

## Genetic Evolution and Adaptation of Population. A Review

Alireza Goodarzi\*

Professor Assistance, Department of biotechnology, Tehran Azad University

\*Corresponding Author: Alireza Goodarzi, Professor Assistance, Department of biotechnology, Tehran Azad University. Email: drgoudarzi80@gmail.com

### ABSTRACT

Genetic evolution has been a topic of interest since antiquity. The science behind it has been questioned and simultaneously answered time and again. The aim of the review is to delineate the importance of the purpose of genetic evolution. Content analysis method is used in this review. It will be prodigious discuss how genetic evolution aids organisms- coming from various backgrounds with numerous unique characteristics- to not become extinct easily. This research mainly focuses on the diverse evolutionary concepts that will expose the secret behind the continuance of species and their populations, despite the drastic changes that repeatedly take place in their surrounding environment. The study, therefore, found how the environment and natural selection cause adaptive evolution among species. Thus, it provides understanding of the survival mechanism of the species in their habitats.

**Keywords:** Adaptation, Evolution, Population, Genetic

### INTRODUCTION

Humans are tremendously interested in human evolution and this topic gets more attention than the evolution of any other species. This is so for several reasons. Beyond the obvious, that we are interested in our own evolution, human evolution is tied up with the interpretation and understanding of diseases with a genetic component and is influenced by human demographic and cultural history of which much is known. For other species than our own less is known about demography and culture. (Jotun Hein. et al 2005)

The evolutionary concept is very fascinating and conspicuous. It gives a broad idea of the apprehension of genetic evolution. Evolutionary concepts paint the picture of the magic behind the survival of living organisms, amidst the shift in time that challenges their survival conditions. To put it in simpler terms, genetic evolution is the study of where variation in genes take place because of evolutionary changes (Frantz et al., 2010). The question is, where do these changes take place that results in novel characteristics of the organisms? To give an easy answer, it can be said that it takes place in the genes of the organisms. This question is also answered by the concept of evolution

Ever since the revolutionary Darwinian evolution theory came out, numerous scientists have come to play the role in investigating the concept of

evolutionary genetics. Basically, the changes in frequencies of genotype, and also how the genes evolve, within populations are held responsible for evolution. The changes that take place can be behavioral or heritable physical, also temporary or permanent, giving selective advantages to the species (Zalta E. 2006). However, this is also important to note that not all changes act in favour of the species. Some changes may cause them to die, or reduce their chances of living.

The eventual source- that results in variations of genes within populations- is the mutation. Moreover, within a precise number of population, mutational variation arises because of random genetic drift and natural selection. Aside from that, natural selection also forms a crucial reason for adaptation of organisms, adjusting the organism and the environment, or preserving genetic information, for a coon's age, in the midst of mutation and drift. When natural selection is studied in-depth, it tells about the ecological genetics, which -in turn- talks about the "phenotypic patterns observed in nature" (Zalta E. 2006). The evolutionary changes can be described in terms of 'micro-evolution' and 'macroevolution'. In the long term, micro-evolutionary changes surge to a macro-evolutionary pattern, by which higher taxonomic groups are characterized (Zalta E. 2006). A seminal study (Zalta E. 2006) shows that these two types of evolution come into existence because of four important evolutionary forces

(mutation, natural selection, random genetic drift, and gene flow).

Morphological adaptation is often seen among populations of species. (Allen H .2005) states that a good amount of genetic changes are involved in morphological evolution. Among these, some particular variation has larger effect- either on the phenotype, or fitness- than the others. Furthermore, Allen study in 2005 (Allen H .2005) declares that when a population moves towards a phenotype that best fits the present environment, their adaptation can then be characterized. For example, Darwin's observations and conclusions, on the evolution of the finches of the Galapagos Islands, were a true eye-opener about the claim that natural selection leads to adaptation. Darwin previously recorded the various forms and adaptations of these finches and speculated on their relationship to mainland species. When his research was studied in the form of a phylogenetic tree, it was detected that the finches that arrived on the Galapagos island, multiplied over time, colonised other islands, and branched out into new species and forms, in order to adapt with their respective ecological niche (predominantly according to the types of food availability). And strong evidence regarding this matter was found when Rosemarie and Peter Grant were studying finches on the islands. They found out that when there was severe food depletion, only a few numbers of finches with specific beak types had a selective advantage over the others (Grant & Rosemary 2006). Thus, it is safe to say that genetic variation plays a crucial role in the survival of the fittest fight.

