

Abstract

Evolutionary conservation and disruption of umami-sweet taste receptor gene family in ecologically diverse platyrrhine primates

Student name: Zhixin WU (吴之欣)

Student ID number: 47226419

Department: Department of Integrated Biosciences

Laboratory: Laboratory of Evolutionary Anthropology

Adviser: Prof, Shoji KAWAMURA

Year and month of completion: September 2024

Introduction

Taste plays a vital role in an animal's fitness by helping them make decisions about ingesting beneficial foods and avoiding harmful substances in their daily life. The umami and sweet taste perception is initiated by the umami-sweet taste receptors (TAS1Rs); umami by TAS1R1-TAS1R3 heterodimer and sweet by TAS1R2-TAS1R3 heterodimer. Although these senses could be considered to be conserved, recent research has revealed diversity of these receptor genes across vertebrate species. However, much information has largely relied on whole-genome assembly (WGA) data which are often incomplete with shallow sequencing depth, especially for multigene families. Platyrrhine primates (monkeys of Americas) are suitable for understanding the evolutionary conservation and diversity of umami-sweet taste receptor gene family because of their remarkable diversity in color vision and diets. This study aims to clarify the compositions of *TAS1R* gene family among platyrrhines by applying targeted capture (TC) with high-depth short-read massive parallel sequencing ("Next-Generation" sequencing: NGS) and to examine if conservation/diversity of the genes is associated with color vision or dietary ecology of the monkeys.

Materials and Methods

I examined 18 species, one individual for each, of platyrrhines from all three Families (Cebidae, Atelidae, Pitheciidae). Probes for the three genes, *TAS1R1*, *TAS1R2* and *TAS1R3*, were designed from available WGA databases of platyrrhines. As references of selective neutrality and single-copy sequencing depth, 85 single-copy non-protein-coding sequences (82 autosomal and 3 X-non-pseudoautosomal) were used. Sequencing reads were mapped to the gene/region sequences and assembled three rounds for accuracy. The sequencing depths and the density of single-nucleotide polymorphism (SNP) sites were evaluated. *TAS1R* genes were

further evaluated for the length of open-reading frame (ORF) and capability of forming 7-transmembrane (7-TM) structure to judge whether the genes were intact, disrupted, or intact-disrupted heterozygous.

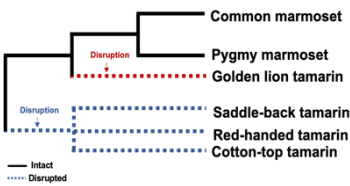
Results

Sequences depth compared between TC and WGA

Genus	Name	Targeted Capture	WGA
Cebidae	Common marmoset	469	63
	Black-eared marmoset	790	NA
	Santarem marmoset	419	35
	Pygmy marmoset	546	35
	Golden Lion Tamarin	804	78
	Red-handed tamarin	472	53
	Cotton-top tamarin	487	55
	Saddle-back tamarin	448	NA
	Azara's night monkey	416	35
	Tufted capuchin	579	43
	White-faced capuchin	762	81
	Bolivian squirrel monkey	439	111
	mantled howler	496	43
Atelidae	black-handed spider monkey	508	57
	Common woolly monkey	480	35
	duky titi	470	35
Pitheciidae	Bearded saki	518	NA
	Pale-faced saki	588	79
	Average	538	56

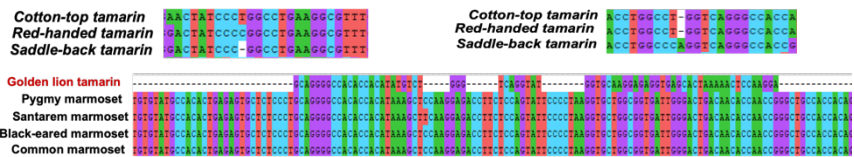
The average sequence depths per nucleotide site of 18 platyrrhine species using targeted capture was 538 and data depth obtained from WGA was 56. On average, the depth of targeted capture was roughly ten times greater than that of WGA (Table left).

TASIR gene composition revealed by TC



The umami receptor *TASIR1* was disrupted in lion tamarin and tamarins. The phylogenetic tree (Figure left) indicates that lion tamarins and tamarins belong to separate branches, and their disruption patterns (Figure below) are notably distinct. Consequently,

based on these observations, I inferred that these disruptions occurred independently. On the other hand, according to the comparison of the non-synonymous and synonymous nucleotide substitutions, other *TASIR* genes of lion tamarin and tamarins and the *TASIR* genes of other platyrrhine species appeared to be under natural selection to conserve their function.



Discussion

The much higher sequencing depth achieved with targeted capture than with WGA enabled significant improvement of sequencing reliability. The disruption of *TASIR1* gene in tamarins and lion tamarins was also confirmed in WGA databases of other tamarin species. The disruption of *TASIR1* in tamarins and loin tamarins implies their loss of umami sensation. While the loss does not seem to be associated with color vision, this might be related to their tree-sap feeding habit. Data obtained from targeted capture and WGA are complementary, providing a more comprehensive understanding when used together. Further analyses are required to determine the ecological factors influencing the evolution of the *TASIR* gene family.