

1. $\int_0^1 x^2 dx = \frac{1}{3}$

2. $\int_0^1 x^3 dx = \frac{1}{4}$

3. $\int_0^1 x^4 dx = \frac{1}{5}$

Heloderma, Pogona, Varanus (2006).

Squamate Genome Size

(2001). (200).

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 (2010) are summarized in Fig1, separated by technique. These estimates (Fig1) 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 cytometry (Fig1a). 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 cytometry methods.

The average squamate haploid genome size estimate based on cytometry is 1.9 Gbp (n=90, range 1.3–3.0 Gbp; Fig2b). 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 Crocodylia 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; Fig2c). The average snake genome size based on flow cytometry is also 1.9 Gbp (n=32, range 1.5–3.0 Gbp; Fig2d). 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

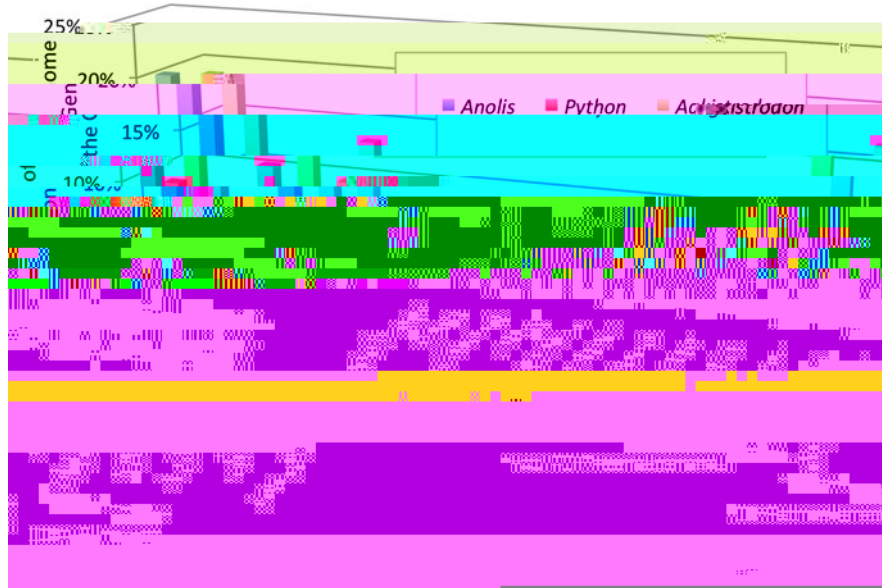
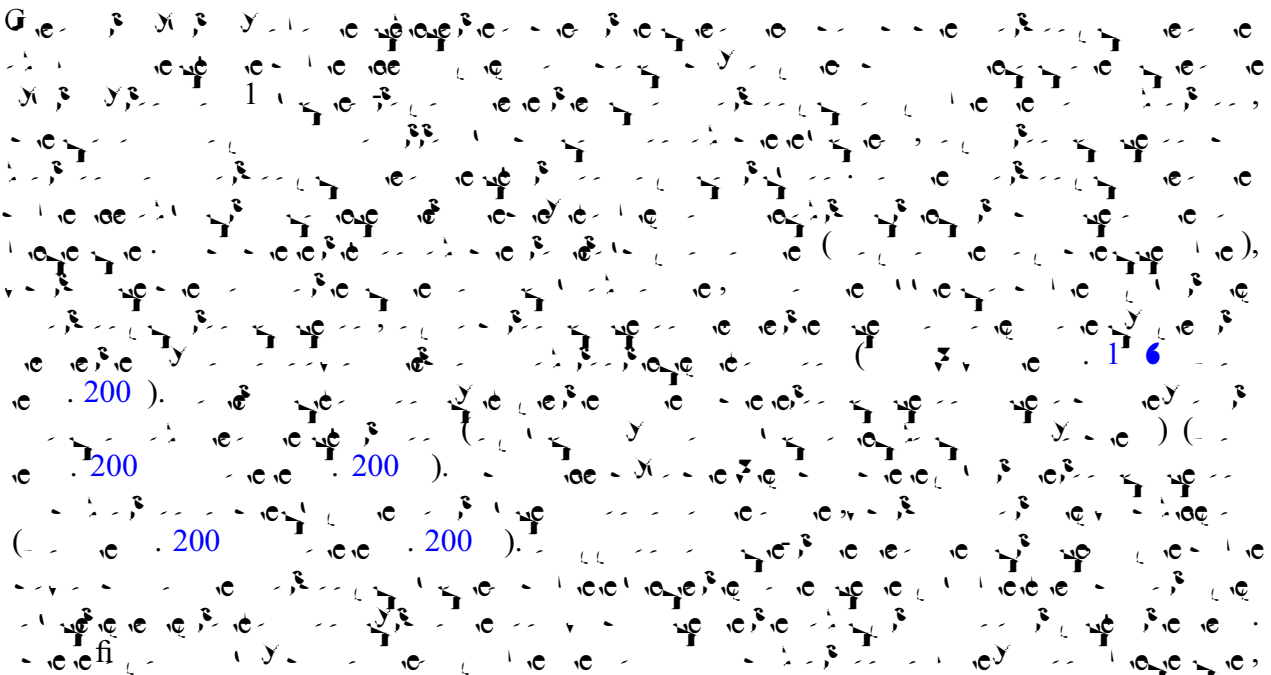