This study will embroil the wide range of evolutionary concepts- such as genomic structural evolution of a species, the genetic groundwork of speciation and adaptation, and selection leading to hereditary changes within populations- and implement the gravity of how they provide advantages to the living organisms.

### Evaluation and Extinction of Genome Structure

These studies have the advantage that they often use traits of direct interest such as brain volume, upright posture, and pathologies. Until recently, longer term human evolution (thousands to millions of years) has mainly been investigated by comparisons of dated fossils and archaeology. Such analysis has brought much understanding of the time of origin of anatomically modern humans, the major migrations and colonization of the earth, and knowledge about demography.

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Firstly, genomic configuration of species has been believed to evaluate according to their surroundings, as its main goal is to adjust and adapt. Such a phenomenon can be seen in hermaphroditism. Hermaphroditism is where one individual has both the male and female sex organs, such as snails, worms, fish and flowers. These type of organisms can self-fertilize. They do not need partners to reproduce. Ghiselin argues that, only under a few conditions, selffertilization occurs: a) when searching a mate is hard; b) where one gender has more advantage at being higher or lower quantity than the others; or c) when there are small populations that are genetically isolated (Ghiselin 1969) believed that pre-Darwinian workers took this circumstance for granted, as they believed that it cut out the need for a mate. However, Ghiselin (1969) made the case that even though selfing might be detrimental at some level, it is still better to self-fertilize than not to reproduce at all. Even though hermaphroditism makes an individual prone to selfing, it is not clearly explained in this study how this hermaphroditism condition takes place in the first place. The thesis has also not shone a light on the matter of explaining the illustration of how the state of hermaphroditism is shifted to the separation of sexes, or vice versa (Ghiselin, 1969).

In essence, (Ghiselin, 1969) tried to explain that an animal's reproductive system is organised in such a way that it aggrandizes the probability of passing the genetic material to the next generation to reproduce. The structure of the population, the differences in the density of population, the gene flow, and various other circumstances play a major role in shaping an animal as a hermaphrodite. To look on the bright side, in small, isolated populations, hermaphrodites can be saved from the deleterious consequences of drift and such related phenomena.

To explain even more clearly about genomic evolution, another example (Freek et al. 2013) of snake venom and its dynamic evolution and adaptation is elucidated. Snakes use venoms to catch preys. They are limbless predators, and their venoms are toxic proteins. The snake venom has been of great intrinsic biological interest for drug discovery, to understand the physiological pathways of vertebrates, and also to estimate how poisonous a snake bite can be to humans. A

fundamental and detailed study (Freek et al. 2013) on king cobra genome was demonstrated to examine venom evolution. Sequencing and comparing with other vertebrates were carried out. The results of this experiment provided an exclusive view of the origin and evolution of snake venom. Furthermore, it also unfolded “multiple genome-level adaptive responses to natural selection in this complex biological weapon system” (Freek et al. 2013).

### Genetic Basis and Adaptation

The adaptation often used to make population more tolerant to environmental stresses has only temporary effect. On the other hand the genetically determined changes have permanent feature. (Ventura et al 2009).

Obviously, due to the explosive growth in contemporary sequence data, the analyses discussed below are soon to be superseded by studies using more data, but the principles and models should remain relevant. (Van Bokhorst et al, 2013) It will be apparent that despite the often impressive amount of data, the statements that can be made about ancestral population behavior are weak (Nordborg, et al, 2002).

An interesting question is the limits of this knowledge as sequence and sample number grows. Data will explode both in length (until whole genomes are reached) and number (until everybody have been sampled). (Ruiz L et al 2013). This will improve reliability of obtained conclusions. Methodologically, the growth in sequence length will make it impossible to ignore recombination in analysis, and the growth in the number of sequences will make the sample size exceed the effective population size at some point. (McVean, G. et al. 2002)

So far, it has been explained how a population can alleviate their chances of extinction in their habitat, caused by natural selection, via transformation of their genomic structures. Now, a deeper context of the previously explained matter will be discussed here. The genetic basis of speciation will give a more in-depth idea on how these organisms acclimate and survive the changes around them.

One enthralling case is where zooplankton showed rapid, local adaptation behavior when the predator pressure around them changed, especially in the absence of neutral genetic changes.

