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Squamate Genome Size

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Fig. 1 Box-plot comparisons of genome size estimates based on three different methods. For all panels, methods are abbreviated: FCM flow cytometry, SFC static flow cytometry, FD Feulgen density. (a) Genome size estimates for all lizard and snake species that have been measured by all three methods. (b) Genome size estimates for all snake and lizard species that have been measured by at least one of the three methods. (c) Genome size estimates for lizard species that have been measured by at least one of the three methods. (d) Genome size estimates for snake species that have been

differences in accuracy and precision. Genome size estimates using each of the three techniques for all squamates with data currently available in the Animal Genome Database (Gregory 2013) are summarized in Fig. 1, separated by technique. These estimates (Fig. 1) show multiple forms of bias across methods. Squamate genome size estimates from Feulgen density and static cytometry are bigger and have a much higher variance than other measurements. These two techniques are thus less precise and possibly less accurate than flow cytometry (Fig. 1a). Thus, previous perspectives of high variance in genome size among squamate reptiles based on these estimates may be artifactual, due to the methodological inconsistency of the techniques used. There is a strong argument for careful interpretation of genome size estimates made by methods other than flow cytometry methods.

The average squamate haploid genome size estimate based on flow cytometry is 1.9 Gbp ($n = 90$, range = 1.3–3.0 Gbp; Fig. 2b). This average is intermediate in size between birds (1.4 Gbp) and mammals (3.5 Gbp) and is also smaller than other non-avian reptiles (3.2 Gbp in Testudines and Crocodilia and 5.0 Gbp in *Sphenodon* (Janes et al. 2010b)). The average lizard genome size based on flow cytometry is also 1.9 Gbp ($n = 58$, range = 1.3–2.8 Gbp; Fig. 2c). The average snake genome size based on flow cytometry is also 1.9 Gbp ($n = 32$, range = 1.5–3.0 Gbp; Fig. 2d). Previous work on the pattern of genome size evolution found that the Reptilia have experienced continuous gradual evolutionary change in genome size with no rapid shifts in genome size since the early reptile radiation (Organ et al. 2008). Other research, however, has found that larger genomes evolve in size

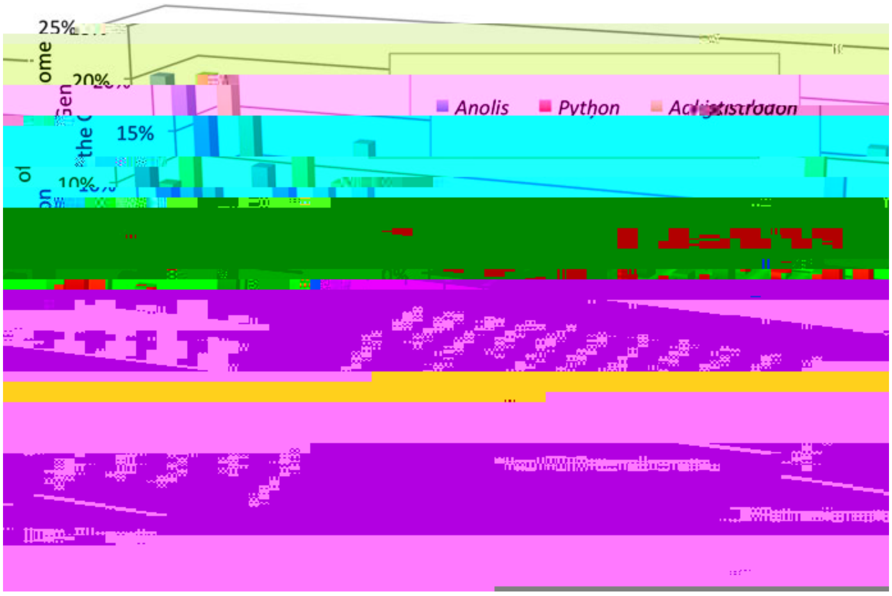

Fig. 2 [illegible] Anolis carolinensis, Python molurus bivittatus, [illegible] Agkistrodon contortrix. [illegible] horizontal axis. [illegible] vertical axis [illegible] (2011) [illegible] Anolis [illegible]

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Squamate Genome Structure

The Mitochondrial Genome

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Genomic GC-Isochore Structure

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Ultraconserved Regions

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Microsatellite Seeding by Transposable Elements

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Genomics of Squamate Venom Toxins

Genetic and Genomic Structure of Squamate Venom Toxins

[illegible]

identified such effects, it is reasonable that there may be epigenetic regulatory effects that additionally modulate expression of venoms. Among vertebrates, snakes in particular possess a tremendous number of unique or extreme phenotypes. A greater understanding of the molecular and genomic basis of these phenotypes holds exciting potential to increase broad understanding of the function and functional flexibility of the vertebrate genome and to illuminate the mechanisms by which such unique phenotypes can be evolutionary created from the raw material of the common vertebrate genome plan.

As more squamate genome and gene expression data become available, the toxinological community might consider a careful reevaluation of the precise language used for putative toxins

References

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[illegible] (Thamnophis sirtalis). [illegible] . 2011 2 – 0.

[illegible] (Python molurus bivittatus). [illegible] . 2011 [illegible]

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Index Terms: