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Usain Bolt. A «hopeful monster»? A descriptive case study
Usain Bolt. Um «monstro esperançoso»? Um estudo de caso descritivo
Usain Bolt. Un «monstruo esperanzado»? Un estudio de caso descriptivo

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Abstract. Usain Bolt's stunning sportive achievements sparked admiration from around the world and raised the question of the genesis of his sport excellence. In the light of the various theories of evolution, we try to understand whether there are evolutionary grounds for considering Usain Bolt a «hopeful monster», i.e. a transgressive phenotype beyond the range of parental phenotypes. This hypothesis would call into question the gradualism defended by Darwin and would give room to saltationism by which profound changes can occur in one or a few generations. It seems that the saltational hypothesis is not scientifically adequate to justify Usain Bolt's sport performance. Not knowing the genetic profile of Usain Bolt and his ancestors, we can hypothesize that his sporting excellence is the result of a given polymorphism or phenotypic changes induced by ecological determinants, among which training and nutrition stand out. We can admit that Usain Bolt is a rare case of developmental plasticity that enables his genome to generate a phenotype associated with a specific competence for sprinting. In the current state of scientific knowledge, there is no way to associate any polymorphism with performance in sporting events related to strength and speed but a challenging field is open for science. Aware of the difficulties in characterizing Usain Bolt, he is undoubtedly the result of an extraordinary combination of genetic and environmental factors.
Keywords: evolutionary biology; athletic performance; genetics; epigenetics.

Resumo. As impressionantes conquistas desportivas de Usain Bolt despertaram admiração em todo o mundo e levantaram a questão da génese de sua excelência desportiva. À luz das várias teorias da evolução, tentamos entender se há bases evolutivas para considerar Usain Bolt um «monstro esperançoso», ou seja, um fenótipo transgressivo além da faixa de fenótipos parentais. Essa hipótese colocaria em questão o gradualismo defendido por Darwin e daria espaço ao saltacionismo, pelo qual mudanças profundas podem ocorrer em uma ou algumas gerações. Parece que a hipótese saltacional não é cientificamente adequada para justificar o desempenho desportivo de Usain Bolt. Desconhecendo o perfil genético de Usain Bolt e de seus ancestrais, podemos hipotetizar que a sua excelência desportiva seja o resultado de um determinado polimorfismo ou alterações fenotípicas induzidas por determinantes ecológicos, entre os quais se destacam o treino e a nutrição. Podemos admitir que Usain Bolt é um caso raro de plasticidade de desenvolvimento que permite ao seu genoma gerar um fenótipo associado a uma competência específica para o sprint. No estado atual do conhecimento científico, não há como associar qualquer polimorfismo ao desempenho em eventos esportivos relacionados à força e velocidade, mas um campo desafiador está aberto para a ciência. Ciente das dificuldades em caracterizar Usain Bolt, ele é, sem dúvida, o resultado de uma extraordinária combinação de fatores genéticos e ambientais.
Palavras-chave: biologia evolucionária; rendimento atlético; genética; epigenética.

Resumen. Los impresionantes logros deportivos de Usain Bolt despertaron la admiración de todo el mundo y plantearon la cuestión de la génesis de su excelencia deportiva. A la luz de las diversas teorías de la evolución, tratamos de comprender si existen bases evolutivas para considerar a Usain Bolt como un «monstruo esperanzado», es decir, un fenotipo transgresor más allá del rango de fenotipos parentales. Esta hipótesis pondría en tela de juicio el gradualismo defendido por Darwin y daría lugar al saltacionismo mediante el cual pueden ocurrir cambios profundos en una o pocas generaciones. Parece que la hipótesis saltacional no es científicamente adecuada para justificar el rendimiento deportivo de Usain Bolt. Sin conocer el perfil genético de Usain Bolt y sus ancestros, podemos plantear la hipótesis de que su excelencia deportiva es el resultado de un determinado polimorfismo o cambios fenotípicos inducidos por determinantes ecológicos, entre los que destacan el entrenamiento y la nutrición. Podemos admitir que Usain Bolt es un caso raro de plasticidad del desarrollo que permite que su genoma genere un fenotipo asociado con una competencia específica para correr. En el estado actual del conocimiento científico, no hay forma de asociar ningún polimorfismo con el rendimiento en eventos deportivos relacionados con la fuerza y la velocidad, pero hay un campo desafiante para la ciencia. Consciente de las dificultades para caracterizar a Usain Bolt, es sin duda el resultado de una extraordinaria combinación de factores genéticos y ambientales.
Palabras clave: biología evolutiva; rendimiento atlético; genética; epigenética.

