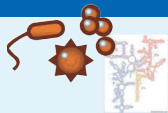
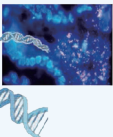


宏基因组测序

产品简介

宏基因组 (Metagenome)即环境中全部微小生物遗传物质的总和,它包含了可培养的和未可培养的微生物的基因。宏基因组测序 (Metagenomics Sequencing) 研究通过二代或者三代测序技术对环境样本中的微生物群落的基因组进行测序,能够全面准确获得样本中物种组成、功能组成、微生物与环境的相互作用关系等,其优势为不依赖于分离培养,为环境微生物研究提供了有力工具。

Meta-omics		Molecule	Knowledge	Limits	Clinical implications
Phylogeny		16S rDNA	<ul style="list-style-type: none"> Bacterial composition & diversity 	<ul style="list-style-type: none"> No information on bacterial functions Except archaea 	<ul style="list-style-type: none"> Composition dysbiosis Healthy or disease specific species
Metagenomics		Chromosomal genomic DNA	<ul style="list-style-type: none"> High resolution Microbiota profiling Genes contents from uncultivated microbes 	<ul style="list-style-type: none"> No information on microbial expressed functions 	<ul style="list-style-type: none"> Functional dysbiosis Healthy or disease specific microbial genes Toward diagnostics functional based studies

宏基因组测序技术特征^[1]

技术优势



单菌组装

contig binning分析,获得单菌草图序列,可进一步进行单菌基因组注释分析;可结合三维基因组分析更有效的区分来自不同菌种的序列;



分析内容全面

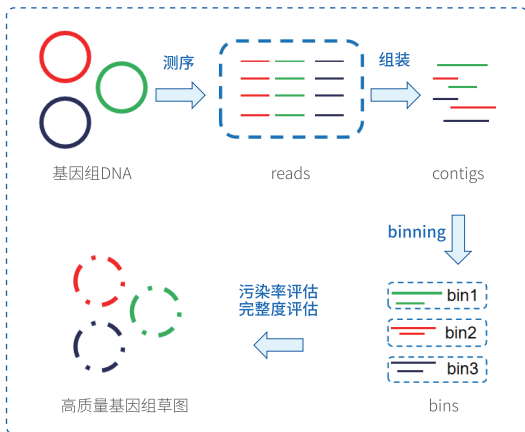
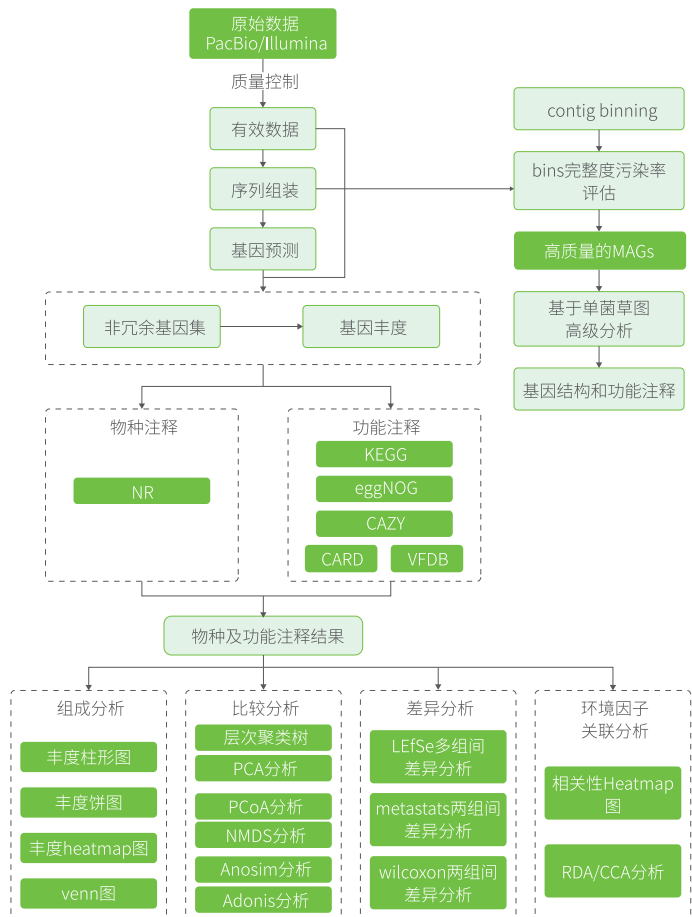
包含KEGG、eggNOG和VFDB等多种数据库分析内容;