Fig. 2 Anolis carolinensis, Python molurus bivittatus, Agkistrodon contortrix. horizontal axis. vertical axis. (2011)

Anolis (200). Python (200). Agkistrodon (200).

Squamate Genome Structure

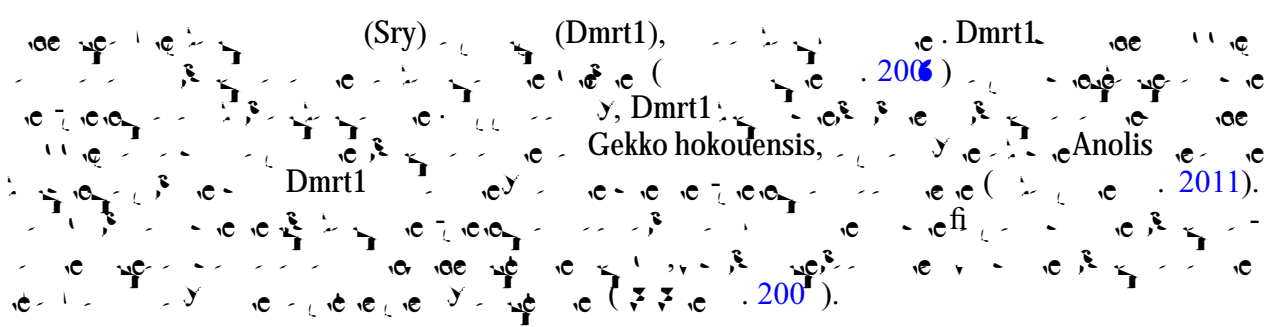
The Mitochondrial Genome



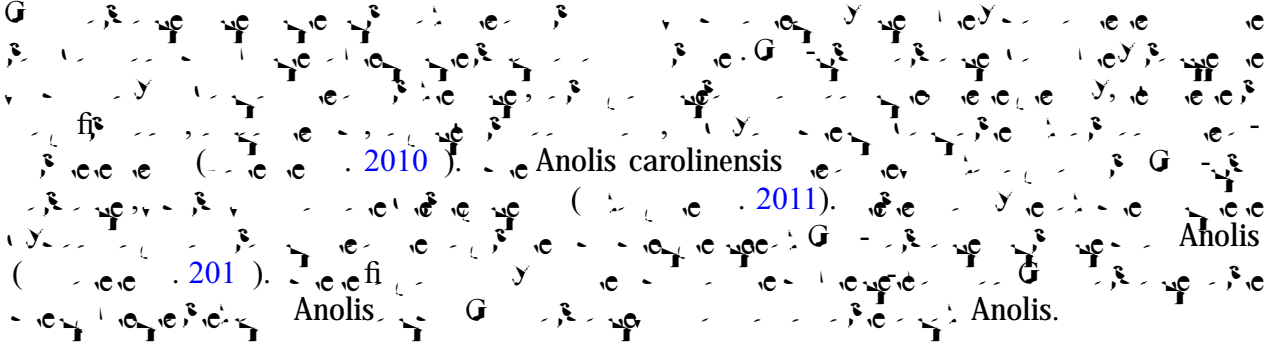
200 ()
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Nuclear Chromosomal Structure

