

COMPLETION REPORT

Geographic variation of colour morphs in tawny dragon lizards: potential causes and role in biodiversity.

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ABSTRACT

Polymorphism is the existence of multiple morphs within a single population and may play an important role in speciation. The Australian tawny dragon lizard, *Ctenophorus decresii* is polymorphic for male throat coloration. Extensive field surveys show that populations of *C. decresii* vary in the number, type and frequency of different colour morphs present. Genetic analysis also indicates three lineages within the species which correspond to major differences in coloration. Divergence in appearance and genetics can lead to incompatibilities between populations and subsequent speciation. Consequently, different lineages of *C. decresii* are likely to be in the early stages of speciation. This study shows that colour variation is associated with genetic divergence, and lineages that differ in coloration show limited admixture, thus supporting a link between colour polymorphism and processes generating new species (speciation).

INTRODUCTION

“What processes generate biodiversity?” remains a fundamental question in evolutionary biology. Some species, termed colour polymorphic, exhibit extreme diversity within populations in the form of discrete colour variants (or morphs; [1, 2]). Colour polymorphism may play an important role in speciation, particularly when populations differ in the frequency of colour morphs or when different morphs are present in different localities. This is because colour morphs often differ in traits other than colour (e.g. behaviour, morphology, physiology, or life history; [3]), therefore populations that differ in morph composition may become incompatible, potentially giving rise to separate species [4]. Although many polymorphic species exhibit inter-populational differences in morph composition [e.g.5, 6, 7], very few studies have looked at this geographic variation or its role in speciation.

The tawny dragon lizard, *Ctenophorus decresii*, provides an ideal species to investigate potential causes and consequences of geographic variation in polymorphism. The species is restricted to rocky outcrops throughout South Australia and western New South Wales (NSW). Males are polymorphic for throat coloration and populations differ in the number, type and frequency of colour morphs present. Previous research (conducted by me as part of this project) identified three genetically distinct lineages, corresponding with major differences in coloration (Figure 1). I discovered that NSW populations are deeply genetically divergent, and clearly comprise a separate species, which I am currently describing (McLean et al, in prep). Within SA, there are two lineages, corresponding to a ‘northern’ and ‘southern’ lineage. Populations throughout the ‘northern’ lineage are polymorphic, exhibiting four discrete male throat colour morphs (orange, yellow, orange and yellow, grey; [8], McLean *et al*, unpublished data). Conversely, the ‘southern’ lineage is monomorphic with a unique blue throat colour morph. For this project, I aimed to 1)

conduct extensive field surveys and investigate population morph frequencies in the polymorphic 'northern' lineage of *C. decresii*, and 2) investigate how divergence in coloration may generate reproductive isolation between the 'northern' and 'southern' lineage.

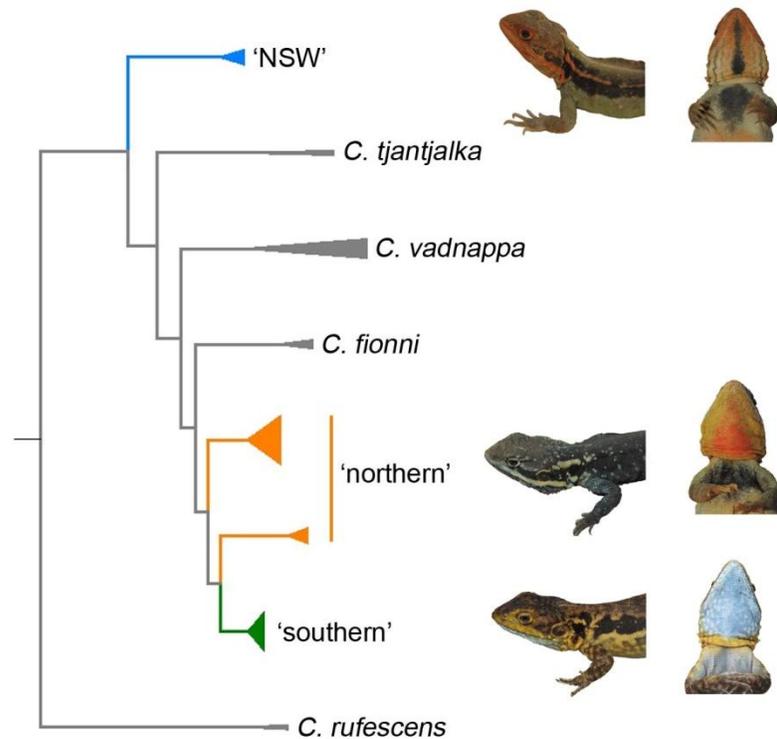


Figure 1. Simplified gene tree showing the three lineages of *C. decresii* (coloured) and closely related species. There are major differences in male coloration (examples shown). Note that the 'NSW' lineage is positioned more basally in the tree.

