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Biotechnology | Aquaculture | Biochemistry 2019: Molecular markers: From sea food mislabeling detection and biodiversity assessment to modern general biology paradigm verification- Kartavtsev Yu- Far Eastern Federal University, Russia

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The evidences of possible impact of gene introgression on species evolution, evolutionary fate of taxa, including reticulations in phylogenetic trees, and consistency of the latest molecular genetic data with the main modern paradigm, Neo-Darwinism, are considered in many of works. In this assignment, the author will focus on animals, although many ideas suit other phyla too. The main issues of the report are as follows: What methods are most appropriate for the hybrid detection and estimation of genetic introgression or gene flow? What facts, obtained on gene introgression by nDNA and mtDNA markers, are the evidence for? Is there in the literature any data on correspondence of molecular diversity in lineages or in taxa with Biological Species Concept (BSC). How frequently are reticulations in gene trees observed, and what is a major signal from their topology? A combination of nDNA and mtDNA markers best suits the hybrid identification and estimates of genetic introgression or gene flow. The available facts for both nDNA and mtDNA diversity seemingly make the introgression among many taxa of animals and plants obvious, although even in wide hybrid zones of Mytilus ex. group edulis, for example, introgression may be quite restricted or asymmetric, thus holding at least the "source" taxon (taxa) intact. If we accept that sexually reproducing species in marine and terrestrial realms are introgressed, as it is still evident for many cases, then we should recognize that the orthodoxal BSC, in terms of complete lack of gene flow among species, is inadequate due to the fact that many zoological species are not biological species yet. However, sooner or later they definitely become biological species. This conclusion is supported by the genetic distance increasing with taxa rank and by the lowest diversity at intraspecies level as for single mtDNA genes, for complete mitogenome, and for nDNA data (Kartavtsev, 2013; Kartavtsev et al., 2016; Hedges et al., 2015). (4) The recent investigation of fish taxa divergence (Kartavtsev, 2017) using vast BOLD (www.boldsystem.org) database shows that gene trees for taxa up to the family level are basically monophyletic, and interspecies reticulations are rare for most of gene trees. All the four above-listed outcomes have a great importance to the paradigms of General Biology, Evolutionary Genetics, and to iBOL (www.ibol.org) science policy, and to the practice of species identification in particular. Evidently, the most common successful delimiting of species based on barcoding technique is possible due to the prevailing species origin throughout geographic speciation mode that allows random accumulation of numerous mutations/substitutions after isolation of sister populations/taxa, which are detectable with molecular markers (barcodes). It seems that claims on the invalidity of the modern BSC paradigm (Arnold, Fogarty, 2009) due to the large-scale gene introgression and phylogeny reticulation are too premature. Contrary to that, the evidences available in the literature show that molecular genetic data are concordant in general with the BSC and Neo-Darwinism.

In genetics, a molecular marker (identified as genetic marker) is a fragment of DNA that is linked with a certain location within the genome. Molecular markers are used in molecular biology and biotechnology to recognize a particular sequence of DNA in a pool of unknown DNA.

In the first 70 years of building genetic maps, the markers on the maps were genes with variant alleles producing detectably dissimilar phenotypes. As organisms became more and more researched, large numbers of such genes could be used as markers on the maps. However, even in those organisms in which the maps appeared to be "full" of loci of known phenotypic effect, measurements showed that the chromosomal intervals between genes had to contain vast amounts of DNA. These gaps could not be mapped by linkage analysis, because there were no markers in those regions. What was wanted were large numbers of additional genetic markers that could be used to fill in the gaps to provide a higher-resolution map. This need was met by the finding of various kinds of molecular markers. A molecular marker is a site of heterozygosity for some type of silent DNA variation not linked with any measurable phenotypic variation. Such a "DNA locus," when heterozygous, can be used in mapping analysis just as a conventional heterozygous allele pair can be used. Because molecular markers can be easily noticed and are so numerous in a genome, when they are mapped by linkage analysis, they fill the voids between genes of known phenotype. Note that, in mapping, the biological significance of the DNA marker is not important in itself; the heterozygous site is merely a convenient reference point that will be useful in finding one's way around the chromosomes. In this way, markers are being used just as milestones were used by travelers in previous centuries. Travelers were not interested in the milestones (markers) themselves, but they would have been disoriented without them.

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