Introduction

Sport, the most pregnant social phenomenon in modern societies, is a territory of excellence, wonderment, and outstanding achievements. The value of socialization through sport has long been recognized and almost all governments worldwide support its spread through physical education in the schools and competitive sport in clubs and federations. Beyond physical expression, sport is an incomparable field of emotions. Emotion is a central feature of all sporting events. Athletic practice per se detonates a medley of emotions, both in the public and in the athletes. The emotions promoted by sport at the highest level are often contradictory - joy, sadness, anger, fear, anxiety, shame,

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guilt, and pride but give the real dimension of man in the face of victory or defeat. The best athletes are successful not only for their physical abilities but also by the way they control emotions, a crucial feature to succeed in the highest-level sport.

When an athlete succeeds in sport, clean of drugs and illicit practices can become a hero and gain the aura of a myth.

Among all-time champions, from the Ancient Olympics to Modernity, stand out for us Usain Bolt. Today, after his retirement he continues being the world record holder in the 100-m, 200-m, and 4 x 100-m relay. He was nine-time Olympic gold medallist in the running races above mentioned. His athletic excellence lasted three consecutive Olympic Games – 2008, 2012, and 2016. To excel in sprint events like Usain Bolt did make us wonder if his physical excellence is something normal derived from training and a special genetic aptitude or if it can be considered a rare case in the normal evolution of the human species.

With this work, we will try to justify Usain's sport excellence speculating in the light of evolutionary biology mainly of microevolution.

The beginning of life

Evolution is the process by which the different living organisms that exist today developed from the last universal common ancestor (LUCA). LUCA is a theoretical construct but helps to shed light on the early stages of life although self-sustaining systems exist before LUCA. Respecting two simple criteria related to the proteins encoded by prokaryotic genomes: (1) the protein should be present in at least two higher taxa of bacteria and archaea, and (2) its tree should recover bacterial and archaeal monophyly, Weiss et al. (2016) identified 355 genes that trace to LUCA by phylogenetic criteria. The three-domain tree of life presents LUCA as the last common ancestor of archaea, bacteria and eukaryotes (Weiss et al., 2018), although LUCA should be considered as an evolutionary intermediate that «links the abiotic phase of Earth's history with the first traces of microbial life in rocks that are 3.8-1.5 billion years of age» (Weiss et al., 2016).

LUCA emerges at the evolutionary separation of the Archaea from the Eubacteria, and before the symbiotic conjugation that resulted in Eukarya (Cornish-Bowden and Cárdenas, 2017). The tree of life conception is called into question when taking into account the genes derived from mitochondria and plastids. More than a tree we should speak of a network that interlace the different domains. Eukaryotes genomes are true chimeras because they display archaeal ribosomes in the cytosol and bacterial ribosomes in mitochondria (Martin et al., 2017).

Since LUCA emergence some billions of years ago, the evolutionary repertoire of cells increased and diversified responding to the conditions imposed by the environment and their intrinsic development. It is not an easy task to draw a complete and satisfactory framework to explain the complexity and diversity of life from its origin. However, and following Margulis (2009) symbiosis is a remarkable step in evolution and it was responsible for the innovative complexity that characterize eukaryotes. From LUCA to the last eukaryotic common ancestor (LECA) a set of evolutionary steps took place in an order difficult to establish but among which mitochondrial acquisition stands out. Mitochondrial acquisition throughout endosymbiosis is a crucial step in eukaryogenesis. Comparative genomics shows that all eukaryotes possess genetic traces from bacteria and archaea. How these traces were introgressed in eukaryotes is still a matter of debate. The full picture for eukaryote development must include several processes as lateral gene transfer (LGT) among prokaryotes, endosymbiosis and gene transfer from organelles to the nucleus (Martin et al., 2015).

