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The Gut Microbiome and Energy Source of the Giant Panda

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The giant panda is a very distinctive species and its highly fibrous diet consists of bamboo to a 99%. Studies have suggested the panda's digestive capacities have adapted to this peculiar diet. Not just that, but their phenotype as well. However, how the panda acquires energy from this plant remains largely a mystery. A metagenomic study was performed to shed light on this subject.

Introduction

The giant panda (***Ailuropoda melanoleuca***) represents one of the endemic flagships of China. The species is distinctive in the sense that, unlike the rest of its superfamily, ***Arctoidea***, the giant Panda species' diet is solely on bamboo .

The bamboo's dry mass is mostly composed of cellulose, hemicellulose and lignin. Previous genomic studies revealed the giant panda lacks the homologues necessary to transcribe proteins capable of degrading cellulose. Moreover, their **gastrointestinal (GI)** tract is characteristic of carnivores.

As a result, it's hypothesized the giant panda needs the presence of cellulose-degrading bacteria. Previous studies have identified some cellulose-degrading bacteria in their faces, while others did not find that the panda gut microbiome had the capacity to degrade cellulose[1, 2].

This study[3] provides evidence on this hypothesis. Wenping Zhang, an expert researcher at the Chengdu Research Base of Giant Panda Breeding, has done previous work on the genetic diversity, gut microbiome composition, and more, on the giant panda. The Research Institute is highly recognised for conservation and research into rare and endangered animals, in particular, the giant panda.

Experiment design

332 feces of 12 giant pandas were analyzed using **shotgun metagenomic sequencing**. Metagenomic analyses consist of studying the genetic material (e.g. DNA) extracted from the environment such as water, solid, stool, and even nutrient medium of cultured microorganisms.

The sample is filtered and purified, leaving only the extracted DNA strands to be sequenced and subsequently put together with assembly methods. Metagenomic analyses are done to understand the **complexity of diversity, host-microbe interactions, metabolic pathways** and **microbiome population**.

Certain sequenced genomes provide useful taxonomic information. Approximately 10 phyla were identified, the most abundant ones being Firmicutes and Proteobacteria. Other phyla identified were *Enterobacteriaceae, Streptococcaceae, Lactobacillaceae, Clostridiaceae, Campylobacteraceae* and *Veillonellaceae*.

