

February 19, 2008. **MOLECULAR DATA IN SYSTEMATICS**

I. Techniques - kinds of data

- intrinsically distance-based data:
 - immunology (cross reaction of antibodies)
 - DNA - DNA hybridization
 - AFLPs - RAPDs -DNA fingerprinting
 - microsatellites

- character-based data:
 - allozymes
 - restriction enzyme sites
 - sequencing methods
 - direct
 - cloning
 - PCR
 - genomic data (gene arrangement)

II. Special features of molecular data

- purported advantages:
 - closer to (or equal to) the genetic information.
 - huge numbers of potential characters, especially useful in organisms with simple morphology.
 - ability to homologize across very broad groups.
 - independence from morphological characters which are perhaps more subject to adaptive convergence.
 - ability to model or weight, because of relatively simple models of change.
 - \$\$\$.

- purported weaknesses:
 - simplicity of characters (i.e., no ontogeny, few possible character states) leading to special problems with homoplasy.
 - sampling problems.
 - fossil taxa generally can't be included.
 - highly conserved regions, used to reconstruct deep branching points, are perhaps *more* subject to adaptive convergence.
 - \$\$\$.

Properties of a good marker, as compared between molecules (i.e., DNA sequence data) and morphology.

	<u>molecules</u>	<u>morphology</u>
1) COMPLEXITY AND COMPARABILITY	-	+
2) DISCRETE STATES	+	-
3) HERITABILITY	+	-
4) INDEPENDENCE	?	?
5) LOW RATE OF CHANGE (λ)	?	?
6) MANY POSSIBLE CHARACTER STATES	-	+

III. Methods of analysis (an overview for now -- more later in the class)

A. Phenetic

- molecular systematics is the last hold-out of phenetic methods as used for phylogenetic reconstruction.
- disadvantages:
 - usually assumes molecular clock.
 - many distance measures used are non-metric, therefore one can't interpret branch lengths.
 - hides homoplasy.
 - throws away the information on individual characters that was so laboriously obtained.
- advantages:
 - ??? (at best able to mimic the results of a phylogenetic analysis)
 - Averaging across whole genome?
 - Avoiding problem of reticulation? (some argue phenetic methods are OK below species level, as in the field of "phylogeography").

B. Phylogenetic

- many molecular systematists are deeply concerned with adapting standard character-based methods of phylogenetic analysis (e.g., parsimony and Maximum likelihood) to these data; most of the issues we have already discussed are involved:
 - homology (including alignment problems)
 - what is a character?
 - nucleotide positions
 - character correlations
 - structural rearrangements (i.e., deletions, inversions) - more below
 - allozymes
 - restriction sites:
 - RFLP's
 - mapping
 - weighting:
 - gains versus losses
 - transitions versus transversions
 - purines A G
 - pyrimidines C T U
 - codon position bias
 - compensatory substitutions in RNA (due to secondary structure)
 - compatibility, "signature nucleotides" (i.e., the "true" synapomorphy approach in a new guise)
 - comparing different data sets (e.g., morphology versus molecules)
 - maximum parsimony versus maximum likelihood (more later)
 - the "window of opportunity": how to tell when it's open?
 - considerations of lambda (λ)

IV. Comparing genomes

- synteny, rearrangements, insertions/deletions
- exon shuffling
- the gene "annotation" problem
- multigene families
 - paralogy vs orthology
 - the fate of duplicated genes: ghost genes, subfunctionalization

V. Recommendations (Mishler's Aphorisms):

-- treat these data as any other; if the object is phylogeny reconstruction, use phylogenetic methods.