From LUCA to Homo sapiens through LECA and other evolutionary intermediaries life expanded without resolving the crucial conundrums - Who we are? Where we come from? Where we are going?

Attempts to explain evolution

Different and alternative theories tried to elucidate the evolutionary process. The triumvirate Mendel-Lamarck-Darwin is of fundamental importance for the analysis of evolution.

George Mendel, coined by some as the «father of modern genetics» discovered the basic principles of heredity through experiences with plant hybrids. Crossing different qualities of peas Mendel established two important laws: the Law of Segregation, which states the emergence of dominant and recessive traits that are randomly transmitted from parents to offspring, and the Law of Independent Assortment that states that those traits are inherited independently of other traits (Mneimneh, 2012). Mendel showed that the diversity of life results from genetic recombination. Some authors

who elect Darwin as the «father of modern genetics» (Liu and Li, 2016) question the paternity of genetics attributed to Mendel. Regardless of this dispute, Mendel and Darwin are both historically important for genetics and evolution.

In 1859, Charles Darwin published his famous book about the origin of species, in which he stated that evolution proceeds from a countless number of very small steps whose main driver is natural selection (Darwin, 1859). This concept was termed «gradualism». Darwinism as a theory of evolution was immediately criticized after its publication. Darwin's evolutionary concepts were questioned concerning the adaptive character of evolution, the gradualness of evolutionary changes, and the random character or variation.

Regardless of all the criticism, two specific tenets of Darwin remain strong on evolution comprehension (Kuhn, 2012):

- Species adapt to changes in the environment (microevolution).

- There is a similarity in the DNA across species (homology).

The other edge of the historical evolutionary triangle was Jean-Baptiste Lamarck who introduces the concept of the inheritance of acquired characters. Before Darwin and Mendel, Lamarck established the first evolutionary laws. The first law highlights the evolutionary role of use and the involutive role of disuse. The second law states that all gains or losses achieved by the influence of circumstances are conserved through generations (Burkhardt, 2013). The evolutionary theory soon developed by Lamarck viewed nature as an unstable set of living beings undergoing the modifying action of the environment that gives rise to multiple morphological changes (Galera, 2017). Species mutability arises from both external agents and reproductive features. Inheritance of acquired characters defended by all neo-Lamarckians contradicts Darwin's claim that variation is random, i.e., non-adaptive. Many Lamarckians accepted the conjugation between the inheritance of acquired features with natural selection. Lamarckism is a conceptual umbrella for even antiscientific evolutionary sights. Lysenko, a soviet Lamarckian, denied the existence of genes and believed that new environments can induce novel characteristics. For instance, Lysenko believed he was able to turn one cereal into another by manipulating growing conditions. These misconceptions underlined many failings in the agricultural programming of the former Soviet Union developed under the aegis of Stalinism.

Other alternative evolutionary theories arise during the 20th century (Levite et al., 2008): Orthogenesis, Mutationism/Saltationism, Scientific Creationism, Old-Darwinism, Idealistic Morphology, Biosphere-Theories, and Modern Synthesis.

Orthogenesis. Defenders of this theory argued that evolution proceeds along with a limited number of definitive trajectories. See the quote of Ernst Mayr a remarkable evolutionist: «until natural selection was fully understood, many evolutionists, from Lamarck to H. F. Osborn to Teilhard de Chardin, postulated the existence of non-physical (perhaps even non-material) forces which drove the living world upward towards ever-greater perfection» (Mayr, 1982). This is the non-scientific tenet of orthogenesis. Orthogenesis assumes the idea of biological progress – a directed evolution towards an increasing perfection of organisms.

Mutationism. Contrary to Darwin's theory, mutationists defend that new species arise through large-effect mutations caused by sudden genome alterations (Stoltzfus and Cable, 2014). Mutationism is a special form of saltationism that advocates that evolution arises through sudden changes and does not proceed through long-term gradual selection. Mutationists assumed that gradual variation could not lead to the origin of new species.

