OMICS Journals are welcoming Submissions

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Dr. Wuyi Liu Biography

- Wuyi Liu **Is a geneticist and animal breeding expert, being good at phylogenetics, bioinformatics, genomics and genetics.** Wuyi Liu **learned from agricultural universities. During 1997-2004,** Wuyi Liu **began the academic career and got my Bachelor and M.Sc. from Anhui Agricultural University, majoring in animal sciences and statistical genetics. During 2007-2010,** Wuyi Liu **was engaged in advanced studies in China Agricultural University and got my Ph.D., majoring in animal genetics and genomics and bioinformatics. At present,** Wuyi Liu **am interested in the following subject areas: phylogenetics and clade inferring, mitochondrial DNA data, genomics, transcriptomics, proteomics, statistical genetics, population genetics and evolution, bioinformatics, biotechnology, statistical genomics, animal ecology.**

Dr. Wuyi Liu Research Interests

- **Presently,** Wuyi Liu **am interested in the following subject areas, i.e. phylogenetics and clade inferring, mitochondrial DNA, genomics, transcriptomics, proteomics, statistical genetics, population genetics and evolution biology, bioinformatics, biotechnology, statistical genomics, animal ecology.**

Dr. Wuyi Liu Publications

- Liu WY and Chen HQ. Study on the Randomly Amplified Polymorphic DNA of Yellow Cattle in Northern Anhui Province. China Cattle Science, 2004, 32(2): 8-11.
- Liu W. and C. Zhao, 2010. Genome-wide identification and analysis of the chicken basic helix-loop-helix factors. Comp. Funct. Genomics, 2010: 1-12.
- Liu W., C. Zhao and J. Li, 2010. A non-invasive and inexpensive PCR-based procedure for rapid sex diagnosis of Chinese gamecock chicks and embryos. J. Anim. Vet. Adv., 9: 962-970.
- Liu W. and C. Zhao, 2010. Comprehensive genetic analysis with mitochondrial DNA data reveals the population evolution relationship between chinese gamecocks and their neighboring native chicken breeds. Asian J. Anim. Vet. Adv., 5: 388-401.
- Liu W. and K. Zhang, 2011. Rapid Salt-extraction of genomic DNA from Formalin-fixed toad and frog tissues for PCR-based analyses. Asian J. Anim. Vet. Adv., 6: 958-965.
- Liu W. and C. Zhao, 2011. Molecular phylogenetic analysis of zebra finch basic Helix-Loop-Helix transcription factors. Biochem. Genetics, 49: 226-241.

Phylogenetics

- Phylogenetics is the study of evolutionary relationships among groups of organisms (e.g. species, populations), which are discovered through molecular sequencing data and morphological data matrices

Phylogenetic systematics

- All life on Earth is united by evolutionary history; we are all evolutionary cousins — twigs on the tree of life. Phylogenetic systematics is the formal name for the field within biology that reconstructs evolutionary history and studies the patterns of relationships among organisms. Unfortunately, history is not something we can see. It has only happened once and only leaves behind clues as to what happened. Systematists use these clues to try to reconstruct evolutionary history (http://evolution.berkeley.edu/evolibrary/article/phylogenetics_01)

Purpose of phylogenetics

- With the aid of sequences, it should be possible to find the genealogical ties between organisms. Experience learns that closely related organisms have similar sequences, more distantly related organisms have more dissimilar sequences. One objective is to reconstruct the **evolutionary relationship** between species.
- An other objective is to estimate the **time of divergence** between two organisms since they last shared a common ancestor.
- (http://users.ugent.be/~avierstr/principles/phylogeny.html)

Disclaimers

- The theory and practical applications of the different models are not universally accepted.
- With one dataset, different software packages can give different results. Changes in the dataset can also give different results. Therefore it is important to have a good alignment to start with.
- Trees based on an alignment of a gene represent the relationship between genes and this is not necessarily the same relationship as between the whole organisms. If trees are calculated based on different genes from organisms, it is possible that these trees result in different relationships.

Terminology

- **node :** a node represents a taxonomic unit. This can be a taxon (an existing species) or an ancestor (unknown species : represents the ancestor of 2 or more species).
- **branch :** defines the relationship between the taxa in terms of descent and ancestry.
- **topology :** is the branching pattern.
- **branch length :** often represents the number of changes that have occurred in that branch.
- **root :** is the common ancestor of all taxa.
- **distance scale :** scale which represents the number of differences between sequences (e.g. 0.1 means 10 % differences between two sequences)

Possible ways of drawing a tree

- Trees can be drawn in different ways. There are trees with **unscaled branches** and with **scaled branches**. Unscaled branches : the length is not proportional to the number of changes. Sometimes, the number of changes are indicated on the branches with numbers. The nodes represents the divergence event on a time scale.
- Scaled branches : the length of the branch is proportional to the number of changes. The distance between 2 species is the sum of the length of all branches connecting them.
- Is is also possible to draw these trees with or without a root. For **rooted trees**, the root is the common ancestor. For each species, there is a unique path that leads from the root to that species. The direction of each path corresponds to evolutionary time. An **unrooted tree** specifies the relationships among species and does not define the evolutionary path.

Methods of phylogenetic analysis

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Thank you.

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