

# The Human Oral Microbiome: A Status Report

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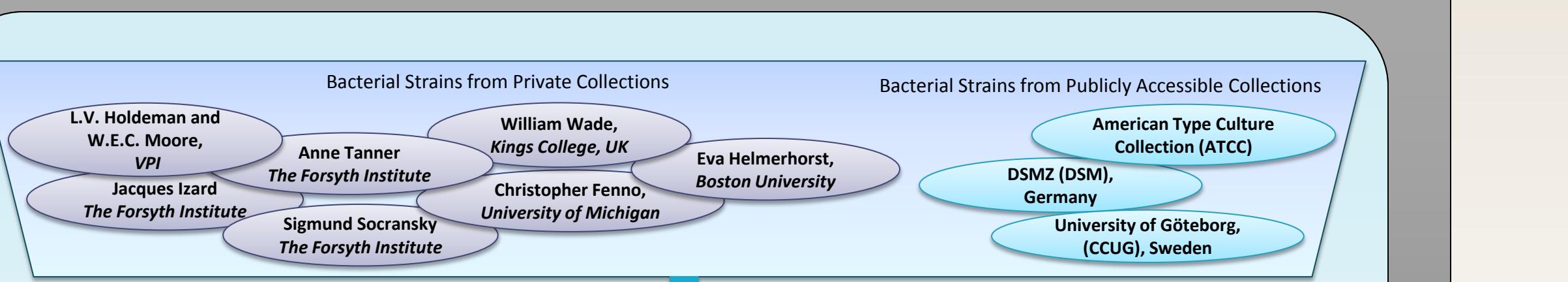
## Abstract

**Objectives:** For the past six years our group has been supported by NIDCR grant DE016937 to fulfill the following major goals: 1) To create a publicly available database with access to a curated taxonomic scheme for provisional naming of the more than 600 oral taxa, and to allow viewing of annotated genomes for all sequenced oral bacteria; 2) To prepare DNA from phylogenetically diverse oral bacteria for genome sequencing by the Human Microbiome Project (HMP) sequencing centers; and 3) To identify isolates of previously uncultivated oral taxa and deposit them with a major culture collection.

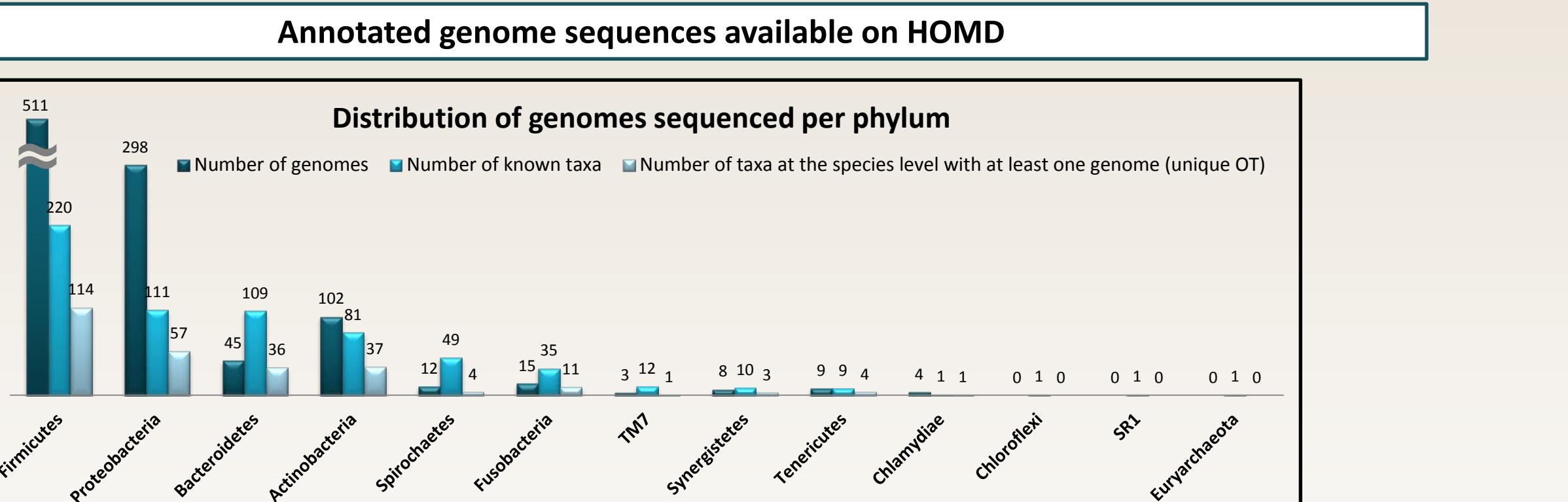
**Methods:** Our approach to this project has been described extensively in the publication (Dewhirst et al. 2010, *J. Bacteriol* 192:5002-17).