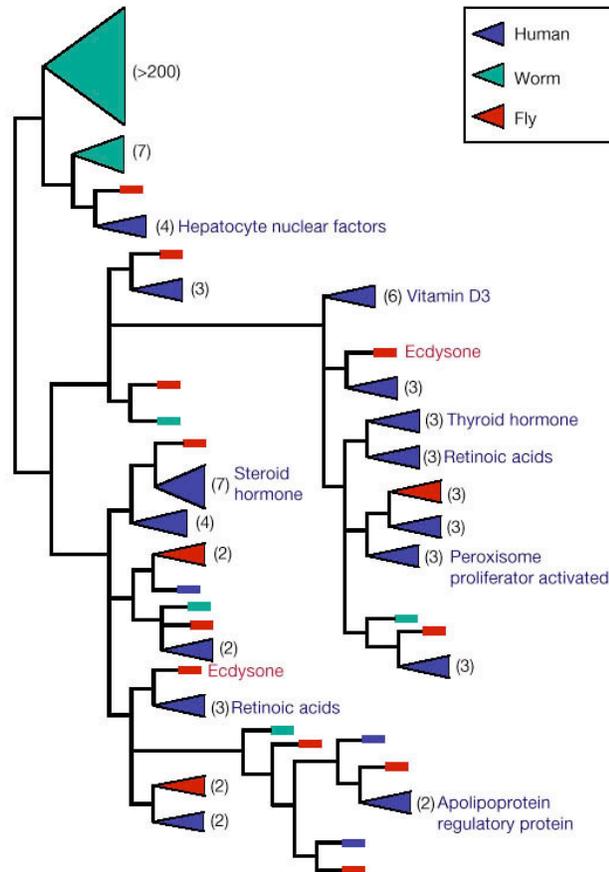
-- include all available data in an analysis, even if your own focus has been on molecules; it makes no sense to ignore older data just because newer data have been generated.

-- be wary of consensus tree approaches; they may be worthwhile as part of the analysis, but it is probably best to combine all putative homologies into one matrix (perhaps with weighting if this can be independently justified).

-- for reconstructing deep splits, it is much better to sequence portions of several different genes, scattered around the nuclear and organelle genomes, than it is to concentrate on extensive sequencing of a single gene (because of the problem of tight selective constraints on any one highly conserved region). Or for that matter, use morphology or genome structure.

-- it is probably better to break large surveys down into reasonable local analyses, to avoid spurious homoplasy (e.g., instead of putting all eukaryotes into one huge matrix, work on relationships within smaller, a priori justified monophyletic groups, and later link those groups together using archetypes: "compartmentalization" -- see earlier lecture on characters).

-- molecular evolutionary studies and phylogeny reconstruction using molecules are two very different goals; for the former purpose, one should use phylogenies based on morphology (and other characters, perhaps including molecules -- but not the molecules that are being studied evolutionary).



Simplified cladogram of the 'many-to-many' relationships of classical nuclear receptors. Triangles indicate expansion within one lineage; bars represent single members. Numbers in parentheses indicate the number of paralogues in each group.

“Synteny”

From: Biochemistry & Molecular Biology of Plants
 edited by Bob B. Buchanan, Wilhelm Gruissem, Russell L.
 Jones. 2000.

