The evolution of two partner LINE/SINE families and a full-length chromodomain-containing Ty3/Gypsy LTR element in the genome of Anolis carolinensis

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ABSTRACT

Transposable elements (TEs) have been characterized in a number of vertebrates, including whole genomes of mammals, birds, and fishes. The Anolis draft assembly provides the first opportunity to study retroposons in a reptilian genome. Here, we identified and reconstructed a number of retroposons based on database searches: five additional subfamilies of Sauria SINE (Piskurek et al. 2006, Piluqué and Okada 2007), SS-Sauvia SINE chimeras, Anolis Bov-B LINE, Anolis SINE 2, Anolis LINE 2, Anolis CR 3, and a chromodomain-containing Ty3/Gypsy LTR element. We focused on SS SINE families and their partner LINE families (Anolis Sairea SINE/Box-B LNE and Anolis SINE LINE 2). We demonstrate that each SINE LINE pair is distributed similarly and that the evolutionarily younger Sauria SINE sequences evolved as part of novel rolling-circle transposons. The evolutionary time frame when Sauria SINEs and BOX-B LNE were two active in their retrotransposition is characterized by a retrotransposition burst of Anolis SINE and BOX-B LNE elements. We also characterized the first full-length chromoviral LTR element in anurans. This newly identified chromovirus has been very well preserved in the Anolis genome. TEs in the Anolis genome account for approximately 20% of the total DNA sequence, whereas the proportion of mammalian genomes in which such elements have important biological functions. Nevertheless, 20% TE sequences are not unique to the Anolis SINE family but also include other TE families that have important biological and evolutionarily relevant functions. The SINEs and LINES and other ubiquitous genomic elements characterized in the Anolis genome will prove very useful for studies in comparative genomics, phylogenetics, and functional genomics.

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We thank Carlos Lloréns for his help in identifying the DNA sequence alignment illustrates the Anolis SINE 2 consensus sequence and its LINE 2-related TRE as a short type of this SINE (Anolis SINE 2), which is just 240 bp long and lacks most of the central region. The pyd and pyf polymerases (I) internal promoter sequences (Box A and Box B) as well as the LINE 2-related region are shaded in gray.

Schematic representation of Sauria SINE/Box-B LINE and Anolis SINE/LINE 2. Identical 3’ ends of LINES and SINES are indicated by the same pattern. EN = apurinic/apyrimidinic endonuclease. RT = reverse transcriptase.

Distribution of five Sauria SINE subfamilies in the genome of A. carolinensis and their sequence divergence from the general consensus sequence.

Distribution of different retroposons in the genome of A. carolinensis and their sequence divergence from the general consensus sequence: (A) Anolis Sauria SINE elements | (B) Anolis Box-B LINE elements | (C) Anolis SINE 2 elements | (D) Anolis LINE 2 elements.

Using the Gypsy Database of Lloréns et al. (2008), we could identify new LTR retroelements in Anolis and show that they represent a novel chromovirus. The approximately 1200 bp long homologous LINEs begin and end in typical 3′ LTRs (−GA-3′) inverted repeats. We named this new Ty3/Gypsy LTR retroelement Amni-1. It displays the canonical LTR-gapped LTR structure of chromoviruses and it represents the first full-length chromoviral genome described in anurans. Ty3/Gypsy LTR retroelements are similar to vertebrate retroviruses in both sequence and genomic structure (Skoobth 1996). The main difference between a retrovirus and a LTR retrotransposon is that the retrovirus has an additional ORF coding for an envelope (env) protein necessary for transferring retroviruses cell-to-cell.

Evolutionary relationships among Anolis Sauria SINE sequences based on a maximum-likelihood analysis and the HEID2 model (Ragoussis et al. 1998). Three Sauria SINE consensus sequences (ACA-3|5) are shown which evolve as partners of Helitrons. Sauria SINE sequences of the common wall lizard (Podarcis muralis, POM) served as the outgroup.