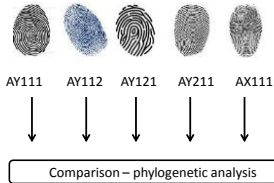


Phylogenetic analyses in fish diseases

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Germany, Insel Riems

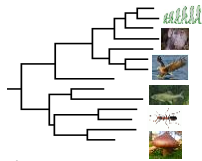


Prerequisite



Phylogenetics

- derives from the Greek terms
 - * *phylé* (φυλή) and *phylon* (φύλον)
 - = "tribe", "clan", "race" and
 - * *genetikós* (γενετικός), of the word *genesis* (γένεσις)
 - = "origin", "source", "birth"
- Evolutionary relationships among groups of organisms (e.g. species, populations)
- discovered through molecular sequencing data and morphological data matrices
- Result = hypothesis about the evolutionary history of taxonomic groups:
 - their **phylogeny**



Molecular phylogenetic

molecular features to portray the phylogeny (= history) of life

- molecular analyses (DNA, RNA), morphology (feather, scale) biochemistry (protein)
- Advantage of molecular analyses is the huge amount of comparative features, which can combine and include in studies (e.g. 200 nt = 200 features, mutation yes or no versus feather yes or no)
- Therefore a better statistic for a better and reliable calculation of „family“ tree and the respective branches

Taxonomic level/ phylogenetic distance ↑

- DNA: nucleotide sequence
- Coding or noncoding regions
 - Introns, intergenic regions (spacer)
 - Single mutations (SNP, RFLP, AFLP etc.)
- population

- Protein: amino acid sequence
- Coding proteins
 - Expression pattern (motifs)
- group

SNP: Single nucleotide polymorphism
 RFLPs: restriction fragment length polymorphisms
 AFLPs: amplified fragment length polymorphisms

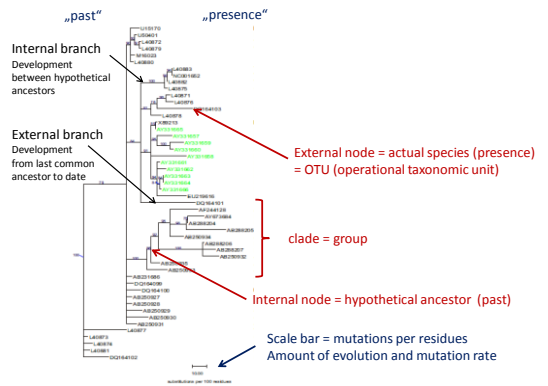
Limitations:

- no way to measure whether a particular phylogenetic hypothesis is accurate or not
- unless the true relationships among the taxa being examined are already known (which may happen with bacteria or viruses under laboratory conditions)
- The best result: a tree with branches that are well supported by the available evidence.

Taxon sampling

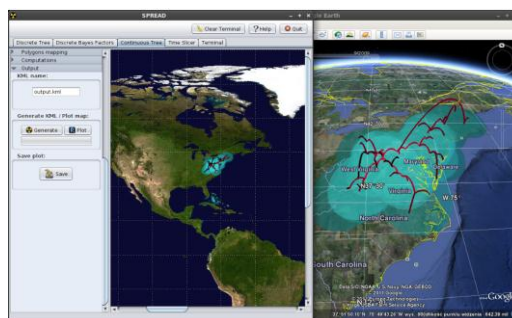
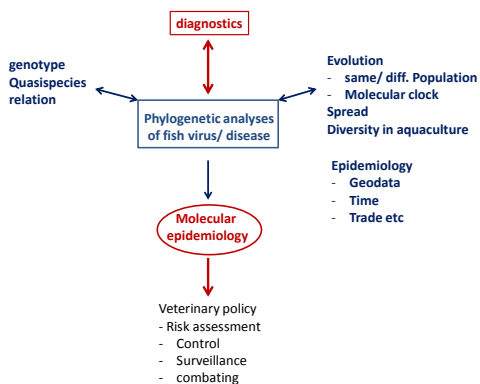
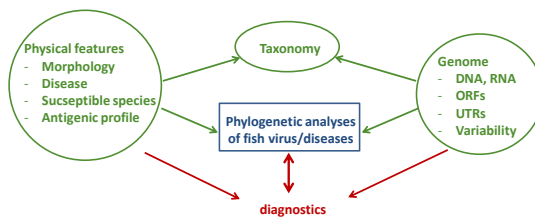
Simulations have shown that it is more important to **increase the number of taxa in the matrix** than to increase the number of character

more taxa → the more accurate → more robust results of phylogenetic tree



veterinary diagnostics

- Characterization and identification of respective agents:
 - genotype: IHNV, VHSV,
 - HPR-type: ISAV
 - EHNV: differentiation from ECV, ESV etc.
- Control of viral pathogens
- Conclusion: origin, relationship and classification
- **Phylogenetic analyses illustrate the development and evolution of the agent**
- **Epidemiology: Correlation between virus distribution and trade channel**



APPLICATIONS NOTE
 Phylogenetics
SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics
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„The good news about computers is that they do what you tell them to do.

The bad news is that they do what you tell them to do.“

Theodor H. Nelson, sociologist and IT-pioneer