**Results:** The HOMD database currently contains 1007 annotated genomes of oral bacteria from 268 taxa (multiple genomes being available for a few taxa). We have sent DNA from 184 oral strains representing 156 taxa to the HMP sequencing centers. Of the 184 strains, 126 are from named taxa and 58 from unnamed taxa. Examination of the Wade, Tanner and Moore's culture collections by 16S rRNA sequencing has allowed us to identify strains for over 200 previously thought to be uncultivated oral taxa. The majority of these isolates represent Human Oral Taxa (HOT) known previously as phylotypes, but a few are totally novel and are assigned new HOT numbers. These isolates will have their genomes sequenced and be deposited with the BEI/ATCC resource.

**Conclusions:** Our group has created the Human Oral Microbiome Database as a bioinformatics resource for the scientific community. We have been the major contributor of highly purified DNA for generating reference genomes for the oral microbiome as part of the HMP. We have successfully identified strains from a large number of previously uncultivated oral taxa and are making them available through a permanent culture collection.



## Methods



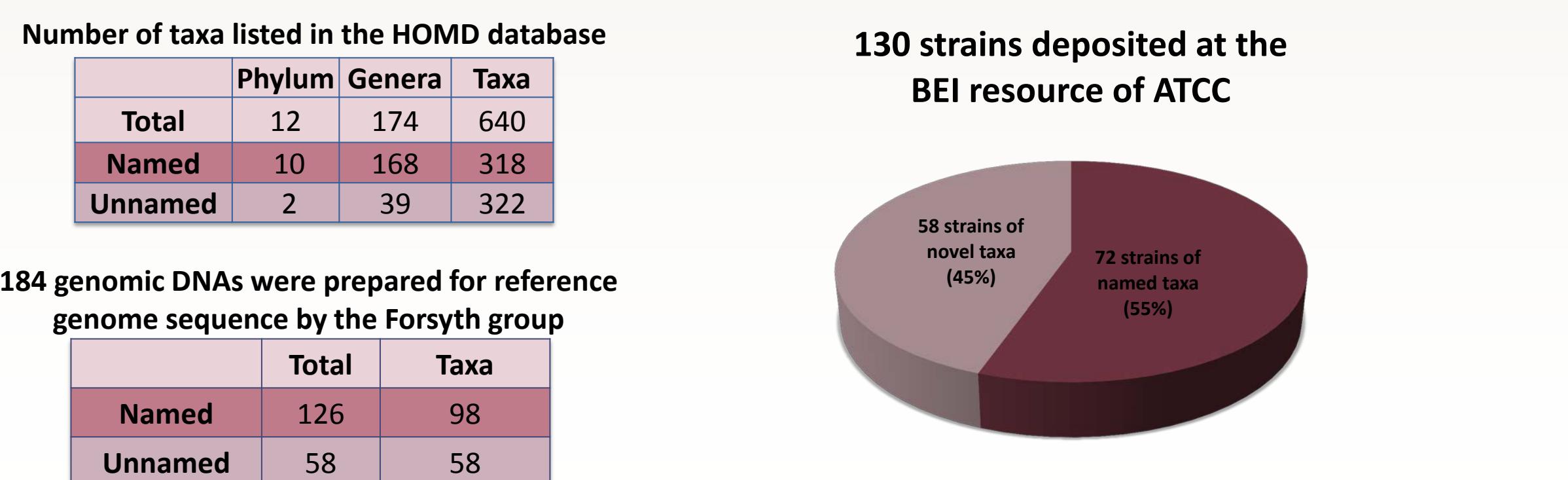
### Identifying unnamed taxa and providing reference strains and genomes

