Traces of Human Migrations in Helicobacter pylori Populations (Falush et al., 2003)

* H. pylori, gut pathogen in humans
* Modern population can be split into 7 subpopulations with geographical distinction
* Modern populations can be traced to ancestral populations from Africa, Central Asia, East Asia
  + 🡪 Spread via human colonization of Polynesia + America, Neolithic farming to Europe, Bantu expansion in Africa, slave trade
* H. pylori has high sequence diversity and frequent recombination between strains
  + 🡪 High information content in H. pylori genome
* Methods
  + Identify 7 housekeeping + antivirulence gene fragments
  + Sequence fragments in 370 strains from 27 human groups (geographic, ethnic, linguistic)
  + `Structure`, Bayesian approach for population structure
* Results
  + Identify four modern populations of H. pylori, denoted:
    - hpAfrica1
      * hspWAfrica
      * hspSAfrica
    - hpAfrica2
    - hpEastAsia
      * hspAmerind
      * hspEAsia
      * hspMaori
    - hpEurope
  + Populations and subpopulations map between ethnic and geographically distinct source regions
  + Unable to split hpEurope into subpopulations
    - Attributed to complex migratory history of Europe
  + Linkage model, reconstructs ancestral populations after hybridization
    - Africa1
    - Africa2
    - EastAsia
    - Europe1 (AE1)
    - Europe2 (AE2)
  + PCA
  + To some extent they propose reconstructed ancestral history of human migration, resolving most cases, e.g., hspWAfrica present in Americas due to slave trade
* Overall
  + High sequence diversity in H. pylori is leveraged to define distinct modern bacterial populations whose ancestry can be traced alongside human migration
  + LD allows for identification of ancestral regions even after hybridization
  + Population subdivision 🡪 virulence factors 🡪 translational applications

Microbial strain-level population structure and genetic diversity from metagenomes (Truong et al., 2017)

* StraingPhiAn 🡪 identify metagenomic strains, characterize genetic structure of thousands of straings from >125 species in > 1500 gut metagenomes
* Correlate microbial population structure with geographic structure of host population
  + E. rectale and P. copri have discrete distributions by subspecies
  + F. prausnitzii is continuous
* Estimate genetic variability of gut microbes
  + Bacteroides most consistent, P. copri most flexible
  + 🡪 Straing level overview of gut microbial diversity
* Results
  + Single strains dominate most species in the gut microbiome
    - Reconstruct each species most abundant strain per sample
    - Assess presence of nondominant strains by searching for SNPs
      * If a low percentage of species-specific marker sites are polymorphic 🡪 single dominant strain
    - When dominant strains are identified, they account for 80% of species in 44% of hosts
    - Difficult to detect non-dominant strains, however, much easier to learn about dominant allele
    - Focus on singular dominant allele
  + Gut microbial stability and uniqueness are explained by subject-specific strain retention
    - When comparing two samples from one host, dominant strain remains 69-79% of time (longitudinal data)
  + High intra-subject strain retention, low inter-subject strain similarity
    - **Shared geography did not increase the fraction of strains shared by different subjects**
  + Strain-level microbial genetics strongly correlate with geographically separated host populations
    - Subspecies clades are often grouped together
  + Sets of related strains associate with geography even in otherwise cosmopolitans species
    - See cool phylogenetic + PCA plots (essentially, geographically close hosts have phylogenetically close strains for species)
  + Genetic diversity of strains in the same species varies significantly for different microbes
    - Bacteroides, which is most common genus, 🡪 genetically consistent with low diversity indices
    - P. copri is 2.74%, F. prausnitzii is 2.94%, L. reuteri is 2.74%.
    - Observed genetic diversity from gut microbiome metagenomics is much larger than from in-vitro isolates.

Dispersal of Mycobacterium tuberculosis via the Canadian fur trade (Pepperell et al., 2011)

* Study of ‘gene flow’, i.e., introduction of genetic material to new populations via interbreeding, for M. tuberculosis in Canada.
  + 🡪 Gene flow from Quebec to Aboriginal populations during fur trade era
* Results suggest two asynchronous processes
  + Dispersal of M. tuberculosis via human migrants
  + Expansion of M. tuberculosis population facilitated by shifts in host ecology
* Low sequence diversity found in M. tuberculosis
* small, widely dispersed pathogenic populations
* M. tuberculosis has population subdivisions on geographic / continental scale
* Results
  + M. tuberculosis may be spread by small numbers of human migrants
  + M. tuberculosis populations can persist at low levels over historical time scales
  + Small bacterial populations may be sustained by ongoing migration + slow disease dynamics
  + Shifts in host ecology favoring the pathogen may be accompanied by bacterial population expansions
* Methods
  + Model for effective population size and `omega`, which parameterized historical Ne to current Ne
    - Compare model to constant population size
  + Time fixed for expansion, based on social history [Is this valid?]
    - Divergence times are estimated using `Ytime`
  + Estimates for population based on symptomatic human hosts [Is this valid?]
  + Estimate for mutation rate is per transmission generation based on intrahost M. tuberculosis population dynamics
  + Simulation study using SIMCOAL (as opposed to fastsimcoal) 🡪 posterior distribution of population expansion and null model (constant size)
    - Method for inferring expansions was tested on simulated data.

Achtman and Zhou 2020 (Metagenomics of the modern and historical human oral microbiome with phylogenetic studies on *Streptococus mutans* and *Streptococcus sobrinus*)

Cornejo 2012 (Evolutionary and Population Genomics of the Cavity causing Bacteria *Streptococcus mutans*)

Eisenhofer 2020 (Investigating the demographic history of Japan using ancient oral microbiota)

Garud 2019 (Evolutionary dynamics of bacteria in the gut microbiome within and across hosts

Groussin 2021 (Elevated rates of horizontal gene transfer in the industrialized human microbiome

Hershberg 2008 (High Functional Diversity in *Mycobacterium tuberculosis* Driven by Genetic Drift and Human Demography)

Ostrowski 2021 (The Food Additive Xantham Gum Drives Adaptation of the Human Gut Microbiota)

Pepperell 2013 (The Role of Selection in Shaping Diversity of Natural *M. tuberculosis* Populations)

Liu (China’s tuberculosis epidemic stems from historical expansion of four strains of *Mycobacterium tuberculosis*)

Sonnenburg 2019 (Vulnerability of the industrialized microbiota)

Tett 2021 (*Prevotella* diversity, niches, and interactions with the human host)

Tett 2019 (The Prevotella copri Complex Comprises Four Distinct Clades underrepresented in Westernized Poplations)

Wibowo 2020 (Reconstruction of ancient microbial genomes form the human gut)

Schnorr 2014 (Gut microbiome of the Hadza hunter-gatheres)