Saltationism. One of the authors who firstly purposed evolution because of discontinuous changes was William Bateson. He also is credited with coining the terms «genetics», «allelomorphs» (later shortened to allele), «zygote», «heterozygote», and «homozygote» (DNA from the beginning; http://www.dnaftb.org/5/bio-2.html). Saltationism, while not completely denying gradual variation, proposed that evolution could arise from instantaneous macro mutations or systematic mutations. New body plans can surge from sudden, discontinuous macromutations. For Goldsmith (1933), individuals bearing such macromutations were coined as «hopeful monsters». In a general way, hopeful monsters are transgressive phenotypes produce by genetic recombination in hybrids through epistatic interactions or additive effects of multiple recombined loci (Dittrich-Reed & Fitzpatrick, 2013).

Idealistic morphology. Typology is roughly synonymous with classification in which the phenomenon of a domain under study is classified into types according to certain common features (Croft, 2003). Idealistic morphology tried combining typology with all methodological and conceptual elements carried by the different evolutionary theories.

The Biosphere Theory. The total sum of living organisms with their environment is considered as a dynamic, self-regulating system, evolving according to their specific rules. After Vernadsky (cited by Levine et al., 2005), the biosphere must be seen as the sum of living and cycling processes of chemical elements exchange between living organisms and their environment. This assumption introduces the geological domain in which life happens and gives rise to the appearance of a new concept – biogeochemistry. Then, evolution must be seen as a global phenomenon which implies all living and non-living systems of the planet.

«Scientific» creationism. This concept is ab initio an oxymoron. Creationism sees all reality as the result of a divine design. «Scientific creationism» try to include the concept of creation into the evolutionary field. The non-scientific support of this pretended theory that accepts some Darwinian assumptions for microevolution but denies the same assumptions for macroevolution makes it impossible to accept as a valid theory. Creationism has nothing to do with evolution and it is a worthless theory (Scott, 2006).

Modern Evolutionary Synthesis (MS) – sometimes referred to as the Neo-Darwinian theory, try reconciling Mendelian genetics with Darwinian principles and other disciplines as systematics, paleontology, population biology, and botany claiming to establish a unified theory of evolution. The five scientists quoted as the architects of the Evolutionary Synthesis were Dobzhansky, Mayr, Stebbins, Huxley, and Simpson (Kulathinal, 2010). One criticism some authors made to MS is that it overlooks development theories. MS explains adaptation through natural selection, however, leaves in the shade the problem of evolutionary novelty and did not introduce ecology in their explanations (Pigliucci, 2008).

Evolution is mainly a gradual process through which species adapt to changes in the environment. However, under certain conditions, e.g., hybridization, new body plans can surge from sudden, discontinuous macromutations (Goldsmith, 1933).

In relation to humans, gradualism is the main driver for evolution. Evolutionary novelty, considered as the appearance of new traits or new conjugation of pre-existing traits that emerge from the evolution of a lineage and corresponds to novel ecological functions (Pigliucci, 2008) is difficult to ascertain in the short term in human evolution.

Today even the hardest defenders of Darwinism recognize that natural selection is not the unique driver of evolutionary change. However, the main scientific research on evolutionary biology reflects gradualism as the most frequent mode of evolution (Gardner, 2009). Other pathways for evolution than natural selection are today recognized particularly at the level of DNA sequence evolution. However, natural selection remains as the major driver for phenotypic variation (Gardner, 2009).

Attempt to characterize Usain Bolt's sport excellence

The human genome is a stabilized structure that regulates growth, development and health. Changes in the normal program of gene expression are the basis for several human diseases. Can we speculate that positive changes in genetic programming can also occur and, instead of the disease, a «super plus» of health can arise, as is the case of extraordinary physical performance? If we consider evolutionary novelties not as absolute discontinuities (genetic driven) but rearrangements of previous existing characters (epigenetic modulation), that affect the evolution of certain lineages (elite athletes kingdom) and respond to a novel ecological function (to cope the high stress imposed by training loads) some clarity can be added to justify sport excellence. If the rationality of this speculation is not an unforgivable mistake it permits consider some elite athletes as evolutionary novelties.

Then, how can we interpret the incredible sport performance shown by Usain Bolt? In this paper, we will try to highlight this question.

Athletic performance is a complex construct influenced by both nature (genetics) and nurture (environment). The relative importance of genetics and environment on athletic performance is difficult to discriminate. Between genetics and environment, genotype and phenotype, a question might be raised: Is high-level sport performance consistent with the fundamental genetic principles of gradual population change or a new insight is needed to explain the sporadic and unusual surge of extremely well developed champions? Would saltational evolution be an answer to this question?

