

Do Time, Heterochromatin, NORs, or Chromosomal Rearrangements Correlate with Distribution of Interstitial Telomeric Repeats in *Sigmodon* (Cotton Rats)?

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Abstract

We studied the chromosomal distribution of telomere repeats (TTAGGG)_n in 8 species of *Sigmodon* (cotton rats) using chromosome paints fluorescent in situ hybridization (FISH) from *Sigmodon hispidus*. In 2 species with the proposed primitive karyotype for the genus, telomere repeats were restricted to telomeric sites. But in the other 6 species that include 3 with proposed primitive karyotypes and 3 with highly rearranged karyotypes, telomere repeats were found on both telomeric sites and within interstitial telomeric sites (ITSs). To explain the distribution of ITS in *Sigmodon*, we gather data from C-bands, silver nitrate staining, G-bands, and chromosomal paint data from previous published studies. We did find some correlation with ITS and heterochromatin, euchromatic chromosomal rearrangements, and nucleolar organizing regions. No one type of chromosomal structure explains all ITS in *Sigmodon*. Multiple explanations and mechanisms for movement of intragenomic sequences are required to explain ITS in this genus. We rejected the hypothesis that age of a lineage correlates with the presence of ITS using divergence time estimate analyses. This multigene phylogeny places species with ITS (*S. arizonae*, *S. fulviventer*, *S. hispidus*, *S. mascotensis*, *S. ochrognathus*, and *S. toltecus*) in the clade with a species without ITS (*S. hirsutus*). Lineages with ITS (*S. arizonae* and *S. mascotensis*) arose independently from a lineage absent of ITS (*S. hirsutus*) around 0.67 to 0.83 Ma. The rearranged karyotypes of *S. mascotensis* and *S. arizonae* appear to be an independently derived autapomorphic characters, supporting a fast rate of chromosomal changes that vary among species.

Key words: BEAST analysis, chromosome evolution, FISH, ITS, *Sigmodon*

Sigmodon is a monophyletic group documented by mitochondrial DNA (mtDNA) and nuclear gene analyses (e.g., Steppan et al. 2004; Henson and Bradley 2009). This monophyletic group is part of a much larger group of rodents, in the subfamily Sigmodontinae (New World rats and mice), of at least 377 species that mainly occur in Central and South America. Species of *Sigmodon* are distributed in Mexico, Central and South America; with the exception of *S. hispidus* that occurs only in the southwestern and southeastern United States. At least 5 different karyotypes have been documented within 10 species from this genus. Diploid numbers range from 22 to 82, autosomes range from entirely acrocentric to mainly biarmed, and X chromosomes include acrocentric and subtelocentric centromere placements.

To better understand karyotypic diversity in *Sigmodon*, studies have used G-banding to describe chromosomal evolution from the ancestral karyotype, which is proposed to be similar to the karyotype of the extant species, *S. hispidus* (Zimmerman 1970; Elder 1980). Swier et al. (2009) tested this ancestral hypothesis through chromosome paints that were constructed from *S. hispidus* (2N = 52; FN = 52) and in situ hybridized to 9 species of *Sigmodon*. Five of these species (*S. hirsutus*, *S. leucotis*, *S. ochrognathus*, *S. peruanus*, and *S. toltecus*) have a diploid number of 52 and a karyotype that is difficult to distinguish from *S. hispidus*. When paints of *S. hispidus* were hybridized to the karyotypes of these 5 species, the paints hybridized to similar sized chromosomes, demonstrating the conservation of the *S. hispidus* paints.