Title:

Can random mutation explain phenotypic variability?

Víctor Alejandro Zapata Trejo[1]

[1]Department of Marine Biology. Autonomous University of Yucatan, Campus of Biological and Agricultural Sciences, Merida 97000, Mexico.

Email: A16018093@alumnos.uady.mx

Abstract: The epigenome regulates the gene expression of all differentiated cells and indicates which specific genes must be transcribed. It is argued that the expression factors that act on specific genes of the somatic cell involved in a behavior also act on the transcription of the same genes in the most undifferentiated cells of the germ line. It is proposed how a probabilistic view of the random mutation can explain the evolution of the phenotypes and integrate all the evidence pointing to a joint evolution with the environment.

Keywords: evolution, gametogenesis, transcription, mutation, epigenome.

Introduction

In the last ten years a discussion has been developed on whether evolutionary theory needs to be rethought, and the cause has been evidence suggesting that phenotypic variability cannot be due solely to random mutation (*1*). For a phenotype to appear it is necessary for the cell to express only a specific portion of the DNA contained in its nucleus. The epigenome is responsible for regulating the expression of specific genes that the cell needs to differentiate in the presence of the factors that regulate transcription (2, 3). Here it is proposed that the expression of specific genes in a given phenotype due to the high demand of gene

resources for the behavior of an organism throughout its development, increases the probability that a random mutation will occur for these genes during gametogenesis, and that the evolution of phenotypes associated with the environment in which it develops is the result of the probability of a random mutation occurring during the transcription of high-demand genes plus the probability that at the same time that gene expression occurs, a random mutation will occur during replication considering for all the processes involved the probability that this mutation is not repaired, adding to this the probability that the mutation will have consequences on the phenotype, the probability that the resulting phenotype will provide an advantage for survival or reproduction, plus the likelihood that natural selection will act in favor of the phenotype (Fig. 1).

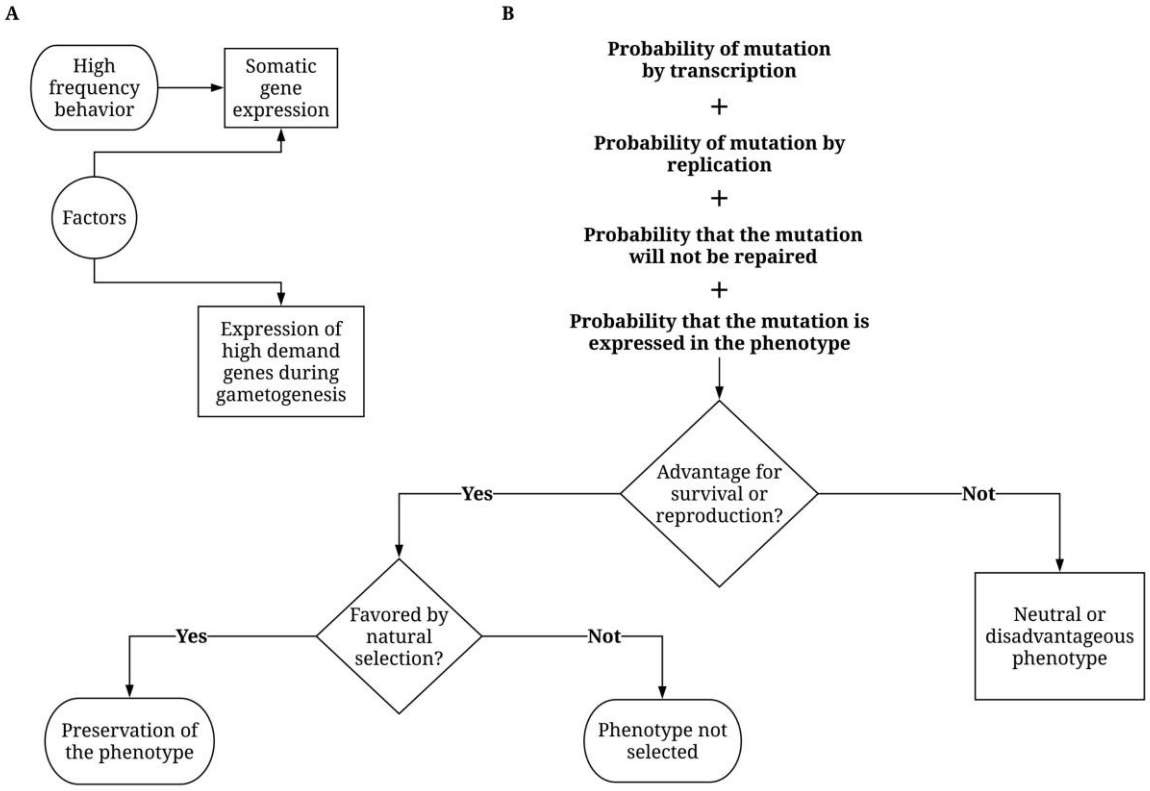

Figure 1. A) Hypothesis of joint gene expression. The factors that regulate expression in somatic cells also act on the most undifferentiated cells of the germ line during gametogenesis. B) Probabilistic view of the random mutation that increases the mutation rate for high demand genes. Natural selection is the mechanism responsible for the conservation of the phenotype.

