Comparative Genomics: Evolution of lizard viviparity

Analysis of oviparous and viviparous individuals of the common lizard reveals the genetic architecture of pregnancy

Camilla M. Whittington

The University of Sydney, School of Life and Environmental Sciences, Sydney, New South Wales, 2006, Australia.

camilla.whittington@sydney.edu.au

There are few more impressive examples of convergent evolution in animals than the repeated origins of live birth. This trait, called viviparity, has evolved from the egg-laying alternative, oviparity, at least 150 times in vertebrates (Figure 1), and many times in invertebrates[1,2]. In squamates alone (lizards, snakes and amphisbaenians), viviparity has evolved at least 115 times[1], and this group includes the only vertebrate examples of a strange phenomenon in which some species use both egg-laying and live-bearing reproductive modes. Writing in *Nature Ecology and Evolution*, Recknagel *et al.*[3] take advantage of the bimodal reproduction of the European common lizard, *Zootoca vivipara*, to investigate the genetic basis of reproductive mode.

Most research into live birth focuses on therian mammals– eutherian mammals and marsupials. But the body of literature exploring viviparity in squamate reptiles and fishes is growing rapidly. Concurrently, physiological similarities are being recognised between viviparous species and egg-laying animals with elaborate forms of parental care, such as the marsupial frogs and syngnathid fishes that brood their embryos in/on the body of the parent[4]. This research identifies a core set of functions that appears to be common to gestational tissues across taxa, in support of internally developing embryos, including adaptations to facilitate respiratory gas exchange, immune modulation to protect developing embryos from the parents' immune system, and in some cases, supply of nutrients through pregnancy [reviewed in 5]. These morphological and physiological similarities highlight the utility of a comparative approach in understanding how, and why, pregnancy evolves.

In just a handful of species of lizards and snakes, there are both oviparous *and* viviparous individuals in different regions of the species range. The strongest evidence of reproductive bimodality comes from two Australian lizards (*Lerista bougainvillii* and *Saiphos equalis*), a water snake (*Helicops angulatus*), and the best-studied, the European common lizard *Zootoca vivipara*[6]. Decades of research has established physiological [e.g. 7], morphological [e.g. 8], and genetic differences, including striking chromosomal alterations [e.g. 9], between egg-laying and live-bearing *Z. vivipara*.

Within a species, these animals presumably have little variation in traits not related to reproductive strategy, making them ideal for interrogating the specific differences supporting egg-laying versus live-bearing. While previous work has revealed interesting genomic and gene expression differences between closely related oviparous and viviparous species pairs[10,11], comparisons *within* a species are rare[12]. Recknagel *et al.*[3] use both genomic and gene expression data in egg-laying and live-bearing European common lizards to identify candidate genes associated with reproductive mode. *Zootoca vivipara* represents a powerful system for this research because hybridisation between the two parity modes occurs both naturally and in the laboratory [e.g. 13]. Hybridisation is probably possible because the oviparous and viviparous populations diverged recently (~4.5 mya[14]). The authors sampled lizards in a natural contact zone of oviparous and viviparous populations, where hybridization occurs. They comprehensively phenotyped clutches for stage of embryonic development at egg deposition, the incubation duration (if any) for eggs, and eggshell traits. Oviparous mothers deposit eggs at earlier stages of embryonic development, with longer incubation periods, and with thicker calcified eggshells, than viviparous mothers. The authors genotyped the mothers to identify genomic differences between oviparous, viviparous, and hybrid individuals. In conjunction, they compared uterine gene expression between oviparous and viviparous mothers. An overlap of the two datasets identifies nearly 100 candidate genes that are both genetically different between parity modes *and* differentially expressed in the uterus. The authors also identified significant overlap of loci under selection and those expressed differently in oviparous and viviparous uteri. Collectively, these candidate genes are intriguing possibilities for future study, with putative functions in tissue remodelling and angiogenesis, control of gestation length, and maternal immune response, as we would predict from studies of other viviparous animals.

Recknagel *et al.*[3] also address the question of whether the convergent evolution of pregnancy involves the same genes by identifying overlap in gene use in gestational tissues between *Z. vivipara* and those in other viviparous (mammals, squamates) and oviparous, brooding (seahorse) species from published datasets. More similarities are observed between closely related taxa (e.g. across amniotes) than those that are distantly related or use non-homologous gestational tissues (e.g. amniotes and seahorse). A strict quantitative comparison is unfortunately ruled out because of methodological variation between studies, but the authors identify interesting parallels in gestational tissue-expressed genes across pregnant species that diverged ~450 mya, a phenomenon also recognised across other animals[e.g. 15].

