Mitonuclear speciation
# Species concepts – archaic constructs

<table>
<thead>
<tr>
<th>Species concept</th>
<th>Property(ies)</th>
<th>Advocates / references</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biological</td>
<td>Intermating (natural reproduction resulting in viable and fertile offspring)</td>
<td>Wright (1940); Mayr (1942); Dobzhansky (1950)</td>
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<tr>
<td>Isolation</td>
<td>*Intrinsic reproductive isolation (absence of interbreeding between heterospecific organisms based on intrinsic properties, as opposed to extrinsic [geographic] barriers)</td>
<td>Mayr (1942); Dobzhansky (1970)</td>
</tr>
<tr>
<td>Recognition</td>
<td>*Shared specific mate recognition or fertilization system (mechanisms by which conspecific organisms, or their gametes, recognize one another for mating and fertilization)</td>
<td>Paterson (1985); Masters et al. (1987); Lambert and Spencer (1995)</td>
</tr>
<tr>
<td>Ecological</td>
<td>*Same niche or adaptive zone (all components of the environment with which conspecific organisms interact)</td>
<td>Van Valen (1976); Andersson (1990)</td>
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<tr>
<td>Evolutionary</td>
<td>Unique evolutionary role, tendencies, and historical fate</td>
<td>Simpson (1951); Wiley (1978); Mayden (1997)</td>
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<tr>
<td>(some interpretations)</td>
<td></td>
<td></td>
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<tr>
<td>Cohesion</td>
<td>*Diagnosability (qualitative, fixed difference)</td>
<td>Grismer (1999, 2001)</td>
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<tr>
<td></td>
<td>Phenotypic cohesion (genetic or demographic exchangeability)</td>
<td>Templeton (1989, 1998a)</td>
</tr>
<tr>
<td>Phylogenetic</td>
<td>Heterogeneous (see next four entries)</td>
<td>(see next four entries)</td>
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<tr>
<td>Hennigian</td>
<td>Ancestor becomes extinct when lineage splits</td>
<td>Hennig (1966); Ridley (1989); Meier and Willmann (2000)</td>
</tr>
<tr>
<td>Monophyletic</td>
<td>*Monophyly (consisting of an ancestor and all of its descendants; commonly inferred from possession of shared derived character states)</td>
<td>Rosen (1979); Donoghue (1985); Mishler (1985)</td>
</tr>
<tr>
<td>Genealogical</td>
<td>*Exclusive coalescence of alleles (all alleles of a given gene are descended from a common ancestral allele not shared with those of other species)</td>
<td>Baum and Shaw (1995); see also Avise and Ball (1990)</td>
</tr>
<tr>
<td>Diagnosable</td>
<td>*Diagnosability (qualitative, fixed difference)</td>
<td>Nelson and Platnick (1981); Cracraft (1983); Nixon and Wheeler (1990)</td>
</tr>
<tr>
<td>Phenetic</td>
<td>*Form a phenetic cluster (quantitative difference)</td>
<td>Michener (1970); Sokal and Crovello (1970); Sneath and Sokal (1973)</td>
</tr>
<tr>
<td>Genotypic cluster (definition)</td>
<td>*Form a genotypic cluster (deficits of genetic intermediates; e.g., heterozygotes)</td>
<td>Mallet (1995)</td>
</tr>
</tbody>
</table>

De Quieroz 2007
Mitonuclear speciation

Mt mutational erosion → Nuclear compensation → Coadapted mt and nuc genotypes → BDMIs → Reproductive isolation → Species
DMIs
Mitonuclear DMIs
F1s vs. F2s and dominance effects

Later hybrids

aabb

VS.

AAm or aaM
Mitonuclear hybrid breakdown

Hill et al. 2019
Nuclear speciation genes

• Gene that follows DMI model and creates reproductive isolation
• Wu and Ting identified 5 in 2004
• Many more have been identified, but the list remains fairly short
• Is there a universal speciation gene or set of genes?
PRDM9

- Only speciation gene identified in mammals (most are in flies)
- Controls recombination hotspots
- One of the fastest evolving genes
An outsized role for mitonuclear DMIs

- Only 13 loci (or 1 linked locus)
- Evolves quickly
- Critical energetic functions
- Can’t tolerate slight incompatibilities?
- Lots of interactions
- May be a hotspot for speciation genes
Evidence for mitonuclear speciation

Table 1 Examples of systems with evidence of a cytonuclear basis of reproductive isolation or cytonuclear effects on fitness. In some cases, the evidence remains indirect and/or speculative

