

Unique small RNA signatures uncovered in the Tammar Wallaby genome

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Although only recently discovered, small RNAs have proven to be essential regulatory molecules encoded within eukaryotic genomes. These molecules, represented by four major class sizes ranging from 20nt to 42nt, are participants in a diverse array of cellular processes including gene regulation, chromatin dynamics and genome defense. The genome sequencing initiative for the tammar wallaby has afforded an opportunity to explore the evolution of each of the major classes of small RNAs, siRNAs, miRNAs, piRNAs, and the newest class of small RNAs, crasiRNAs (centromere repeat associated short interacting RNAs), first discovered in the tammar wallaby. Our analysis includes the detailed examination of these small RNAs, salient features that define their canonical members and the constitution of species-specific members derived from mobile genetic elements. Understanding the evolution of these important regulators and surveyors of the genome in this unique marsupial model brings valuable insights to the community of small RNA researchers.