – an exploration of genetic divergence and cryptic morphology in the Kimberley *Gehyra nana*

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Background

The rugged terrain of the Kimberley Plateau in north-western Australia is a recognised hotspot of gekkonid diversity. The availability of moist, rocky refugia may have supported species survival and diversification during past climatic fluctuations. The Kimberley *Gehyra*, which currently comprise eight species, are one component of a diverse fauna endemic to the region. The *Gehyra* genus displays considerable within-species variation yet conservative interspecific morphology, and this is reflected in the frequent misidentifications in *Gehyra* of broadly similar appearance, including the common and widespread rock-inhabiting *Gehyra nana*. Thus, our goal was to complete a genetic and morphological review of these 'small brown spotty geckos'.

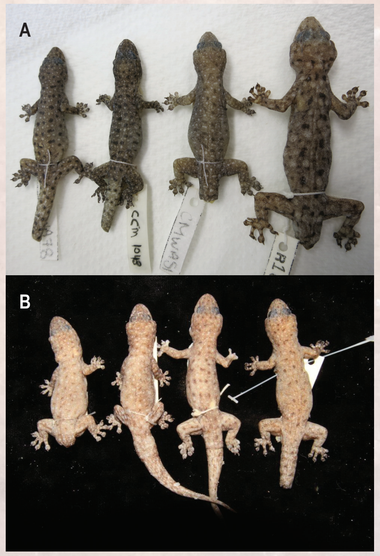

Figure 1: SPOT the difference:
A: (L to R) nana1, nana4, nana6, nana5
B: variation in type nana (nana4)

Results & Discussion

- *G. nana* is paraphyletic for mtDNA with high lineage diversity. Candidate lineages and species in the 'nana complex' have an average sequence divergence of 20-30%, on a par with that across the *Australis* group.
- Morphological data was obtained from ~20 specimens of each candidate lineage and sister species (genotypes were based solely on MtDNA results).
- Multivariate analyses (Principal Components and Discriminant Function) analyses were performed on 13 body measurements and 8 meristic characters.
- There is considerable overlap in body size and meristic characters; however, *G. occidentalis*, nana5 and south Kimberley sp. can be differentiated from a group consisting of nana1, nana4 and nana6, and *G. multiporosa*.
- Our ability to separate *multiporosa* from sympatric 'nana' in the north Kimberley would be compromised if *multiporosa* mtDNA introgresses locally into nana4 & nana6
- Results suggest multiple overlapping lineages in both the north and south of the Kimberley. The southern lineages should be diagnosable using a combination of body size, meristic characters and dorsal pattern. The northern lineages are more problematic, and it is difficult to reliably identify ungenotyped individuals.
- Currently there are eight described *Gehyra* species in the Kimberley. Diversity of this region remains underestimated and the number of recognised *Gehyra* species could at least double.

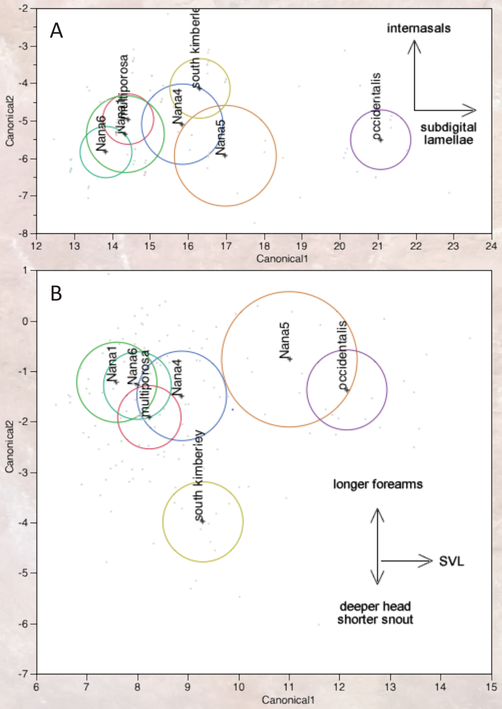

Figure 2: Canonical plots of A) meristic characters, and B) body size

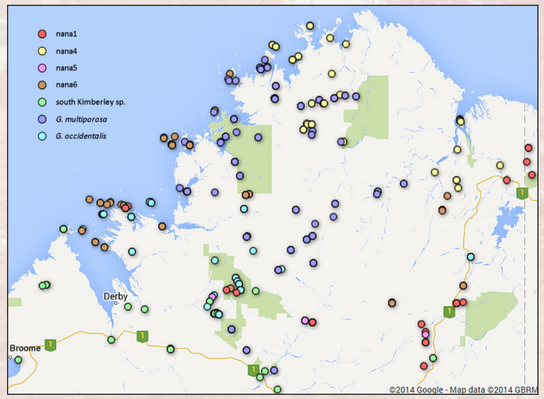

Figure 3: Distribution of genotyped *Gehyra* (Kimberley 'nana' groups, south Kimberley sp., *G. multiporosa* & *G. occidentalis*) in the Kimberley region, WA.

