INTELLIGENT DESIGN TO GENERATE BIODIVERSITY

Fernando Castro-Chavez
Independent Biotechnologist
Website: http://www.geocities.com/plin9k

The classic work of Mendel on the precise inheritance of characters demonstrated an Intelligent Design behind the Laws of Heredity. Those Laws can be linked now to our modern knowledge of molecular biology to provide a clearer account of the molecular basis and limits to biological change as well as to generate biodiversity.

Here are some approximations on such endeavor:

1. By comparing different varieties of the same kinds of organisms, frequently misclassified as if they were members of different 'species', a database or catalog can be prepared referencing dominant versus recessive genes between groups of organisms that are able to produce fertile offspring. For example, within the different finches, cranes, ducks, Camelids, Delphiniums, Cetaceans, Coleopteran, Brassica, Canis, etc. *I. E.*, dogs can naturally be crossed with wolves and with coyotes; also finches interbreed among themselves; preserving furthermore the genetic load of endangered animals like in the case of cranes (see below).

2. The aforementioned classification can thus be useful for the natural Mendelian engineering of biodiversity, to preserve endangered organisms. For example, by using the old and well proven method of backcrosses described by Mendel near the end of his classical article [1], through reciprocal crosses of the desired resulting F2 phenotypes. This approach will produce new varieties, expanding our biodiversity without the primary need of using artificial cloning, recombinant DNA, or any of the artificial and of the Molecular Biology's techniques. Those methodologies may be used only in extreme cases.

3. This databases classifying and comparing dominant versus recessive genes specific for different organisms will be useful in helping us understand the molecular basis of their segregation in the second hybrid generation, or F2. Enabling us then to answer the question: Which molecular difference makes a gene able to become dominant or recessive? The answer to that question will also help us to better understand the natural span and limits to biological change, discarding 'anagenesis' and 'speciation', speculations both of fictitious origins and transmutations of one species into another. The novel use of the Laws of Heredity proposed here for ecosystems may help us in the production of varieties, races, lineages or sub-species under different and new environments, thus preserving endangered species and generating biodiversity through the intelligent use of those designed Laws of Heredity discovered by Mendel.

We can still declare today, as William Bateson declared 103 years ago: "In these pages I have only touched the edge of that new country which is stretching out before us, whence in ten years' time we shall look back on the present days of our captivity. Soon every science that deals with animals and plants will be teeming with discovery, made possible by Mendel's work. The

breeder, whether of plants or of animals, no longer trudging in the old paths of tradition, will be second only to the chemist in resource and in foresight. Each conception of life in which heredity bears a part - and which of them is exempt? - must change before the coming rush of facts" [2].

Next, I will present few examples of organisms that putatively interbreed producing a fertile offspring; few of them, identified below, are pending to the final report of the F2 presence, which will mean that the initial offspring (the F1) was fertile. Leading that result at the same time to conclude that those so-called different 'species' or 'genus', are only varieties of the same kinds of organisms. Numerous other examples exist today and many others will be discovered.

As stated before, frequently and mistakenly organisms have been classified as if they were members of different species, and even as if they were members of different genus. Below, in example 5, we can see that in Hawaii a fertile offspring was obtained from a whale *Pseudorca crassidens* and a bottlenose dolphin *Tursiops truncatus*. Then, indeed, they are only varieties of the same kind of organism. That error seems to be very easy to occur in the human attempt to classify nature. It is like mistakenly classifying varieties of dogs as if those were members of different 'species' and 'genus'. Few examples are:

