

Some Implications for the Study of Intelligent Design Derived from Molecular and Microarray Analysis

Fernando Castro-Chavez
Independent Biotechnologist
fdocc@yahoo.com

There are several implications for intelligent design of molecular work using microarray analysis. Here are some of them:

- 1- The discovery of real genes being expressed in a particular tissue [1] can be contrasted from artifacts, which are products of the methodologies used, as the host-vector interactions leading to an artificial rearrangement-splicing described elsewhere [2].
- 2- The discovery of genes expressed only in particular organisms or species (“species specific genes”) can be emphasized as a product of intelligent design, as these are not present in any other organism, discarding a continuous evolutionary way of transmission of genetic material, and enforcing the discontinuous, non-linear origin of the genomic organization of living beings.
- 3- The discovery of genes expressed only in a particular tissue can also help us understand the precise and meticulous design to fulfill the specific purpose for that tissue in particular, every cell working as a coordinated machinery with an intense molecular communication in order for the complete body of an organism to be able to work as it was intended to be.
- 4- The significance of these primary points can be applied to other areas of knowledge with the same confidence; for example, regarding dating methodologies that lead to wrong interpretations, as they are based solely on the imaginations of their producers and users; or, i.e., the interpretations of the experiments related to the work of Stanley Miller, are based in imaginary scenarios that upon a further review became inconsistent, even among themselves, and correspondingly, useless as a mistake.
- 5- A discontinuous presence of genes specific for humans, not present in any other living organism, disproves the continuous and linear order of events conceived by the minds of the promoters of “evolution” and its followers, a fact that is also reflected by the birth of new stars, which disproves a linear derivation of mass if only originated at the moment of the “big bang,” etc.
- 6- New genes can be found as being expressed in unexpected tissues or cells fulfilling their own and particular function inside a specific environment; i.e., inside a cellular organelle.

- 7- Under environmental alterations, specific cells can start producing genes not supposed to be there, starting the process of disease. If those strange genes can be detected at its genesis, using methodologies like a customized microarray analysis, this can help to prevent them for further development. This in itself also demonstrated that any environmental mutation altering the normal disposition of the gene expression brings with itself negative side effects, not bringing any “evolution,” but instead, bringing a pathological state for the organism.
- 8- By comparing different lineages of the same species, we can be able to discover the real and natural plasticity of the genes, in order to allow the organisms to become adapted to diverse environments, but always under a clear and natural boundary, taking one step forward the study on “the natural limits to biological change” [3]. We can in that way further the study and teaching of the molecular basis of biological change, considering recent molecular discoveries as the molecular quality control mechanisms, all of that explains how a cow can be in a dwarf or a tall line but that it can not change to become, i.e., “a whale”.
- 9- By learning how a normal cell or organism works genetically we can also be able to detect the abnormal and anti-natural characteristics of ancient remains, i.e., skulls and bones of ancient hominids or even to compare the already found frozen remains of mammoths with living elephants, and maybe, if one of them is found frozen on the north pole, of Neanderthals also.

References:

[1] Castro-Chavez, F., Yechoor, V.K, Saha, P., Martinez-Botas, J., Wooten, E., Sharma, S., O’Connell, P., Taegtmeier, H., and Chan, L. (2003) Coordinated upregulation of oxidative pathways and downregulation of lipid biosynthesis underlie obesity resistance in Perilipin knockout mice. A microarray gene expression profile. *Diabetes* 52, 2666-2674. URL: <http://diabetes.diabetesjournals.org/cgi/content/abstract/52/11/2666>

[2] Castro-Chavez, F. (2004) A family of artificial heterotranscripts in *Genbank* and their *EcoRI* - related palindromic linkers (*Submitted*). URL: <http://www.geocities.com/fdocc3/ht.htm>

[3] Lester, L. P. & Bohlin, R. G. (1989) The Natural Limits to Biological Change. *Probe Books*, 207 pp. URL: <http://www.probe.org/docs/natlim.html>