

Turtle genome analysis sheds light on the development and evolution of turtle-specific body plan

28 April 2013



Pelodiscus sinensis. Credit: Wikipedia.

The Joint International Turtle Genomes Consortium, led by investigators from RIKEN, BGI, and Wellcome Trust Sanger Institute, has completed the genome sequencing of soft-shell turtle (*Pelodiscus sinensis*) and green sea turtle (*Chelonia mydas*). These achievements shed new light on the origin of turtles and applied the classical evo-devo model to explain the developmental process of their unique body plan. The findings were published online in *Nature Genetics*.

The evolution of turtles is an enigma in science. Their distinct body design—with a sharp beak and protective hard shell has changed very little over the past 210 million years. As the smallest species of soft-shell turtles, Chinese [soft-shell turtle](#) was once commonly sold in pet shops. [Green sea turtle](#) is considered as the largest of all the hard-shelled [sea turtles](#) and is named because of the green fat

beneath its shell. Its population sizes has been drastically reduced recently and it has been listed as an endangered species.

To reveal the evolutionary history of turtles and the mechanisms underlying the development of their unique [anatomical features](#), researchers in this project sequenced and analyzed the genomes of soft-shell turtle and green sea turtle. They found the evidence that turtles are likely to be a sister group with the [common ancestor](#) of [crocodilians](#) and birds from whole genome phylogenetic analyses. The turtles were diverged from archosaurians approximately between 267.9 and 248.3 million years ago, which coincides with the time range of the Upper Permian to Triassic period that overlapped or followed shortly after the end of [Permian extinction](#).

In the study, researchers performed the brief research on genes may be associated with the turtle-specific characteristics, and found some olfactory receptor (OR) [gene families](#) were highly expanded in both turtles. This finding suggests that turtles have developed superior olfaction ability against a wide variety of hydrophilic substances. In addition, many genes involved in taste perception, hunger-stimulating, and energy homeostasis regulating hormone ghrelin have been uniquely lost in turtles. Researchers suggested that the loss of these genes may be related to their low-metabolic rate.

The consortium also investigated the association of embryonic gene expression profiles (GXP) and their morphological evolution pattern, based on ENSEMBL soft-shell turtle gene-set. By integrating RNA-seq technology, comparative genomics method, and mathematical statistical approaches, researchers confirmed GXP divergence during embryogenesis of soft-shell turtle and chicken

indeed follows the developmental hourglass model. They also revealed that the maximal conservation stage occurred at around the vertebrate phylotypic period, rather than at later stage that show the amniote-common pattern.

To clarify the morphological specifications of turtle embryogenesis in late development, especially the formation of the carapacial ridge (CR), researchers investigated into CR-specific miRNA expression, found existence of tissue-specific miRNAs and involvement of Wnt signaling. Also they revealed the Wnt expression involved in the carapacial ridge (CR) formation of the turtle shell, researchers annotated all the Wnt genes in the two turtle genomes, identifying a total of 20 Wnt genes. Intriguingly, they discovered Wnt5a is the only Wnt gene expressed in the turtle CR region, supporting the possible co-option of limb-associated Wnt signaling in the acquisition of this turtle-specific novelty.

Zhuo Wang, Project Manager from BGI, said, "The genome-wide phylogenetic analysis of two turtles in our project, along with two crocodile genomic data additionally, makes clear the evolutionary history of turtles in diverging from other species and settles the disputes about the phylogenetic position of reptiles. The genomic analyses and embryonic gene expression profiles have been combined to reveal the fundamental evo-devo questions on turtle evolution and development. These works have been highly appreciated by the editor and reviewers. Besides the interesting story, the genomic data we released here will provide a platform for more scientists to initialize their genome-wide studies on turtles. "

Dr. Hongyan Zhang, Regional Director of BGI Tech Solutions Co., Ltd. for Japan, said, "The completed [genome sequencing](#) of soft-shell turtle and green sea turtle give an important hint to uncover the development and evolution mechanism of [turtles](#). This scientific achievement is a joint effort supported by BGI's advanced sequencing technologies and excellent bioinformatics capabilities, the profound basis research background of developmental biology from RIKEN, and other partners' great contributions. We are looking forward to having more collaboration with

other scientists for better exploring the secret of life together in the near future."

More information: The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle specific body plan, [DOI: 10.1038/ng.2615](https://doi.org/10.1038/ng.2615)

Provided by BGI Shenzhen

APA citation: Turtle genome analysis sheds light on the development and evolution of turtle-specific body plan (2013, April 28) retrieved 1 October 2020 from <https://phys.org/news/2013-04-turtle-genome-analysis-evolution-turtle-specific.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.