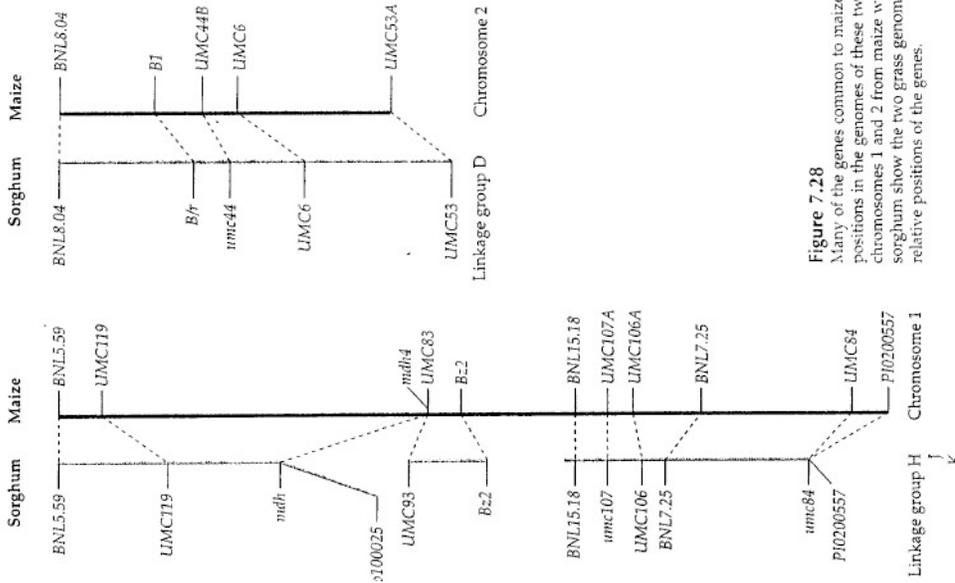


Figure 7.28
 Many of the genes common to maize and sorghum are organized into similar positions in the genomes of these two plants. A comparison of genetic maps of chromosomes 1 and 2 from maize with the maps of several linkage groups from sorghum show the two grass genomes similarly organized with respect to the relative positions of the genes.

Multiple gene inversion characters across Green Plants

22 gene inversion
 in LSC
 Grasses

28 gene inversion
 in LSC
 euphyllophytes

13 gene inversion
Adiantum (other
 leptosporangiate
 ferns, but not
Osmunda)

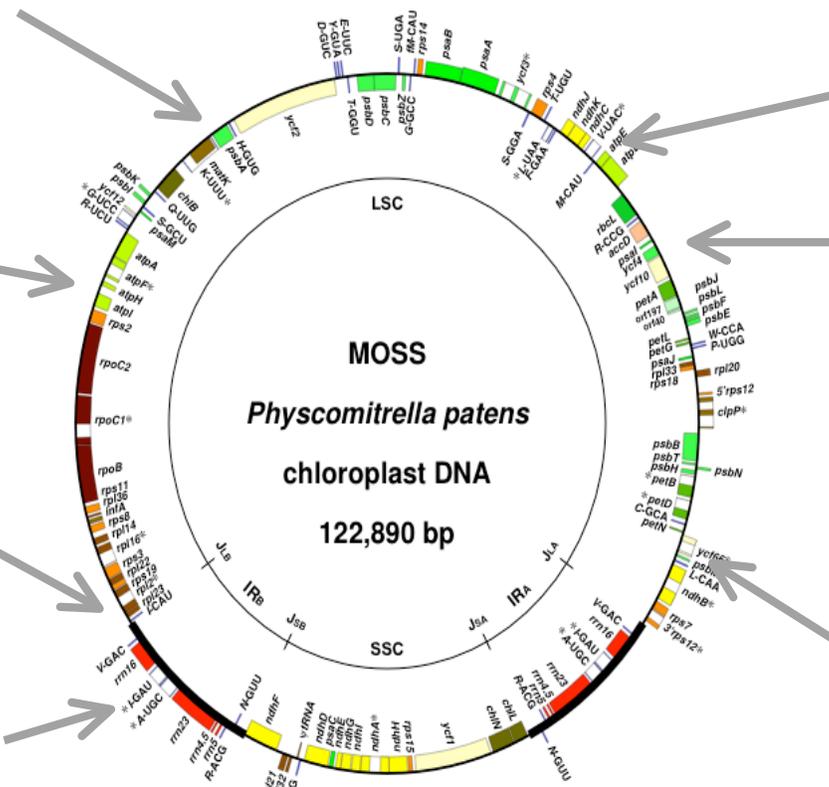
11 gene inversion
Pinus (associated
 with loss of IR in
 conifers)

5 gene inversion in
 LSC
 Pteridophytes s.s.

12 gene inversion
 and 13 gene
 inversion and
 translocation in
 LSC
Chaetosphaeridium

33 gene inversion
 in LSC
Oenothera

75 gene inversion
 in LSC
Physcomitrella



D.G. Kelch, A. Driskell, and B.D. Mishler. 2004. Inferring phylogeny using genomic characters: a case study using land plant plastomes. In B. Goffinet, V. Hollowell, and R. Magill (eds.), *Molecular Systematics of Bryophytes* [Monographs in Systematic Botany 98], pp. 3-12. Missouri Botanical Garden Press, St. Louis.