<table>
<thead>
<tr>
<th>Taxon</th>
<th>References</th>
</tr>
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<tbody>
<tr>
<td>Animals</td>
<td></td>
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<tr>
<td>Nematodes (Caenorhabditis)</td>
<td>Zhu et al. (2015), Chang et al. (2016)</td>
</tr>
<tr>
<td>Fungi</td>
<td></td>
</tr>
<tr>
<td>Yeast (Saccharomyces)</td>
<td>Zeyl et al. (2005), Lee et al. (2008), Chou et al. (2010), Paliwal et al. (2014), Spirek et al. (2015)</td>
</tr>
<tr>
<td>Plants</td>
<td></td>
</tr>
<tr>
<td>Angiosperms (numerous)</td>
<td>Reviewed in Levin (2003), Greiner et al. (2011)</td>
</tr>
</tbody>
</table>

Sloan et al. 2017
Best case study

- Fast mt evolution
- Good evidence for nuclear coevolution
- Hybrids show mito dysfunction as predicted
- Incompatibilities map to N-mt genes
DNA barcode gap

- First proposed as a taxonomic tool
- Hill considers it diagnostic of the speciation process
- Works well in birds
- Doesn’t work well in lineages with slow mt mutation rates (e.g., corals)

Craft et al. 2008
Adaptive vs. neutral mitonuclear speciation
Mitonuclear coevolution and reproductive isolation

Some fallacies

Populations are reproductively isolated without gene flow, but aren’t species yet

How long might this take?
Mitonuclear speciation provides a mechanism for the biological species concept

- a species is a population that is genetically isolated from other populations by incompatibilities in uniquely coadapted mt and N-mt genes (Hill, 2016, 2017, 2018).
Some other evidence for mitonuclear speciation

![Graph showing asymmetry of reciprocal hybrid crosses vs. time since divergence (my).](image)

Bolnick and Near 2005
Clinal data

[Diagram showing nucleotide sequence and geographic distance with a graph depicting the proportion of X. malinche ancestry at different elevations.]
Darwin’s corollary to Haldane’s rule
Introgression

• Nuclear introgression across species boundaries via hybridization is common
• Mt introgression is also common
• ~20% of phylogenetic studies show mitonuclear discordance
• Often mt genomes are captured w/o nuclear gene flow

Good et al. 2015
Causes for mt introgression

• Many authors invoke adaptive reasons, but do not follow up
• Good evidence for adaptive introgression of pt in sunflowers (reciprocal transplants)
• Lots of neutral reasons too:
  • Sex-biased dispersal
  • Haldane’s rule
  • Sexual selection
  • Haplodiploidy
  • Selfish genes/drive
Paradox of mt introgression

• How can mt genomes create species boundaries and then blatantly disregard them?
Resolutions

A) Nuclear coevolution restores mitonuclear “match”

mt and N-mt genes interact to form the COX enzyme

population divergence → mt mutation accumulation → restoration of “match”

B) mt “rescue” introgression may also restore mitonuclear “match”

“rescue” introgression

hybridization can reveal mitonuclear incompatibilities
Rescue introgression

• Little evidence – 2 case studies
Co-introgression

• Allows mt introgression without breaking up coadapted mt and N-mt complexes
• A few cases
• Including NDUFS5
Difficulties in co-introgression

Sloan et al. 2017
Table 3 Predicted conditions that would favour alternative evolutionary responses to mitochondrial mutation accumulation

<table>
<thead>
<tr>
<th>Conditions promoting:...</th>
<th>Compensatory co-evolution and mitonuclear incompatibilities</th>
<th>Adaptive mitochondrial introgression/replacement</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mitochondrial mutation rates</td>
<td>Higher rates</td>
<td>Lower rates</td>
</tr>
<tr>
<td>Effective Population Size</td>
<td>Large or symmetric population sizes</td>
<td>Small or asymmetric population sizes</td>
</tr>
<tr>
<td>Population Subdivision</td>
<td>More subdivision</td>
<td>Less subdivision</td>
</tr>
<tr>
<td>Divergence Time</td>
<td>More ancient divergence</td>
<td>More recent divergence</td>
</tr>
<tr>
<td>Cotransmission of nuclear and mitochondrial loci (e.g. inbreeding)</td>
<td>More cotransmission</td>
<td>Less cotransmission</td>
</tr>
<tr>
<td>Constraints on mitochondrial function</td>
<td>Intense constraints</td>
<td>Relaxed constraints</td>
</tr>
</tbody>
</table>

Sloan et al. 2017
Final thoughts

• Mitonuclear speciation definitely occurs, but how important is it in eukaryotic reproductive isolation?
• Active area of research...