1 - Cichlids [3],
2 - The fishes *Xiphophorus* [4],
3 - Sunfish *Lepomis* [5], pending their report of the F2,
4 - Porpoises [6], many individuals with intermediate pigmentation have been observed, indicating that such offspring may be viable, but still pending their report of the F2,
5 - Dolphins [7], to see an example of a fertile offspring from false killer whale (*Pseudorca crassidens*) x bottlenose dolphin (*Tursiops truncatus*) in Hawaii [8],
6 - Whales [9, 10], the first example of any cetacean hybridization giving rise to a fertile offspring,
7 - *Acropora* Corals [11], suggesting a large potential for natural hybridization and extensive introgression,
8 - Finches [12], to read a comment on them [13]; Darwin took them as if they were different species in an attempt to document his theory of evolution. However, finches always were and have been just varieties of the same kind of organism.
9 - Macaques [14],
10 - Red wolves (a fertile offspring of coyotes x wolves) [15, 16]. Varieties of dogs, many of them product of a deliberate process of artificial selection; dogs interbreed with wolves, coyotes, jackals and dingos producing fertile offspring, being all varieties of the same kind of organism. If we can do the "engineering of the perfect dogs" [17], we can do the same with all other living organisms.
11 - Squirrels [18], hybridizations and backcrosses,
12 - Voles [19]
13 - *Hieracium* [20], successful backcrossings,
14 - *Banksia* [21], F2 unspecified,
15 - *Tilia* [22], F2 unspecified,
16 - *Rhododendron* [23, with an evidence of frequent backcrossing],
17 - *Drosophila* (fruit fly) [24],
18 - Carabid beetles *Carabus* [25], introgressive hybridization has occurred multiple times,

19 - *Parnassius* Butterflies [26], F2 unspecified,
20 - *Saccharomyces* (yeast) [27], the allopolyploid strains were able to undergo further hybridizations.

Additionally, the Bison [28], and a more recent work awaiting its final results on fertility presents the offspring of crossbreeding between camels and llamas [29].

The weakness in the evidence for 'speciation' is present in all published articles on the subject. The next is a clear example on the fallibility for the classification of 'species', if based only on phenotype or genotype without including the fact of the fertile descendants. We read in relation to birds: "Among our sample more than half the crosses between species in the same genus produce fertile hybrids" "...viable hybrids have been produced between taxa..." [30]. What the authors are telling us here is that those birds, in the same way as the finches and like multiple other examples, are just varieties of the same organism.

Other frequent position is the fearful and passive take regarding natural crossbreeding. For example: "Identification of which species are likely to hybridize after contact is of critical importance to prevent the further loss of native species... species at risk of introgression... the extent and effects of hybridization in fishes, crayfishes, mussels, and other invertebrates... this approach may be the first step in addressing the potential threat of hybridization between many of the closely related species in North American fresh waters" [31]. The same negative and fearful 'spin' exists in contemporary ecology opinions related to animals [16] and plants [21].

It can be seen that the three last references are opposed to the interbreeding of subspecies because, they argue, the diversity of the parental line may 'disappear'. However, under a strictly rational and controlled interbreeding between subspecies, instead of the 'disappearance' of the parental lines, we will have just the opposite: a more increasingly diversity! Being that, only a question of doing it ecologically wisely. This is a straight and dismissed Mendelian application, which is also useful to preserve the genetic pool of endangered species before their extinction, destroying any 'speciational' fallacy, as we are only dealing with varieties or subspecies here.

When I found that the finches of Galapagos were able to interbreed and to produce fertile offspring, that information opened my eyes to see the flaws in the weak definitions of 'species' used by evolutionists to support their own unfounded hypotheses and claims. Those finches are the very same that were used by Darwin as his inspiration for his theory on evolution. You can see how the Grant's, the discoverers of the ability of the finches to interbreed producing fertile offspring, struggle to try to fit their findings within the wrong theory of 'speciation', a supposed foundational 'evidence' for the theories of 'evolution' (as it was put in *National Geographic*, Nov. 2004). However, there is no transformism or 'transmutation' of one organism into another, there is not a 'molecular evolution' leading to a gradual differentiation of species through millennia, other two of the flawed 'evolutionary' claims.

On thinking of the finches, I thought that, if also all those cranes were also only varieties of one same species, as the finches are amongst themselves, then different cranes could also be able to interbreed having a fertile offspring (the second-generation fertility test). It is known that the two Australian 'species' of cranes can interbreed and have a fertile offspring. In such a way we can

save the genetic load of the varieties of cranes which are endangered (the Canadian, the Siberian, and the Korean), through crossing some of them with not endangered varieties. According to Mendel's Laws, at least 1/4 of the F2 will present features corresponding to the endangered ones, and if we cross those amongst themselves, plus back-crosses with the original endangered ones, we can gradually increase and take out them of the list endangered varieties. Those cranes have never been endangered 'species' but 'varieties'. We don't want to see the same organisms always present on endangered lists.