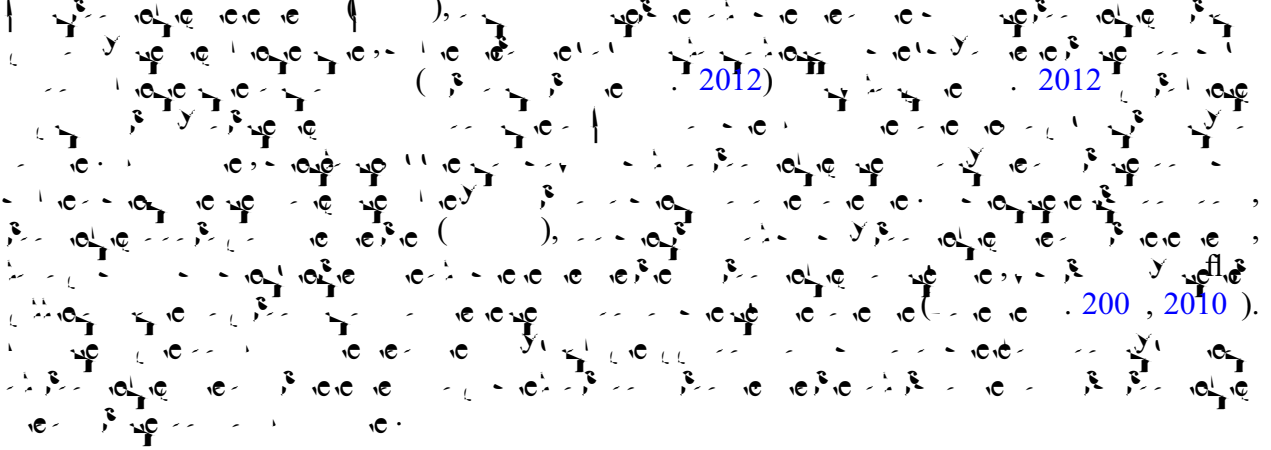
(200)
 1 6) (2000)
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 2n = 10
 (200)
 200



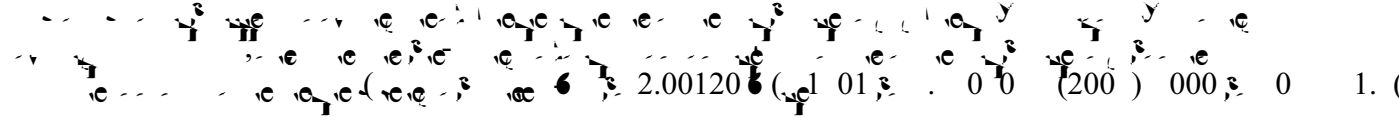
Genomic GC-Isochore Structure



Ultraconserved Regions



Transposable Element Diversity



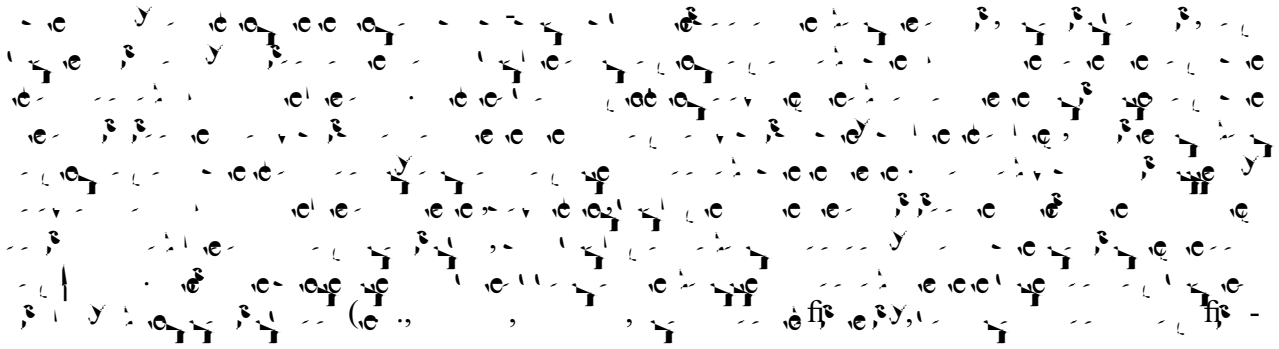
Anolis (.201).
1

Microsatellite Seeding by Transposable Elements

Microsatellite seeding by transposable elements is a process where repetitive DNA sequences are introduced into a genome by mobile genetic elements. This process can lead to the expansion and diversification of microsatellite regions, which are often used as markers in genetic studies. The mechanism involves the insertion of transposable elements into existing microsatellite repeats, creating new alleles with different lengths and structures. This process is particularly significant in the evolution of highly polymorphic microsatellite loci.

Genomics of Squamate Venom Toxins

Genetic and Genomic Structure of Squamate Venom Toxins



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 exibility 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

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Index Terms:

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