Comparative Genomics Reveals a Convergent Signature on the Vitamin D Receptor (VDR) in Herbivorous Mammals

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Research

Keywords: vitamin D receptor, intestinal fermentation, herbivorous adaption

Posted Date: May 11th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-483507/v1>

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Abstract

Background: Dietary adaptation is one of hot topics in adaptive evolution of mammals. Herbivorous mammals generally digest structural carbohydrates (such as cellulose and hemicellulose) via intestinal microbial fermentation. However, the mechanism by which the host supports the intestinal fermentation capacity is still not well understood. To address this question, we conducted convergent amino acid scanning to identify candidate genes involving intestinal fermentation across mammalian phylogeny.

Results: Among 4886 one-to-one orthologous genes, we found that 122 genes showed a significant increase of convergent signature in two foregut-fermenting families (Cercopithecidae: *Rhinopithecus roxellana*, Bovidae: *Bos taurus* and *Ovis aries*) and particularly, in the vitamin D receptor (VDR), a convergent cysteine to serine substitution at amino acid 410 (VDR C410S) occurred in 14 mammalian families with intestinal fermentation capacity. As a critical role of VDR in the regulation of intestinal microbes and adaptive immunity, we employed phylogenetically independent contrast analysis to test whether the evolution of the VDR gene influenced intestinal fermentation and found this convergent amino acid substitution (VDR C410S) possess significant positively correlations with the intestinal fermentation capacity and the dietary components (plant parts except for fruits, seeds and nectar) consumed by 107 mammalian species, which indicated VDR have a positive impact on the herbivorous adaptation of intestinal fermentation.

Conclusions: Our results suggest that nuclear receptor gene VDR involved in intestinal adaptive immune show rapid adaptive fixation of convergent amino acid substitutions (C410S) among herbivorous mammals with convergent methodology.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Figures

Get 1:1 orthologous protein sequences of 14 mammals

OrthoMCL ↓ 4886 genes

Identify parallel amino acid substitutions

Paml JAVA script ↓ 228 genes

Neutral simulation with JTT-f substitutions model

Zou script ↓ 122 genes

Validating convergent genes with 100+ mammals

OrthologuesV10B database ↓ 118 genes

Identify candidate convergent genes related to intestinal fermentation capacity among the 107 mammalian species

Phylogenetically independent contrasts (PIC) ↓ 17 genes

Vitamin D receptor

Figure 1

Search and verification procedures for candidate genes related to the fermentation capacity showing convergent evolution.

Figure 2

Information on VDR amino acid 410 substitutions and intestinal fermentation capacity in 107 mammalian species. Red indicates species showing fermentation, and black indicates species not showing fermentation. Information for species with S substitutions is indicated in red. The purple indicated the different proportions of 107 mammalian species eating plant components (except for fruits, seeds and nectar).

Figure 3

The specificity of VDR410 substitutions in mammalian taxa with and without fermentation. (A) Phylogenetically independent contrast (PIC) test of the VDR S410 substitutions of VDR 410 site (with padded VDR sequence data) and intestinal fermentation capacity in 107 mammalian species. (B) Phylogenetically independent contrast (PIC) test of plant parts other than fruits, seeds, and nectar and S substitutions of VDR 410 site (with padded VDR sequence data) in 107 mammalian species. (C) The

amino acid proportions of VDR amino acid 410 site in 107 mammalian species (non-fermentation (N=54)), fermentation (N=53)). (D) The amino acid proportions of VDR amino acid 410 site among 107 mammalian species eating different proportions of plant components (except for fruits, seeds and nectar).

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