With a better understanding of the real or true 'species', the plan for the full use of our natural resources makes sense, as for example, not forever an organism like the salmon must be present in a specific region on its list of 'endangered species'.

I am proposing here an organized and exhaustive research project focused on the "second generation fertility test" of fauna, flora and micro-organisms, to set also a higher standard in our understanding of which of them are real species, and which of them are just varieties, that is to say, 'sub-species'.

This is another practical example of a perspective based on 'Intelligent Design' and in total opposition to evolution and to the multiple mistakes of the official 'morphological' classification of organisms.

This is also the opposite of a static conservationism *versus* a practical Intelligent Design Research, as Mendel and our contemporary breeders are very well aware of. We have been given the natural resources and here is a proposal to use them more adequately.

I am aware that to do such recoveries of 'endangered' organisms a lot of wise work is necessary, but it is worthy, as that also will help us to shut down the wrong idea of 'speciation', while deliberately preserving and producing biodiversity in different and new locations.

Keeping those organisms producers of fertile offspring under the category of "subspecies" or 'varieties' will be closer to the facts. Then, we could be able to produce a wonderful array of varieties and subspecies in the most diverse environments, like more diversity within those cranes [32]. Obtaining new subspecies of cranes, as I have proposed before; a process already done with many varieties of dogs that have been developed by man like the 'doberman'.

An expanded list of animals pertaining to the same kinds of organisms that remain mistakenly classified as if pertaining to different species will be of great use for practical purposes; the support of the readers is requested in this area. Preventing at the same time the further and deliberate exploitation of biological ignorance by evolutionists. For example, 'dominant' evolutionists, instead of the evaluation of misclassified organisms actually corresponding to the same kind of organism through checking if they produce fertile offspring, are rather fully assuming *a priori* as "fact" an evolutionary transformism reflected by all of those speculated phylogenies [33], products of the human imagination. Those are just contradictory and multiple guessworks [34-44].

In conclusion, what I propose here is to take the natural ability of the biodiversity to hybridize producing a fertile offspring, in a controlled and rational way. Wisely to prevent ecological disasters [45, 46] and at the same time promoting a biodiversity more than abundant!

Acknowledgements: To Tracy Lynn Duncan for her faithful support and to Dr. William Dembski for his encouragement to improve this document.

References:

