

## Short Communication

# Fisher, Haldane and Wright would be proud owing to population genetics has become in a defiant study area in the genetics researches

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Population genetics is one of the most dynamic areas of investigation within biological sciences. Moreover, this discipline offers a challenge, which is not encountered in most others biological sciences because its main challenge is theoretical rather than experimental [1]. However, its theoretical development come up from analysis of empirical data although in some cases the empirical support arises after the theoretical development. Hence, it could be seen as a feedback between empirical data and theoretical development to understand and explain in the best possible way how natural populations evolve. Mathematical models are widely employed in population genetics; these models represent a simplification of a complex situation and inevitably they are unable to show all the relationships of the real situation [2]. Hence, the choice of few identifiable factors to describe the real and complex situation is a challenge. Population geneticist are interested in complex situations that involved several factors such as birth, death, population size, patterns of mating, geographical distribution of organism, among others [3]. In this way, the population geneticist tries to describe the effect of a large number of individual events by complete while physicist or chemist work with statistical average of molecular behavior of each individual molecule [2].

The beginning of this discipline can be dated in 1908 when Godfrey H. Hardy and Wilhelm Weinberg, independently, formulated their principle. With random mating, the Hardy-Weinberg principle states that the allele frequencies from parents determine the genotype frequencies in the progenies. In this way, this principle emphasizes the genetic continuity in time between generations and also, it expands the Mendelian familiar ratio to level of population Mendelian ratio. Thus, the mathematical model behind Hardy-Weinberg principle establishes the mathematical relation between the allele frequencies and the genotype frequencies is given by:  $AA:p^2$ ;  $Aa:2pq$  and  $aa:q^2$ , in which  $p^2$ ;  $2pq$  and  $q^2$  are the frequencies of the genotypes  $AA$ ,  $Aa$  and  $aa$  in zygotes of any generation while  $p$  and  $q$  are the allele frequencies of  $A$  and  $a$  in gametes of the previous generation [3].

However, the real discussion and development of population genetics as a discipline did not begin until 1918. For that time, Ronald A. Fisher, John B.S. Haldane and Sewall G. Wright made a brilliant synthesis from all the previous works and discussions between statistician and evolutionists. In appearance, this synthesis was unrealizable because it had to achieve a linkage between two antagonistic disciplines: Mathematics and Genetics. However, these men were capable



to develop mathematical models that extract the essence of the real and complex situation of population genetics in a formulation that could be handled mathematically [2]. In strict sense, an accurate definition of population genetics is hard to state because of the great and fast development of technologies: by one hand technologies for producing data and on the other hand technologies for analyzing data. In this way, we can state that modern population genetics has been enriched by three different revolutions: conceptual revolution, empirical revolution and computational revolution [3]. Perhaps, an accurate definition of this discipline is that population genetics studies the origin, quantity and distribution of genetic variability in populations and the fate of this variability through the time and the space [4]. Thus, it is evident the crucial role of population genetics in the evolutionary biology owing to it is involved in the study of the mechanisms by which evolution occurs.

Population genetics definition can be broken down taking in account the underlying causes of its aims. By one hand, the study of microevolutionary processes and on the other hand, the study of historical-demographic events. Also, there is other possible break down within the microevolutionary processes that has largely been discussed, it means the played role of natural selection or genetic drift in modeling the genetic variation of natural populations. All these discussions are still current and, without doubt, they have been useful for the enrichment of theoretical and empirical development of population genetics.

In the birth of population genetics as a discipline, the researchers were strongly influenced by natural selection and Darwinian thought. Fisher analyzed the influence of the natural selection in large populations. He understood the natural selection as a deterministic process that increase the frequency of advantage alleles by slow action. In a similar way, Haldane developed a mathematical model for analyzing the fate of alleles under natural selection, although he emphasized the speed of action of natural selection [5]. Wright, for his part, proposed a model for small populations where the inbreeding generates new genetic systems, i.e. means rearrangement of alleles, and afterward the natural selection acts on this new arrangement of alleles increased the frequency of the advantage alleles in the populations [5]. The assumption underlying all these models is that a great number of mutations would have an adaptive effect being the fate of these mutations determined by natural selection [6]. Based on this assumption and on empirical evidences from protein polymorphism data, Kimura proposed the neutral theory of molecular evolution. The empirical support shows that two or more polymorphic alleles are included in 15 to 50% of the genes coding for enzymatic proteins, it means that polymorphic alleles occurred with frequencies considering high to result from equilibrium between adverse selection and mutation [3]. Thus, the neutral theory of molecular evolution places at the genetic drift in the center of the discussion because of it establishes that this microevolutionary process determines the allele frequencies dynamics in a population as results of most observed molecular polymorphisms are selectively neutral [7].

The neutral theory meant a new challenge for population genetics because of it moved the core of the discipline happened a departure from the orthodox population genetics theory. In this way, the value of neutral theory is that it became in a null hypothesis and it brought fresh air to population genetics by including the molecular data into the analysis of empirical data and converting population genetics into a most realistic discipline. Also, the development of neutral theory stimulated the collecting of huge amount of molecular data from RNA, coding and noncoding DNA, aminoacid sequences, proteins expressed, entire genomes and make the most of computational development because this theory symbolizes, without doubt, one of the most complete and elegant mathematical theory developed in the core of biological sciences [3]. However, the population genetics definition includes the action of historical-demographic events on the genetic variability makeup in natural populations. The action of these events implies study the variability in natural populations looking back the past while the classical study of action of microevolutionary processes considers the variability in natural populations at the present to predict its future. The Wright-Fisher model of genetic drift derived the expected distribution of allele frequencies forward in time [3] while coalescent model consider that the allele frequencies are the results of genealogical and mutational history of all allelic states [8]. In this way, the coalescent model considers the present, while taking the past into account and fill the gap between forward and backward in time of the distribution of population's genetic variability. Also, the coalescent theory together with statistical phylogeography gave a new impetus to population genetics opening a door to new ideas, models and theories [9]. One more time, population geneticist revisited the Hardy-Weinberg principle for adapting its assumptions, left from classical model, i.e. Wright-Fisher model, and developed the mathematical theory for supporting their ideas. Hence, they got a new starting point for revitalizing their exciting field of research and for developing new questions and hypothesis to unravel the history, to know the dynamics, and to predict the future of the genetic variability in natural populations.

Nowadays, models and theories of population genetics provide the framework for studying a wide number of situations and topics, such as plan and implement of management strategies of wild and captive populations of threatened species [10], infer local adaptation by means the identification of potential adaptive loci [11], understand the demographic history and ancestral relationships of domestic and endangered species [12], take conservation and management decisions in urban landscapes [13], reconstruct of phylogeography and revelate the origin of migrant species [14], among other studies which include the most recently study regarding to COVID-19 pandemic by a genetic, epidemiological and evolutionary perspective [15]. Along this brief summary about the protruding landmarks in the development of population genetics, we can see that Fisher, Haldane and Wright sowed their ideas in a fertile field. Nowadays an uncountable number of researchers are still sowing new questions, harvesting answers, formulating hypothesis, generating challenges and testing models because of population genetics is an alive and dynamics discipline that



demands creative minds as a consequence of its defiant subject of study, i.e. past, present and future of the genetic variability in the populations.

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