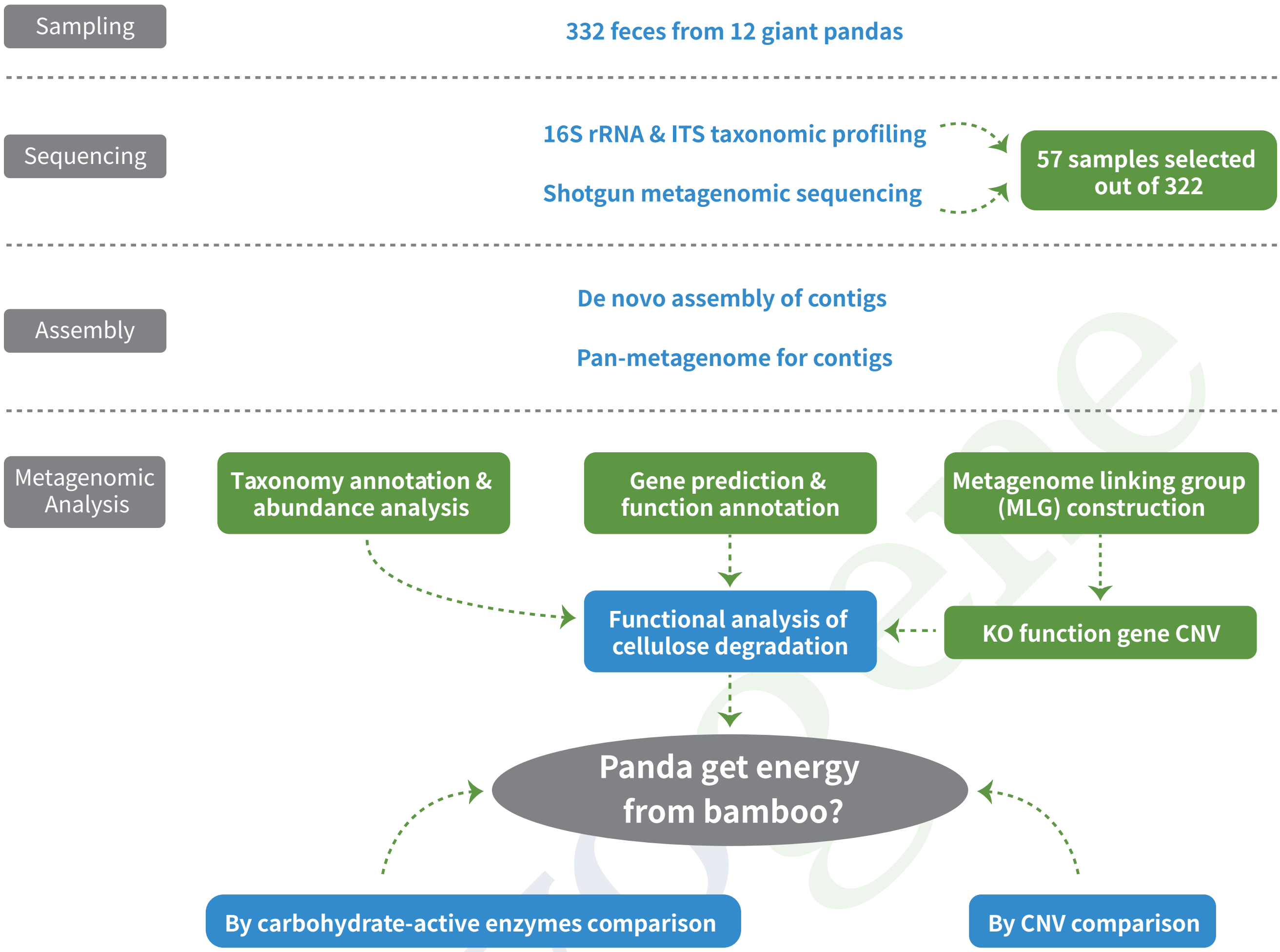

Figure 1. Research pipeline of the study

KO models and comparative metagenomic studies were performed to pinpoint the cellulolytic and hemicellulose activity, lignin metabolism and overall carbohydrate activity genes in the giant panda's genome.

The workflow consisted of taking 332 feces from 12 giant pandas, identifying their taxonomic profile using 16S rRNA sequencing. Out of the 332, only 57 samples were analyzed using Shotgun Metagenomic techniques, and the sequenced fragments were assembled. Afterwards, came the functional analysis of the samples:

a) taxonomy annotation and abundance analysis;
b) identifying the gene-encoding genome regions in the DNA;
c) using the aforementioned KO models to pinpoint the involved genes.

The final results are analyzed comprehensively to build hypothesis on how the panda extracts the much-required energy from the fiber-rich bamboo.

Conclusion

The research demonstrated there is an age-associated variability of the giant panda's life stages and its intestinal flora. Fecal material analyses demonstrated the panda's **gut microbiome** composition remains stable after the first year of life. The GI of very young pandas possess a higher expression of genes-encoding enzymes capable of metabolizing simple sugars. Comparative analyses of metagenomic showed that the giant panda also expressed two pancreatic amylase gene copies, while carnivore species only display one[4].

The panda's digestive physiology is adapted to surviving on hemicellulose, maximizing the amount of energy that is possible to acquire from its degradation. NGS technology allowed specialized teams, such as the one from Great Panda Research base, to acquire more knowledge on the topic of the giant panda's genomic expression, GI composition and how it affects each one of its life stages.

Novogene continues to supply trusted next-generation sequencing services to help researchers achieve their goals. By combining metagenomics study, Novogene uses NGS technologies with the latest advancements in bioinformatics for data analysis, and helps researchers capture metagenomes without the painstaking steps of isolation and cultivation of each individual species in the lab.
Novogene has vast experience in multiple microbial sequencing, including 16S/18S/ITS rRNA amplicon metagenomic sequencing, metagenomics sequencing for genomic profiling and meta-transcriptomic sequencing for transcriptome studies. Bioinformatics package is offered to assist with the complete data analysis, from taxonomic diversity to functional annotation of genes.

References

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