#### Number of taxa listed in the HOMD database

	Phylum	Genera	Taxa
Total	12	174	640
Named	10	168	318
Unnamed	2	39	322

#### 184 genomic DNAs were prepared for reference genome sequence by the Forsyth group

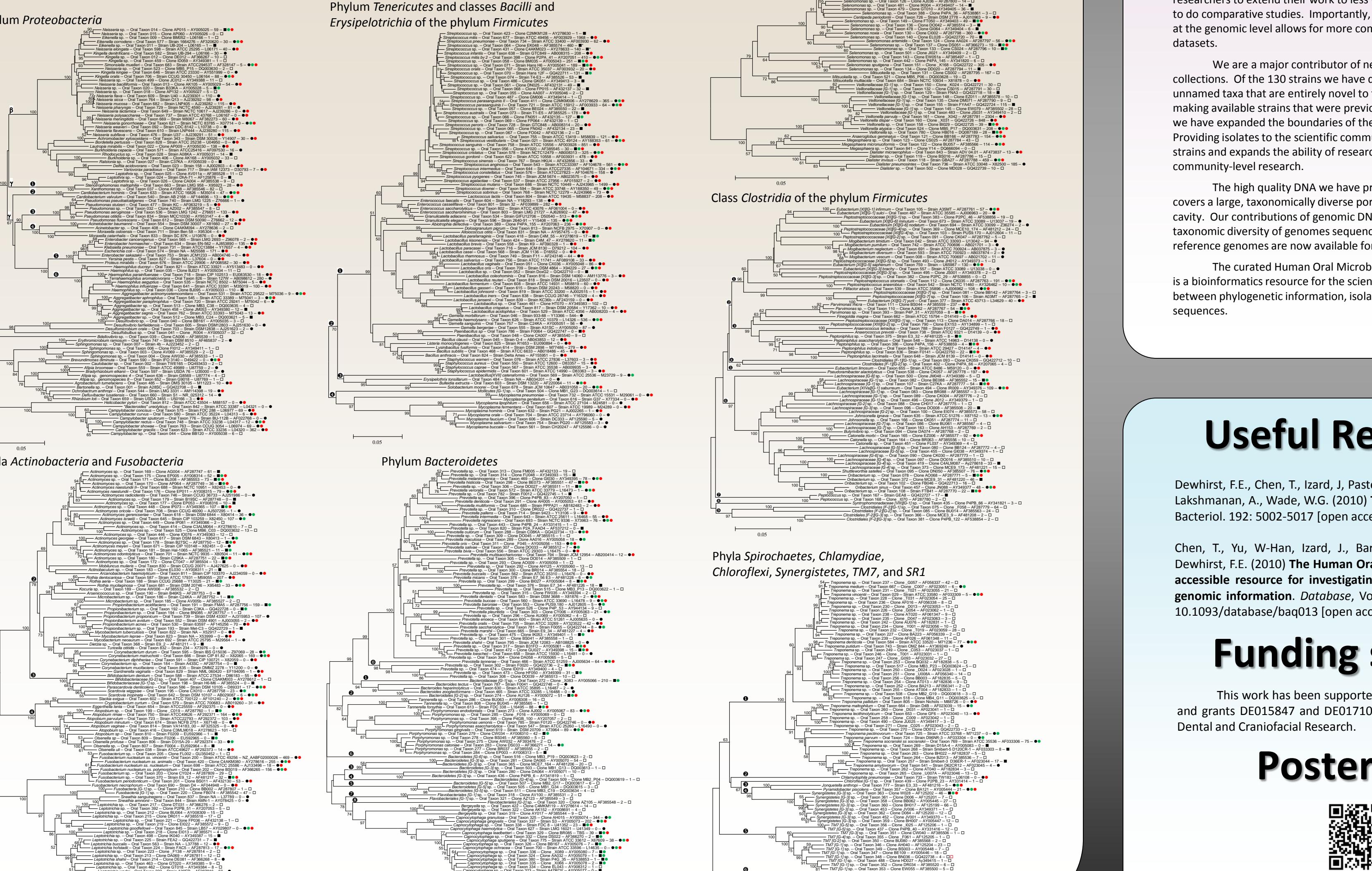
	Total	Taxa
Named	126	98
Unnamed	58	58



## Phylogenetic distribution of genome availability

**Genome availability is described on neighbor-joining trees of the human oral taxa.**

(●) Genome available for at least one strain of taxon, (○) DNA prepared by the Forsyth group for at least one strain of taxon  
 (□) Genome available from uncultivated taxa,  
 (●) Named species, (■) Unnamed species, (□) Phylotype (uncultivated taxon known from cloning studies)



## Conclusions

We have created a curated, phylogenetically based database that we continue to expand. Currently, there are a total of 640 taxa listed on the Human Oral Microbiome Database, with 322 (over 50%) being unnamed taxa. By focusing on increasing the phylogenetic coverage of available strains and reference genome sequences, this database enables researchers to extend their work to less well-characterized organisms and at the genomic level allows for more complex analysis of metagenomic datasets.

We are a major contributor of new strains to permanent culture collections. Of the 130 strains we have deposited, 58 (45%) are from unnamed taxa that are entirely novel to the scientific community. By making available strains that were previously thought to be uncultivable, we have expanded the boundaries of the human microbiome cultivability. Providing isolates to the scientific community enables hands-on analysis of strains and expands the ability of researchers to perform multi-strain, community-level research.

The high quality DNA we have provided for reference genomes covers a large, taxonomically diverse portion of the taxa found in the oral cavity. Our contributions of genomic DNA account for over 64% of the taxonomic diversity of genomes sequences available. These annotated reference genomes are now available for metabolic and functional studies.

The curated Human Oral Microbiome Database at [www.HOMD.org](http://www.HOMD.org) is a bioinformatics resource for the scientific community. It provides a link between phylogenetic information, isolated strains, and genome sequences.

## Useful References

Dewhirst, F.E., Chen, T., Izard, J., Paster, B.J., Tanner, A.C.R., Yu, W.-H., Lakshmanan, A., Wade, W.G. (2010) *The Human Oral Microbiome*. *J. Bacteriol.* 192: 5002-5017 [open access].

Chen, T., Yu, W-H., Izard, J., Baranova, O.V., Lakshmanan, A., Dewhirst, F.E. (2010) *The Human Oral Microbiome Database: a web accessible resource for investigating oral microbe taxonomic and genomic information*. *Database*, Vol. 2010, Article ID baq013, doi: 10.1093/database/baq013 [open access].

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## Poster QRC



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