This study highlights the utility of bimodally reproductive squamates in understanding the mechanistic basis of pregnancy. The option to compare extremes of reproductive phenotype *within* a species is uniquely powerful. These lizards also present the opportunity to answer ultimate questions surrounding the evolution of pregnancy, including under which conditions viviparity is favoured, as well as why such extreme phenotypic variation is maintained within species with bimodal reproduction.

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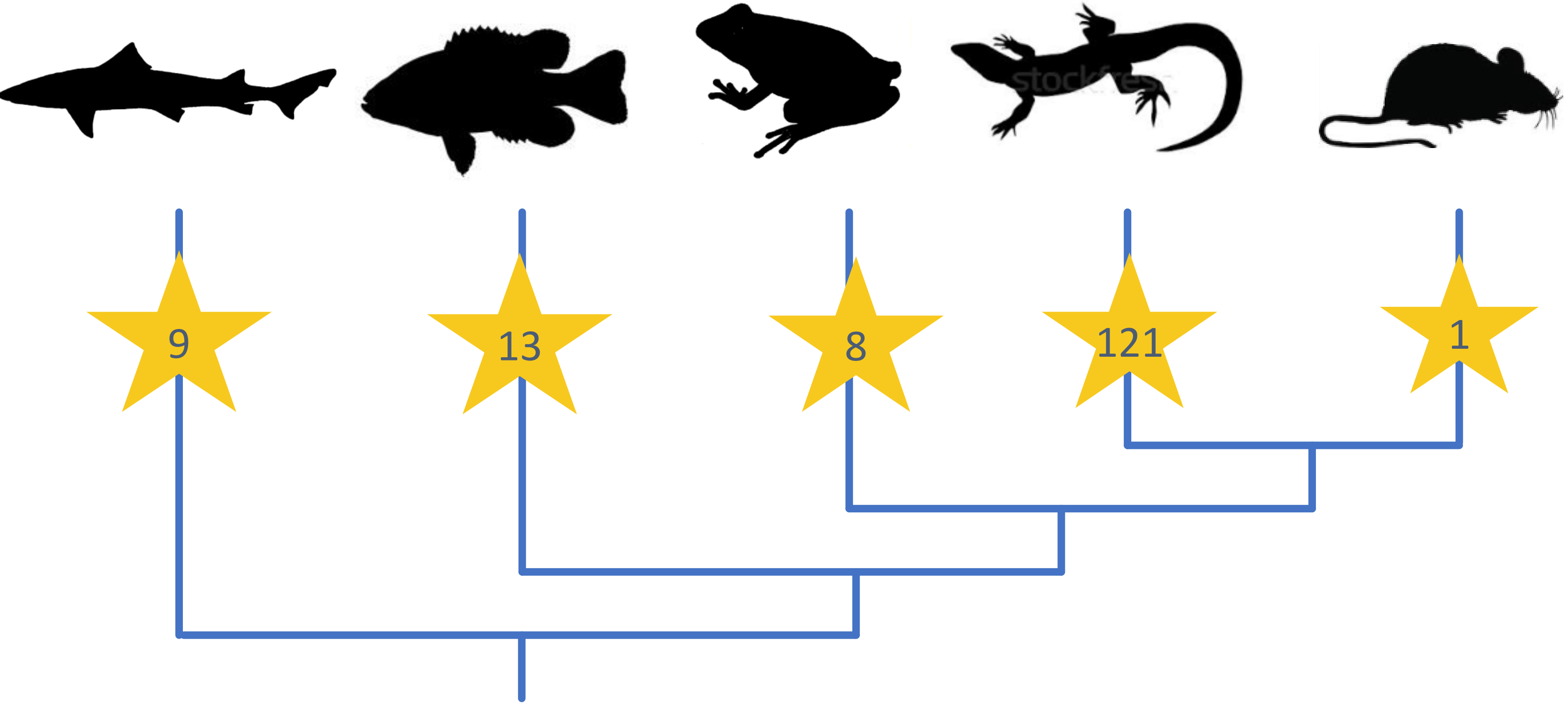
Figure 1. Evolution of viviparity in vertebrates.

Viviparity has evolved multiple times independently, including 121 origins in reptiles, 115 of which are in extant squamates (lizards, snakes, and amphisbaenians)[1]. Only very few vertebrate species, all of which are squamates, exhibit reproductive bimodality (individuals of the same species are either oviparous or viviparous). The numbers within the stars indicate the number of independent evolution events of viviparity in each lineage (L-R silhouettes represent: Chondrichthyes; paraphyletic group of fishes, Actinopterygii and Sarcopterygii [excluding Tetrapoda]; Lissamphibia; Reptilia; Mammalia). There is an additional origin of viviparity in Placodermi, not shown.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