[1] Mendel, Gregor. Versuche über Pflanzen Hybriden. *Ver. Natur. Verein. Brünn*, Bd. IV für das Jahr 1865, Abhandlungen, 3-47. English version: URL: http://www.mendelweb.org/Mendel.html
[2] p. 208, in: William Bateson, Mendel's Principles of Heredity a Defence, 1902. *Cambridge University Press*. 212 pp. URL: http://www.esp.org/books/bateson/mendel/facsimile (PDF files)
[3] Turner GF, Seehausen O, Knight ME, Allender CJ, Robinson RL. How many species of cichlid fishes are there in African lakes? *Mol Ecol.* 2001 Mar;10(3):793-806.
[4] Li HY, Savage T, Obermoeller RD, Kazianis S, Walter RB. Parental 5-methylcytosine methylation patterns are stable upon inter-species hybridization of *Xiphophorus* (*Teleostei*: *Poeciliidae*) fish. *Comp Biochem Physiol B Biochem Mol Biol.* 2002 Dec;133(4):581-95.
[5] Avise JC, Saunders NC. Hybridization and introgression among species of sunfish (*Lepomis*): analysis by mitochondrial DNA and allozyme markers. *Genetics*. 1984 Sep;108(1):237-55.
[6] Baird RW, Willis PM, Guenther TJ, Wilson PJ and White BN. An Intergeneric Hybrid In The Family *Phocoenidae*. *Canadian Journal of Zoology* 76:198-204. 1998.
[7] Gray AP, Mammalian Hybrids, 1972, *Commonwealth Agricultural Bureaux*, Farnham Royal, Bucks, England.
[8] URL: http://hotspotshawaii.com/Wolphin.html
[9] Spilliaert R, Vikingsson G, Arnason U, Palsdottir A, Sigurjonsson J, Arnason A. Species hybridization between a female blue whale (*Balaenoptera musculus)* and a male fin whale (*B. physalus*): molecular and morphological documentation. *J Hered.* 1991 Jul-Aug;82(4):269-74.
[10] Arnason U, Spilliaert R, Palsdottir A, Arnason A. Molecular identification of hybrids between the two largest whale species, the blue whale (*Balaenoptera musculus*) and the fin whale (*B. physalus*). *Hereditas*. 1991;115(2):183-9.
[11] Van Oppen MJ, Willis BL, Van Rheede T, Miller DJ. Spawning times, reproductive compatibilities and genetic structuring in the *Acropora aspera* group: evidence for natural hybridization and semi-permeable species boundaries in corals. *Mol Ecol.* 2002 Aug;11(8):1363-76.
[12] Grant PR, Grant BR. Genetics and the origin of bird species. *Proc Natl Acad Sci U S A.* 1997 Jul 22;94(15):7768-75. URL: http://www.pnas.org/cgi/content/full/94/15/7768
[13] Carl Zimmer. Darwin's Avian Muses Continue To Evolve. *Science* 26 April 2002; 296: 633-635. URL: http://www.carlzimmer.com/articles/2002/articles_2002_Finch.html
[14] Evans BJ, Supriatna J, Melnick DJ. Hybridization and population genetics of two macaque species in Sulawesi, Indonesia. *Evolution Int J Org Evolution.* 2001 Aug;55(8):1686-702.
[15] Reich DE, Wayne RK, Goldstein DB. Genetic evidence for a recent origin by hybridization of red wolves. *Mol Ecol.* 1999 Jan;8(1):139-44.
[16] Miller CR, Adams JR, Waits LP. Pedigree-based assignment tests for reversing coyote (*Canis latrans*) introgression into the wild red wolf (*Canis rufus*) population. *Mol Ecol.* 2003 Dec;12(12):3287-301.
[17] http://www.funzone.ws/zones/dogs_pets.html , http://dogs.about.com/b/a/070494.htm
[18] Ermakov OA, Surin VL, Titov SV, Tagiev AF, Luk'ianenko AV, Formozov NA. Study of hybridization in four species of ground squirrels (*Spermophilus*: *Rodentia*, *Sciuridae*) by molecular genetic methods. *Genetika*. 2002 Jul;38(7):950-64.
[19] Iwasa MA, Suzuki H. Intra- and interspecific genetic complexities of two *Eothenomys* species in Honshu, Japan. *Zoolog Sci.* 2003 Oct;20(10):1305-13.
[20] Morgan-Richards M, Trewick SA, Chapman HM, Krahulcova A. Interspecific hybridization among *Hieracium* species in New Zealand: evidence from flow cytometry. *Heredity.* 2004 May 12.
[21] Lamont BB, He T, Enright NJ, Krauss SL, Miller BP. Anthropogenic disturbance promotes hybridization between *Banksia* species by altering their biology. *J Evol Biol.* 2003 Jul;16(4):551-7.
[22] Fromm M, Hattemer HH. Inheritance of allozymes and hybridization in two European *Tilia* species. *Heredity*. 2003 Sep;91(3):337-44.