In easier terms, zooplankton eggs have this characteristic of going through a ‘resting stage’,

where the diapausing eggs can be found in an inert state (Cousyn et al. 2001). This fact was considered revolutionary in the studies of species adaptation, as this state could last for centuries, providing a unique opportunity of rebuilding the genetic history of natural populations. A significant study (Cousyn et al. 2001) used fish as the predation pressure, and water-flea *Daphnia* as the subject. Fish were used as they are known to have an unyielding effect on the structure of the community of zooplankton and their evolution as a population. Cousyn et al. (2001) chiefly focused on studying the quantitative trait of the subject by using phototactic behavior (observing movement of the subject around the light) in presence of fish kairomone (a chemical released by fish to fight against the prey). In an experiment, when water-flea *Daphnia* was studied, (Cousyn et al. 2001) revealed that when there was a “variable and well documented levels of fish predation over the past 30 years”, the differentiation in genetic construction, through time, was superior for the studied behavioral trait than for the neutral genes. It implemented a strong proof that natural selection, indeed, was the propulsive force that drives the observed and rapid evolutionary changes in the zooplankton behavior.

### Other Reasons of Genetic Evolution

DNA sequences do not directly relate to morphological traits, but they are abundant in quantity, can be determined with accuracy and have the advantage that their evolution can be analyzed by well-defined models. The smaller importance of subjective interpretation and the use of exact modelling also facilitates comparison of results among different investigations (Song and Hein, 2004).

Although much progress has been made, there are still many contentious issues. It is unfortunate that it is so hard to obtain reliable ancestral genomic DNA on any scale, since this could settle many issues and allow a combined analysis of data from archaeology and evolutionary genetics. (Wiuf 2002) To get the absolute dates of events, information on the age of fossils corresponding to some internal node in the genealogy has to be used. (Rosenberg, et al, 2002).

Until recently, longer term human evolution (thousands to millions of years) has mainly been investigated by comparisons of dated fossils and archaeology. Such analysis has brought much understanding of the time of origin of anatomically modern humans, the major

migrations and colonization of the earth, and knowledge about demography (Jobling, et al, 2004).

Lastly, two more paradigms will be portrayed to further clear the concept of genetic evolution and how it leads to speciation and adaptation. Number one is how the construction of a niche causes genetic evolution. What is a niche construction, to begin with? According to Day, Laland and Odling-Smee (2003, p.80), it “refers to the capacity of organisms to construct, modify, and select important components of their local environments, such as nests, burrows, pupal cases, chemicals, and nutrients.” Naturally, a population builds its surroundings according to its own living preference. A study (Day, Laland and Odling-Smee 2003) made the case that many scientists considered it as an evolutionary process, as organisms not only affect the nature of their own world, but also determine the kind of selection pressure that they- and their descendants- are unsealed to. Day, Laland and Odling-Smee’s study in 2003 also established that natural selection and niche construction interact in a reciprocal manner, where the presence of the natural selection determines the arrangement and construction of the niche done by the organisms. This study also stated that adaptation is scrutinized as a mechanism by which natural selection progressively sculpts the living things, in its habitat, to be well-fitting to the environment. Moreover, in many situations, the offspring can be affected by the changes brought by the niche construction -done by the ancestors- as the successors not only inherit genes from their parents, but also from the altered niche construction- previously made by their genetic or ecological ancestors. It goes without saying that there are considerable amount of evidences proving that the change in ecological arrangement- by niche construction carried out by individuals of a population- for their own benefit, regularly modifies selection pressures, which in turn has some type of effects on the offspring, along with the other types of species in that similar habitat. This phenomenon is continuous, evidencing the diversification we witness in our environment.

Second example is where it is experimented if sex chromosomes have any impact on the susceptibility to influenza virus infection by the two different sexes. Dimitry et al (2017), declared that looking into sex and gender should be mediated when displaying the means contributing to sex differences in health and diseases. Previously it was hold that only because

of the male sex hormones, testosterone, males were more prone to being affected with influenza A virus than females. Nonetheless, nowadays, scientists are intrigued to research if the sex chromosomes also play a crucial part in this matter. A critical study (Dimitry et al. 2017) set forth that when there was genetic variation in chromosome Y, that certainly had a control and influence on the perceptivity of the male mice, which were under experiment, to the influenza A virus.

### CONCLUSION

Thus, it can be comprehended that more than one factor can administer the behavior of a species, be it either environmental or genetic. Living organisms are bound to change and evaluate, because nature itself is never stable. Even though mother nature has its own way of challenging the survival of living things, evolutionary wizardry always acts as the knight in shining armor, accommodating the individuals in their habitats, giving its utmost effort to defend them and proliferate their chances in this gamble of life and death.

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