

Nanopore-only reads to improve genome scaffolds at the chromosome level for low complexity organisms

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INTRODUCTION

- ◆ *Malassezia* is a skin commensal yeast in humans and warm-blooded animals
- ◆ *M. pachydermatis* is the most concerning veterinary species (opportunistic pathogen)
- ◆ Although rare, *M. pachydermatis* relates to human bloodstream infections.
- ◆ *M. pachydermatis* has a compact genome of less than 9 Mb, with six chromosomes.

◆ **De novo assembly** - GenBank SAMN14981974 - BioProject PRJNA631787



◆ Genome assemblies for *Malassezia pachydermatis*

Sample	Size	Scaffolds	contigs	N50	Genome	Reference
dog ear	8.24 Mbp	10	10	1.42 Mbp	SAMN14981974	This study
dog ear	8.15 Mbp	91	118	0.64 Mbp	GCF_001278385.1	(Wu et al., 2015)
CBS 1879	8.16 Mbp	61	80	0.64 Mbp	GCA_001264975.1	(Triana et al., 2015)

RESULTS

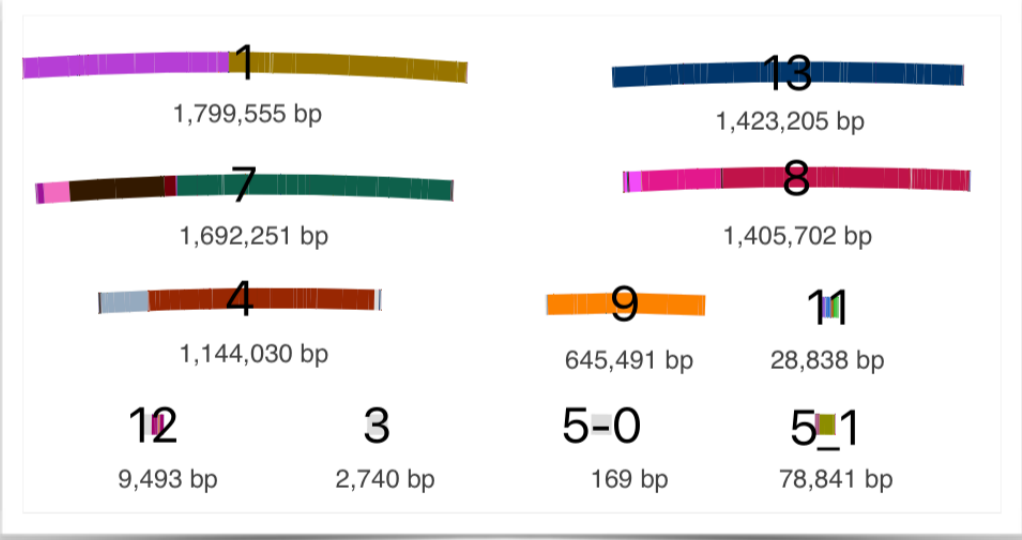
◆ **Completeness** - 76.6% (1,764 genes)
Similar to reference genome (78.5%)

◆ **Scaffold** - 6 contigs (1.8 Mbp - 0.6 Mbp)
Putative 6 chromosomes *M. pachydermatis*

```
# BUSCO version is: 4.0.1
# The lineage dataset is: basidiomycota_odb10 (Creation date: 2019-11-20,
# number of species: 133, number of BUSCOs: 1764)
# Summarized benchmarking in BUSCO notation for file consensus_medaka2.fasta
# BUSCO was run in mode: genome

***** Results: *****

C:76.6%[S:76.5%,D:0.1%],F:3.8%,M:19.6%,n:1764
1350 Complete BUSCOs (C)
1349 Complete and single-copy BUSCOs (S)
1 Complete and duplicated BUSCOs (D)
67 Fragmented BUSCOs (F)
347 Missing BUSCOs (M)
1764 Total BUSCO groups searched
```



METHODS

SAMPLE

M. pachydermatis isolate from a dog with otitis externa

DNA EXTRACTION & SEQUENCING

ZYMOBIOMICS MiniPrep - SQK-RBK004 + MinION FC R 9.4

BIOINFORMATICS

Basecalling + Demultiplexing - Guppy v2.3.7 HQ & Deepbinner
De novo assembly - Flye 2.6 + racon 1.4.10 + medaka 0.11.4 (*2)
In-depth characterization - BUSCO v4.0.1, Bandage 0.8.1

TAKE-HOME MESSAGE

Nanopore-only de novo assembly improves the scaffolding of genomes, even at the chromosome level for yeast



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