Discussion

There is evidence that exposure to specific stimuli can regulate the gene expression of the somatic cells involved (*4*). This is notorious in birds of the Passeriformes order where song behavior is sexually dimorphic, implying that during embryogenesis, oogenesis and spermatogenesis, different genes involved in such behavior are expressed (*5*). A similar epigenetic mechanism biased by sex has recently been documented also in mammals (*6*). It has been proposed that the type of mechanism that regulates a behavior can influence the probability that phenotypic plasticity will evolve (*7*). Here it is suggested that the factors that regulate the gene expression of somatic cells involved in a high frequency behavior can induce the transcription of high demand genes in the most undifferentiated cells of the germ line.

It has been shown that in regions of DNA with high GC content, replication begins earlier than in regions with low GC content (*8*). A high-demand gene network results in a high transcription rate, so a high gene demand should be associated with regions of DNA with high GC content for rapid translation (*9*, *10*). In birds of the Passeriformes order, platelet phosphofructokinase is a tissue enzyme that should not be expressed during gametogenesis, and yet it does so in one or several steps of this process. It has been suggested that the phosphofructokinase gene in birds of this order has raised its GC content not only by mutation

pressure by replication but also by mutation pressure by transcription (*10*). The autonomous transcription of genes that should not be expressed during gametogenesis can be explained with the probabilistic hypothesis presented here considering all the variables that suggest a random mutation pressure by transcription and replication.

Factors that regulate gene expression in somatic cells can increase the mutation rate by transcription and replication depending on the frequency of the stimulus, but these cannot be inherited, and this has been the barrier that prevents accepting the fact that the environment does influence the evolution of phenotypes (*1*, *7*). Although not directly, high gene expression of somatic cells due to behavior, such as the construction of the niche (*11*, *12*), can influence what during gametogenesis, spermatogonia and oogonia. undifferentiated cells and what give rise to the gametes that do transmit the genetic information to the next generation, a mutation occurs due to joint probability due to the presence of the factors that regulate the transcription of the genes involved in the behavior, increasing in this way the mutation rate for such genes. It should be clarified that the function is independent of the structure, and it cannot be said that a structure evolved to perform a specific function because the mutation was a random event. So, the evolutionary theory does not really need to be rethought, since a probabilistic view of the random mutation can integrate all the evidence pointing to an evolution of the joint phenotype with the environment.

References

1. K. Laland, T. Uller, M. Feldman, K. Sterelny, G. B. Müller, A. Moczek, E. Jablonka, J. Odling-Smee, G. A. Wray, H. E. Hoekstra, D. J. Futuyma, R. E. Lenski, T. F. C. Mackay, D. Schluter, J. E. Strassmann, *Nature* **514**, 7521 (2014).

2. A. Jeltsch & M. G. Rots, *Epigenome Editing* (Humana Press, New York, 2018).

3. C. Carlberg & F. Molnár, *Human Epigenomics*, (Springer, Singapore, 2018).

4. P. H. Gunaratne, Y. C. Lin, A. L. Benham, J. Drnevich, C. Coarfa, J. B. Tennakoon, C. J. Creighton, J. H. Kim, A. Milosavljevic, M. Watson, S. Griffiths-Jones, D. F. Clayton, *BMC Genomics* **12**, 1 (2011).

5. G. Z. Luo, M. Hafner, Z. Shi, M. Marrón, G. H. Feng, T. Tuschl, X. J. Wang, X. Li, *BMC Genomics* **13** (2012).

6. M. Warnefors, K. Mössinger, J. Halbert, T. Studer, J. L. VandeBerg, I. Lindgren, A. Fallahshahroudi, P. Jensen, H. Kaessmann, *Genome Research* **27**, 12 (2017).

7. C. C. Rittschof & K. A. Hughes, *Nature Communications* **9**, (2018).

8. M. M. Martin, M. Ryan, R. Kim, A. L. Zakas, H. Fu, C. M. Lin, W. C. Reinhold, S. R. Davis, S. Bilke, H. Liu, J. H. Doroshow, M. A. Reimers, M. S. Valenzuela, Y. Pommier, P. S. Meltzer, M. I. Aladjem, *Genome Research* **21**, 11 (2011).

9. M. Costantini & G. Bernardi, *PNAS* **105**, 9 (2008).

10. V. V. Khrustalev, E. V. Barkovsky, T. A. Khrustaleva, S. V. Lelevich, *Gene* **546** (2014).

11. J. B. Saltz & S. V. Nuzhdin, *Trends in Ecology & Evolution* **29**, 1 (2014).

12. S. F. Gilbert, T. C. G Bosch, C. Ledón-Rettig, *Nature Reviews Genetics* **16** (2015).

Acknowledgements:

To Dr. Carlos González Salas for the valuable observations made to the final draft of this document.