METHODOLOGY

To determine morph composition and frequencies in different localities, 20-30 *C. decresii* males were captured and photographed in 11 populations in South Australia and New South Wales (7 in the Flinders Ranges, 1 in the Mt Lofty Ranges, 1 on Kangaroo Island, 1 in the Olary Ranges, and 1 near Broken Hill). Each male was classified into a discrete throat colour morph using quantitative colour analysis of photographs [9]. I also surveyed an area between the Flinders and Mt Lofty Ranges, which represent a genetic break between the 'northern' and 'southern' lineage (Figure 2), to investigate if and where the lineages come into contact and the level of admixture between them. Tissue samples for genetic analysis were also collected from across the species entire distribution. A section of mitochondrial DNA (ND4), five nuclear genes (α -enolase intron 8, BACH1, FSHR, MKL1, and SLC8A1), and 10 microsatellite markers were used to infer the genetic relationship between populations, and assess population history and gene flow between lineages.

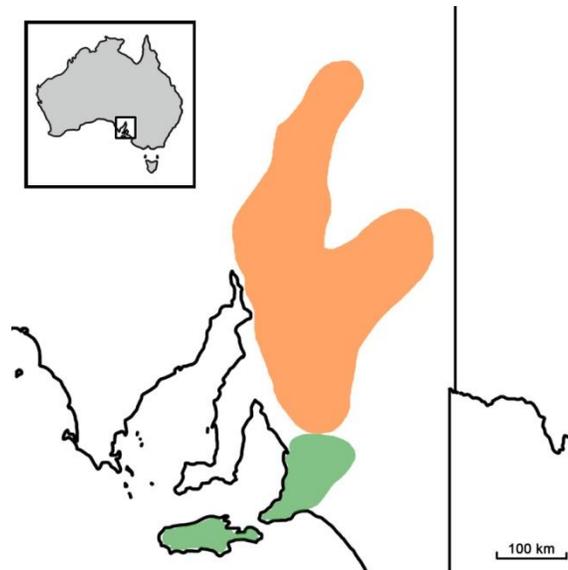


Figure 2. Map showing the distribution of ‘northern’ (orange) and ‘southern’ (green) *C. decresii* and indicating the area of contact between the two lineages.

RESULTS AND DISCUSSION

All populations of *C. decresii* throughout the ‘northern’ lineage are polymorphic and the eight populations surveyed contained all four recognised morph types (orange, yellow, orange and yellow (pictured, Figure 1), and grey; [8]);). The relative frequency of morph types varied considerably among populations. For example, orange and grey males were generally rare, however, orange was the most common morph type in the most eastern population (Bimbowrie Station) and grey was the most common morph type in the most northern population (Aroona). This suggests that local evolutionary processes (selection, gene flow, chance) are influencing morph frequencies throughout the ‘northern’ lineage. Conversely, in the ‘southern’ lineage all males had blue throat coloration (Figure 1). Genetic analysis indicated that the ‘northern’ and ‘southern’ lineages may have been isolated to the Flinders Ranges and Mt Lofty Ranges respectively during historical glacial cycles [10, 11], resulting in divergence in coloration during isolation. I found a zone of secondary contact between the lineages in the Barossa Valley (Figure 2), where limited genetic admixture was occurring. However, I found a sharp discontinuity in coloration (as opposed to a smooth clinal change from ‘northern’ to ‘southern’ coloration) and no individuals of intermediate coloration. Consequently, it appears that there may be some level of reproductive isolation between the two lineages. As coloration is likely to be an important social signal involved in species recognition [11-13], divergence in coloration may be acting as a barrier to gene flow between the ‘northern’ and ‘southern’ lineage. Therefore, the lineages of *C. decresii* may be in the process of becoming separate species, supporting a link between geographic variation in polymorphism and speciation.

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