



Microbiomes in the São Paulo Zoo

João Carlos Setubal

2022

Since 2000, the main new topic (for me) has been metagenomics-microbiomics

A few definitions

- Microbiota: microbial community in a given environment
- Metagenome: the result of metagenomic sequencing (no isolation) of a sample
- Microbiome: genomes + gene sequences + gene product sequences identifiable in a metagenome

Targeted and total DNA (shotgun) sequencing

- Amplicon (targeted)
 - 16S (prokaryotes)
 - ITS (eukaryotes)
 - Species identification is difficult or impossible
 - "metataxonomics"
- total DNA (shotgun)
 - Access to the microbiome
 - Species and even strain identification is possible

Metagenome-Assembled Genome (MAG)



MAGs are at the left end of a contamination spectrum



The MAG explosion

nature microbiology

ARTICLES DOI: 10.1038/s41564-017-0012-7

OPEN

Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life

Donovan H. Parks[®], Christian Rinke[®], Maria Chuvochina, Pierre-Alain Chaumeil, Ben J. Woodcroft, Paul N. Evans, Philip Hugenholtz[®] and Gene W. Tyson^{*}

Article

https://doi.org/10.1038/s41467-022-32805-z

A compendium of 32,277 metagenomeassembled genomes and over 80 million genes from the early-life human gut microbiome

A Catalog of over 5,000 | Genomes from the Capri

Received: 16 February 2022

Shuqin Zeng¹, Dhrati Patangia^{2,3,4}, Alexandre Almeida ^{0,5,6}, Zhemin Zhou⁷, Dezhi Mu⁰, R. Paul Ross^{2,4}, Catherine Stanton^{2,3} & Shaopu Wang ⁰ ⊠

Accepted: 16 August 2022

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Projeto MetaZoo

Estudos da diversidade microbiana no Parque Zoológico do Estado de São Paulo

(BIOTA/FAPESP: Microrganismos / Processo 2011/50870-6)

Coordenadores: João Carlos Setubal, IQ/USP Aline Maria da Silva, IQ/USP 2013-2018

Whose idea it was

Luiz Juliano Neto Unifesp

• 2009

- Professor Kohei Oda (U. Kyoto) visits the Zoo
- "compost is a gold mine!"
- LJN proposes Microbiology lab in the Zoo
- FAPESP grant (2010-2012) to study composting (pilot)
- Thematic project was the successor of this pilot

Composting Unit at the São Paulo Zoo Park

Facility designed to compost 4 tons/day of all organic waste produced in the park: 44 concrete chambers of 1 m³

- Feces from ~ 400 species (3000 animals)
- Bedding materials and animal feed waste
- Plant debris from the park's Atlantic rain forest fragment and gardens
- Water treatment sludge

São Francisco Reservoir

Aim: understand its microbiota seasonal variation

Howler monkey gut microbiome

Compare the microbiomes of free-living and captive individuals

Composting: Pilot results (2013)

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RESEARCH ARTICLE

Metagenomic Analysis of a Tropical Compositng Operation at the São Paulo Zoo Park Reveals Diversity of Biomass Degradation Functions and Organisms

Layla Farage Martins , Luciana Principal Antunes , Renata C. Pascon, Julio Cezar Franco de Oliveira, Luciano A. Digiampietri, Deibs Barbosa, Bruno Malveira Peixoto, Marcelo A. Vallim, Cristina Viana-Niero, Eric H. Ostroski, Guilherme P. Telles, Zanoni Dias, João Batista da Cruz, [...], João Carlos Setubal [] [view all]

Published: April 24, 2013 • https://doi.org/10.1371/journal.pone.0061928

Bacteria are dominant

Unassembled shotgun reads from two independent Zoo composting samples

Follow-up (2016)

SCIENTIFIC REPORTS

Received: 03 August 2016 Accepted: 14 November 2016 Published: 12 December 2016

OPEN Microbial community structure and dynamics in thermophilic composting viewed through metagenomics and metatranscriptomics

Luciana Principal Antunes¹, Layla Farage Martins¹, Roberta Verciano Pereira¹, Andrew Maltez Thomas^{1,2}, Deibs Barbosa^{1,2}, Leandro Nascimento Lemos^{1,2}, Gianluca Major Machado Silva^{1,2}, Livia Maria Silva Moura^{1,2}, George Willian Condomitti Epamino^{1,2}, Luciano Antonio Digiampietri³, Karen Cristina Lombardi¹, Patricia Locosque Ramos⁴, Ronaldo Bento Quaggio¹, Julio Cezar Franco de Oliveira⁵, Renata Castiglioni Pascon⁵, João Batista da Cruz⁴, Aline Maria da Silva^{1,2,*} & João Carlos Setubal^{1,2,6,*}

Compost-derived consortium (2017)

ORIGINAL RESEARCH published: 19 April 2017 dol: 10.3389/fmicb.2017.00644

Genome-Centric Analysis of a Thermophilic and Cellulolytic Bacterial Consortium Derived from Composting

OPEN ACCESS

Edited by: Eric Altermann, AgResearch, New Zealand

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Composting MAGs (2021)

Braga et al. BMC Genomics (2021) 22:652 https://doi.org/10.1186/s12864-021-07957-9

BMC Genomics

RESEARCH

Genome-resolved metagenome and metatranscriptome analyses of thermophilic composting reveal key bacterial players and their metabolic interactions

Lucas Palma Perez Braga¹⁺, Roberta Verciano Pereira¹⁺, Layla Farage Martins¹⁺, Livia Maria Silva Moura^{1,2+}, Fabio Beltrame Sanchez^{1,2}, José Salvatore Leister Patané³, Aline Maria da Silva^{1*} and João Carlos Setubal^{1*}

Open Access

ZC4: 49 hq MAGs

The dynamics of composting based on MAGs & metatranscriptomics

increase at the end

MAG08 and MAG20 appear to be good lignin degraders

- Both have several genes for ligninolytic enzymes
- MAG08 Pseudomonas thermotolerans
- MAG20 A novel gammaproteobacterium

Still ongoing!

- New samples
 - Inocula
 - Mature compost
- More liberal MAG quality criteria
 - 50% completeness instead of 80%

Current MAG numbers

samples	# MAGs
ZC3	31
ZC4	93
inoculum	22
mature compost	20
total	166

Howler monkeys: 58 hq MAGs

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Raquel Franco (howler monkeys) Suzana Guima (composting)

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