

1
Name of Journal: *World Journal of Gastroenterology*

Manuscript NO: 50819

Manuscript Type: ORIGINAL ARTICLE

Basic Study

Characterizing the composition of intestinal microflora by 16S rRNA gene sequencing

Wen-Jia Wang, You-Lian Zhou, Jie He, Zhi-Qiang Feng, Long Zhang, Xiao-Bo Lai, Jun-Xiao Zhou, Hong Wang

Abstract

BACKGROUND

This study determined the composition and diversity of intestinal microflora in patients with colorectal adenoma (CRA), which may provide evidence for investigations of the role of intestinal microflora in the pathogenesis of colorectal tumors and the composition of intestinal microflora closely related to CRA, and further validated the possibility of intestinal flora as a biomarker of CRA.

AIM

Match Overview

1	Internet 15 words crawled on 27-Jul-2019 f6publishing.blob.core.windows.net	<1%
2	Internet 14 words crawled on 06-Sep-2018 www.esp.org	<1%
3	Internet 12 words crawled on 29-Dec-2019 www.nature.com	<1%
4	Crossref 12 words Yu Gao, Zhiming He, Zilian Wang, Yanmin Luo, Hongyu Sun, Yi Zhou, Linhuan Huang, Manchao Li, Qun Fang, Shiwen	<1%
5	Internet 12 words crawled on 31-Jul-2019 tessera.spandidos-publications.com	<1%

Characterizing the composition of intestinal microflora by 16S



ALL

IMAGES

VIDEOS

关闭取词

29,200 Results

Any time ▾

16S rRNA Gene Sequencing of Human Intestinal Microflora ...

<https://www.lcsciences.com/discovery/16s-rna-gene-sequencing-case-study> ▾

16S rRNA Gene Sequencing of Human Intestinal Microflora Case Study Human gut microbiota plays important roles in harvesting energy from the diet, stimulating the proliferation of the **intestinal epithelium**, developing the immune system, and regulating **fat storage** in the host.

High-throughput 16S rRNA gene sequencing reveals ...

<https://www.sciencedirect.com/science/article/pii/S1075996415000050>

The aim of this study was to investigate the effects of gamma irradiation on the **compositions** of the large and small **intestinal microbiotas**. The **gut microbiotas** in control mice and mice receiving irradiation treatment were characterized by **high-throughput sequencing** of the **bacterial 16S rRNA gene**.

Cited by: 25

Author: Young Suk Kim, Jinu Kim, Soo-Je Park

Publish Year: 2015

Characterization of bacterial community shift in human ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4094692>

The samples were collected by colonoscopy and were processed immediately for isolation of DNA. **Mucosal microbiota** was analyzed by means of 16S rRNA gene-based Illumina high throughput sequencing. **Quantitative real-time PCR (qPCR)** was performed to determine total ...

Cited by: 55

Author: Sandeep A Walujkar, Dhiraj P Dhotre, Na...

Publish Year: 2014

Fecal metabonomics combined with 16S rRNA gene ...

<https://www.sciencedirect.com/science/article/pii/S037887411931428X>

Simultaneously, 16S rRNA gene sequencing analysis based on the Illumina HiSeq sequencing platform and ANOVA analysis were used to analyze the **composition** of the **intestinal microbiota** in the stool samples and to screen for the significant altered **microbiota** at the genus level.

Author: Ruiqun Chen, Jia Wang, Runhua Zhan... Publish Year: 2019

(PDF) Characterization of mid-intestinal microbiota of ...

https://www.researchgate.net/publication/334536881_Characterization_of_mid-intestinal...

The microbiota of 30 farmed Chinook salmon from a single cohort was surveyed using metabarcoding



国内版

国际版

Characterizing the composition of intestinal microflora by 16S



ALL

IMAGES

VIDEOS

开启取词

29,700 Results

Any time ▾

Characterization of the Fecal Microbial Communities of ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4341109>

High-throughput 16S rRNA gene pyrosequencing offers a more qualitative and quantitative overview of microbial communities than other culture-dependent and -independent techniques, thereby providing substantial insight into the presence of both known and unclassified bacteria in the **microflora**.

Cited by: 19

Author: Edward Alain B. Pajarillo, Jong Pyo Chae...

Publish Year: 2015

16S rRNA Gene Sequencing of Human Intestinal Microflora ...

<https://www.lcsciences.com/discovery/16s-rna-gene-sequencing-case-study> ▾

16S rRNA Gene Sequencing of Human Intestinal Microflora Case Study Human gut microbiota plays important roles in harvesting energy from the diet, stimulating the proliferation of the **intestinal epithelium**, developing the immune system, and regulating **fat storage** in the host.

Characterization of the intestinal microbiota of the sea ...

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0208011> ▾

High-throughput 16S rRNA gene sequencing has been used to identify the intestinal microbiota of many animal species, but that of marine invertebrate organisms remains largely unknown. There are only a few high-throughput sequencing studies on the intestinal microbiota of echinoderms (**non-vertebrate Deuterostomes**).

Cited by: 1

Author: María Pagán-Jiménez, Jean F. Ruiz-Cald...

Publish Year: 2019

A Novel Method for Determining Microflora Composition ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3168955>

A common method for studying the diversity of the **microflora** is through **sequencing** of the 16S ribosomal RNA **gene** (16S rRNA). This **gene** is required in all prokaryotic cells and its DNA sequence has highly variable regions flanked by conserved regions which allows for i) amplification using universal primers and ii) phylogenetic analysis and ...

Cited by: 9

Author: Ernest R. Chan, James Hester, Matthew ...

Publish Year: 2011

(PDF) Characterization of mid-intestinal microbiota of ...

https://www.researchgate.net/publication/334536881_Characterization_of_mid-intestinal...

The microbiota of 30 farmed Chinook salmon from a single cohort was surveyed using metabarcoding of the V2-V4 hypervariable region of the bacterial 16S rDNA gene.

See results for

Gene (Journal)

Gene is a peer-reviewed scientific journal in genetics and molecular biology, focusing on the cloning, structure,...