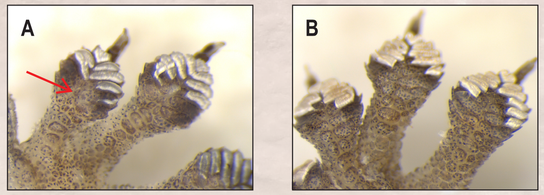

Figure 4: Toe pads of nana6 individuals showing A) granule present between proximal subdigital lamellae, and B) granule absent

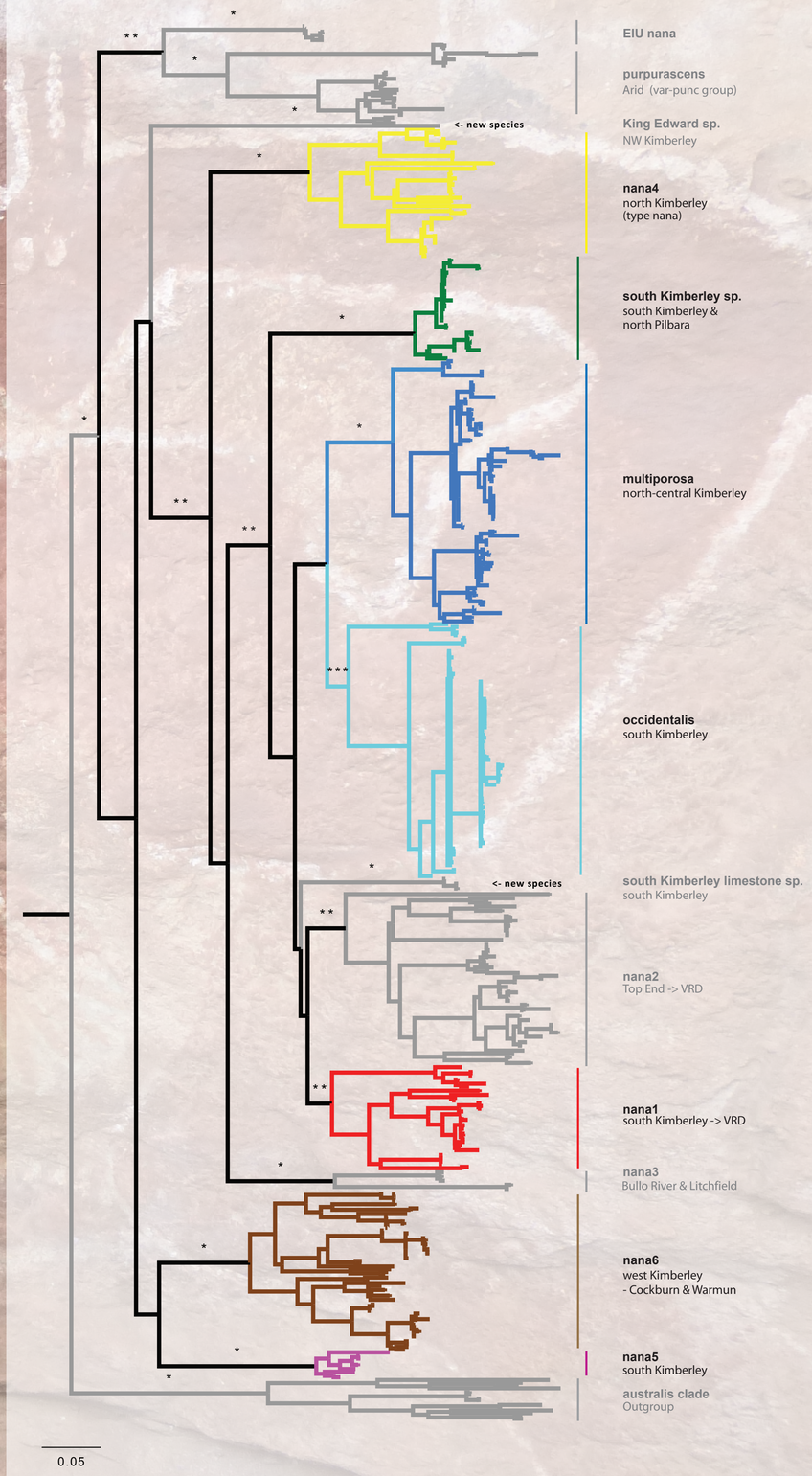

Figure 5: Preliminary phylogenetic tree using RAxML with GTR+G model for 504 individuals for 1124bp of ND2 gene. Model selection was carried out using PartitionFinder (* = 100, ** = 95 – 98, *** = 94 bootstraps).

Future directions

- Analysis of >20 nDNA loci using sequence capture is underway to test lineage boundaries and resolve their relationships, and to check for introgression.
- More intensive analysis of emerging contact zones
- Further molecular investigation of new lineages, including EIU nana, south Kimberley limestone sp., nana5 and King Edward sp.
- Further morphological investigation, including CT scanning of bone structure

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