[23] Milne RI, Abbott RJ, Wolff K, Chamberlain DF. Hybridization among sympatric species of *Rhododendron* (*Ericaceae*) in Turkey: morphological and molecular evidence. *Am J Bot.* 1999 Dec;86(12):1776-1785.
[24] Sainz A, Wilder JA, Wolf M, Hollocher H. *Drosophila melanogaster* and *D. simulans* rescue strains produce fit offspring, despite divergent centromere-specific histone alleles. *Heredity.* 2003 Jul;91(1):28-35.
[25] Sota T, Ishikawa R, Ujiie M, Kusumoto F, Vogler AP. Extensive trans-species mitochondrial polymorphisms in the carabid beetles *Carabus* subgenus *Ohomopterus* caused by repeated introgressive hybridization. *Mol Ecol.* 2001 Dec;10(12):2833-47.
[26] Zakharov EV. The demonstration of natural hybridization between two swallowtail species *Parnassius nomion* and *Parnassius bremeri* (*Lepidoptera*, *Papilionidae*) using RAPD-PCR technique. *Genetika.* 2001 Apr;37(4):475-84.
[27] de Barros Lopes M, Bellon JR, Shirley NJ, Ganter PF. Evidence for multiple interspecific hybridization in *Saccharomyces sensu stricto* species. *FEMS Yeast Res.* 2002 Jan;1(4):323-31.
[28] http://www.csew.com/cattletag/Cattle%20Website/Fact_Sheets/American_Bison/American_Bison.htm
[29] Wright, W. Camel centre tries to produce three more camas. *Gulf News*. 25th February 1999. URLs: http://www.datadubai.com/cama1.htm , http://www.taylorllamas.com/Camel-LamaCrossPhotos.html
[30] Price TD, Bouvier MM. The evolution of F1 postzygotic incompatibilities in birds. *Evolution Int J Org Evolution.* 2002 Oct;56(10):2083-9.
[31] Perry WL, Lodge DM, Feder JL. Importance of hybridization between indigenous and nonindigenous freshwater species: an overlooked threat to North American biodiversity. *Syst Biol.* 2002 Apr;51(2):255-75.
[32] http://magma.nationalgeographic.com/ngm/0404/feature2/map.html
[33] *National Science Foundation*. Assembling the Tree of Life (*ATOL*). *Program Solicitation. NSF 05-523*. URL: http://www.nsf.gov/pubs/2005/nsf05523/nsf05523.htm
[34] Felsenstein, J. Confidence limits on phylogenies: An approach using the bootstrap. *Evolution.* 1985. 39:783-791. (more references on contradictory phylogenics at URL: http://ib.berkeley.edu/courses/ib200a/readings.html)
[35] Sarich, V. M., Schmid, C. W., and Marks, J. DNA hybridization as a guide to phylogeny: A critical appraisal. *Cladistics*. 1989. 5:3-32.
[36] Marks J. What's old and new in molecular phylogenetics. *Amer. J. Phys. Anthropol.* 1991. 90:237-46.
[37] Sanderson, M.J. Objections to boostraping phylogenies: a critique. *Syst. Biol.* 1995. 44(3):299-320.
[38] Bryant, D. A classification of consensus methods for phylogenetics. In Janowitz, M., Lapointe, F.J., McMorris, F., Mirkin, B. Robers, F. (eds.) *Bioconsensus. DIMACS-AMS*. 2003. 163-184.
[39] Grant, T, and A. G. Kluge. Data exploration in phylogenetic inference: scientific, heuristic, or neither. *Cladistics*. 2003. 19:379-418.
[40] Curnoe D. Problems with the use of cladistic analysis in palaeoanthropology. *Homo*. 2003;53(3):225-34.
[41] Templeton AR. Statistical phylogeography: methods of evaluating and minimizing inference errors. *Mol Ecol.* 2004 Apr;13(4):789-809.
[42] Holland BR, Huber KT, Moulton V, Lockhart PJ. Using consensus networks to visualize contradictory evidence for species phylogeny. *Mol Biol Evol.* 2004 Jul;21(7):1459-61.
[43] Makarenkov V, Legendre P. From a phylogenetic tree to a reticulated network. *J Comput Biol.* 2004;11(1):195-212.
[44] de Queiroz, A., M. J. Donoghue and J. Kim. Separate versus combined analysis of phylogenetic evidence. *Ann. Rev. Ecol. Syst.* 1995. 26: 657-681.
[45] J.A. Holmes. Lecture 10: Introduced Species In Communities. *BGY C61S* - March 28, 2001. Environmental Research and Teaching, *University of Toronto*. *Environmental Information Office at I.E.S.* URL: http://www.utoronto.ca/env/jah/ace/C61_lc10.htm
[46] "Introduced Species", references from 1996 to present. *Sea Web, Ocean Citations*. I.E.: http://www.seaweb.org/background/abstracts/introduced/2004/04introducedindex.html