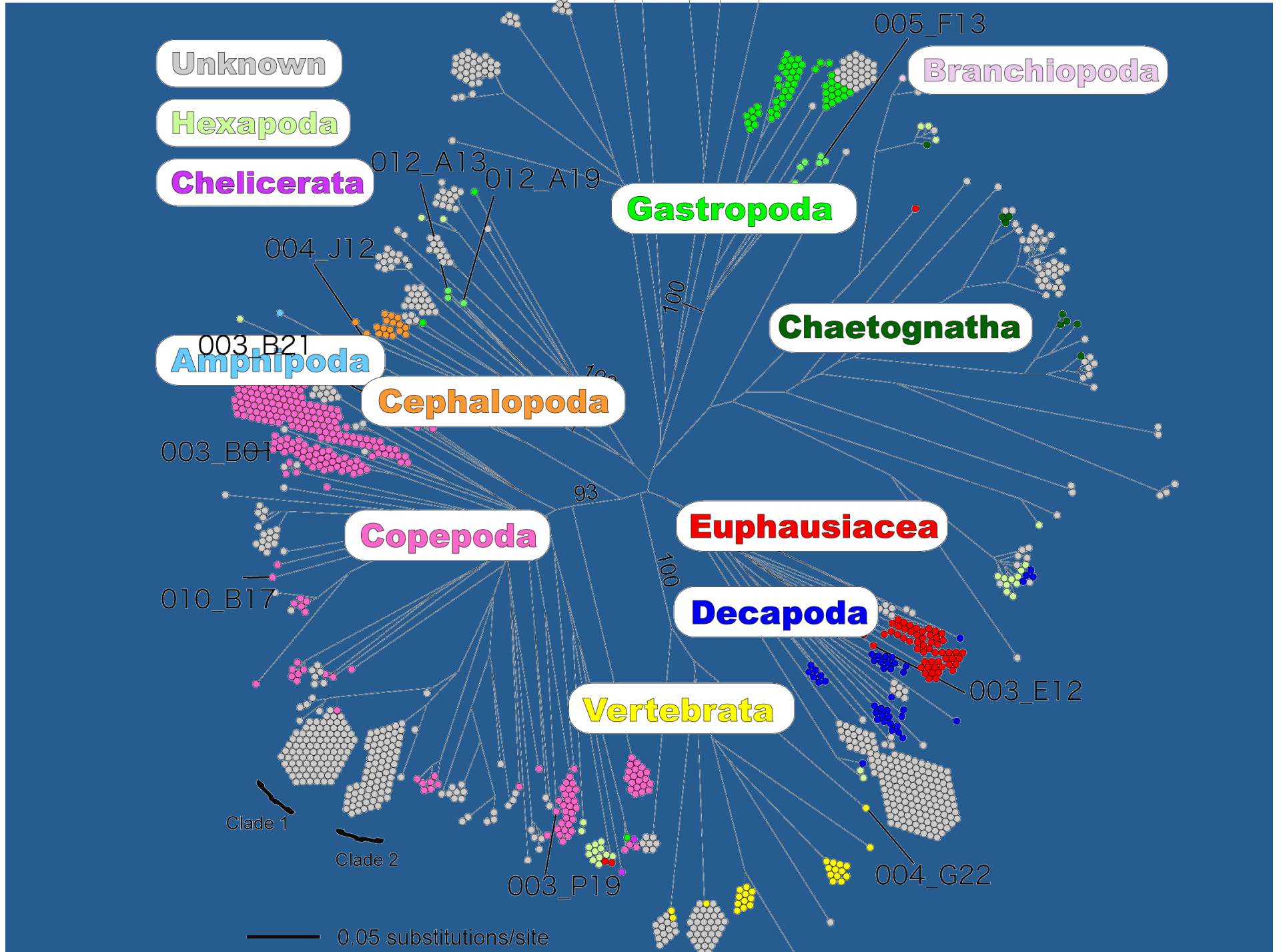


Metagenomics, metagenetics, metatranscriptomics

Ryuji J. Machida

Smithsonian National Museum of
Natural History



Genetic analysis

- Individual based (Phylogeny, Population genetics, Barcoding)
 - Sampling
 - Identification
 - DNA extraction
 - PCR
 - Sequence
- Community based (metagenomics, metagenetics, metatranscriptomics)
 - Sampling
 - Homogenization
 - DNA or RNA extraction
 - PCR (or without PCR)
 - Sequence

What we will know?

- Estimation of diversity
 - Functional diversity
- Genomic architecture of community
 - Population genetics, Phylogeny
- Monitoring
 - Climate change, pollution
- Laval dispersals
 - Fish, Benthic animals

Next generation sequencer

- 454 (Roche)
 - 4M base pairs, read length=400 bp
- Solexa (Illumina)
 - 200M base pairs, read length=100 bp
- SOLiD (ABI)
 - 300G base pairs, read length=75 bp