更准确的功能分析

不同于扩增子的功能预测,宏基因组可更准确地在基因功能层面进行研究;

分析流程



binning原理示意图

技术参数

产品	测序平台	测序数据量	送样要求	项目周期
二代宏基因组测序	Illumina/BGI	10G/样	DNA浓度 \geq 20ng/ μ L 总量 \geq 2 μ g	40个自然日
三代宏基因组测序	PacBio Sequel II	>20G/样	DNA浓度 \geq 50ng/ μ L 总量 \geq 8 μ g	50个自然日

案例分析

宏基因组学揭示曙古菌门的代谢与进化^[2]

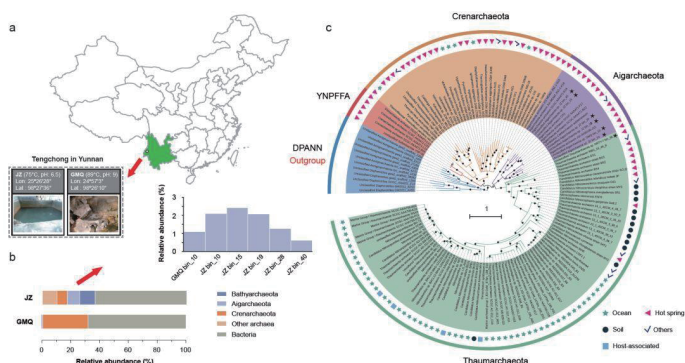
发表期刊: *Nature Communications*

时间: 2018年7月

影响因子: 12.353

样本: 云南腾冲温泉沉积物样品: JZ和GMQ

摘要: 曙古菌门 (Aigarchaeota) 微生物在地热环境中广泛分布, 但其生理生态作用却鲜为人知。作者利用宏基因组测序技术及binning分析从中国云南陆生热泉生境两个沉积岩样本中组装出6个曙古菌门基因组。Thaumarchaeota和Aigarchaeota的共同祖先起源于高温生境, 通过水平基因转移增强了各自对不同环境的适应性, 该研究加深了我们对古菌支系的理解。



bins系统发育分析

Aigarchaeota和Thaumarchaeota bins数据统计表

Bins	Aigarchaeota						Thaumarchaeota
	GMQ bins_10	JZ bins_10	JZ bins_15	JZ bins_19	JZ bins_28	JZ bins_40	DRTY7 bin_36
No. of scaffolds	10	79	25	54	17	25	167
Genome size (bp)	1,230,238	1,086,093	1,473,345	1,654,953	1,440,436	1,471,612	1,241,443
GC content (%)	53.7	55.4	37.48	62.32	51.83	51.92	36.12
N50 value (bp)	239,895	18,760	82,890	59,043	161,320	136,575	10,470
No. of protein coding genes	1,398	1,222	1,524	1,734	1,581	1,566	1,443
Coding density (%)	90.0	92.5	90.0	89.9	94.7	92.7	91.2
No. of rRNAs	3	4	4	5	2	4	3
No. of tRNAs	44	36	36	38	41	45	46
No. of genes annotated by COG ^a	904(64.6%)	859(70.3%)	1099(72.1%)	1097(63.3%)	1080(68.3%)	1055(67.4%)	757(50.7%)
No. of genes annotated by KOG ^a	341(24.4%)	323(26.4%)	398(26.1%)	396(22.8%)	405(25.6%)	385(24.6%)	283(18.9%)
No. of genes annotated by KO ^a	712(50.9%)	686(56.1%)	898(58.9%)	870(50.2%)	913(57.7%)	835(53.3%)	623(41.7%)
No. of genes annotated by InterPro ^a	710(50.8%)	669(54.7%)	847(55.6%)	904(52.1%)	849(53.7%)	848(54.1%)	664(44.4%)
No. of genes annotated by MetaCyc ^a	338(24.2%)	327(26.8%)	432(28.3%)	436(25.1%)	442(28.0%)	388(24.8%)	276(18.5%)
Completeness (%) ^b	98.06	97.09	99.03	97.09	97.57	98.06	93.69
Contamination (%) ^b	0	0	0	0	0	0	0.97

^aFunctional annotation for the seven genomes was conducted by uploading to IMG database

^bGenome completeness and contamination were estimated using CheckM (ref. 10)

参考文献:

[1]Lepage P, Leclerc M C, Joossens M, et al. A metagenomic insight into our gut's microbiome[J]. *Gut*, 2013, 62(1): 146-158.

[2]Zheng-Shuang Hua, et al. Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. *Nature Communications*, 2018.

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