In nature, it often happens the emergence of new forms out of the slow and progressive steps proposed by Darwinism. The sudden appearance of evolutionary novelty through hybrid recombination often occur in nature. The rapid development of new forms through hybridization disclosed by some authors is a concept with many points of contact with saltationism.

However, the principles of gradual population change

can be accompanied by abrupt jumps on evolution. This is the «saltational» hypothesis defended by some authors (Levit et al., 2008; Theißen, 2009). Saltational changes can occur quickly in one or few generations giving place to the so-called «hopeful monsters». It seems that both gradual and saltational theories are required to explain the complexity and diversity of life on earth. These «hopeful monsters», seen as an evolutionary novelty, can arise from hybrid genetic recombination through epistatic interactions or additive effects of multiple recombined loci consistent with the principles of modern population genetics (Dittrich-Reed and Fitzpatrick, 2013) or can arise also from sudden, non-adaptive, random saltations occurring without transitional forms in single steps (Levit et al., 2008).

In terms of genetic evolution, can we say that each junction of an ovum with a spermatozoon in humans is a special case of hybridization? The answer seems to be negative because species are groups of actually or potentially interbreeding natural populations that are reproductively isolated from other such groups (Mayr et al., 1953). It is not reasonable and scientifically appropriate to speak of hybridization for human chromosome conjugation. Then, Usain Bolt, descending obviously from two beings of the same species cannot be justified as an evolutionary novelty from hybrid recombination.

One mechanism for evolutionary novelty is transgressive segregation. Transgressive segregation refers to the fraction of a population that exceeds parental phenotypic traits in either a negative or a positive direction. These extreme phenotypes are more frequent in intraspecific crosses involving inbred, domesticated plant populations than in interspecific crosses between outbred, «wild animals» species (Rieseberg et al., 1999). Can we speak in transgressive segregation within the same species? Can Usain Bolt be a transgressive segregation from his parents knowing that the current evolutionary point of a given group or individual is the result of successive transformations induced in previous generations? Theoretically and philosophically, this hypothesis is very challenging but its scientific support seems not to be possible.

The journey from Africa: enhancing factor or reducing factor

Apart from moral considerations that the trafficking of slaves involved, we should try to understand the possible results of this nefarious practice on the sport value of the current descendants of the African diaspora. The migratory movement from West Africa was directed mainly towards South America and the Caribbean and minority towards the United States.

The journey between Africa and the Americas could last until three months and it was carried out in the most degrading conditions. The terrible conditions of captivity and transport resulted in the death of about two million men, women, and children. About half of the Africans brought to America were from Angola and Senegambia. The ancestry of African Americans is predominantly from Niger-Kordofanian (~71%), European (~13%), and other African populations (~8%) (Tishkoff et al., 2009). African American populations, which are less admixed with non-Africans, cluster more closely with West Africans (Tishkoff et al., 2009).

Through genotyping data from 2841 SNPs (single nucleotide polymorphisms) Sikora et al. (2011) showed that populations of the West Africa (Yorubas and Mandenka), Niger-Congo speaking population, present a remarkable genetic similarity clearly distinctive from the Eastern populations like Bantu, Pygmy and Khoisan populations.

Genome-wide research showed higher levels of genetic diversity in Africans compared to non-Africans. A survey of 1327 nuclear microsatellite, insertion/deletion, and single nucleotide polymorphism markers indicated that African as well as African-American populations displayed greater genetic diversity than non-Africans (Tishkoff et al., 1996). It seems that there is greater genetic diversity in a Maasai village than in the entire non-African population (Wagh et al., 2012).

The selection of a previous healthy slave population for emigration induced a first bottleneck effect. The high mortality rate during travel induced a second bottleneck effect.

Bottleneck effect arises from the drastic reduction of the population size in a given ecological niche due to some natural or artificial cause. Population size reduction could lead to reduction in genetic diversity and correlative effects on fitness (considered here as reproductive success and not physical conditioning capability). In the Africa-America migratory movement, the bottleneck effect is mainly epigenetic because the number of individuals that arrived in the Americas was sufficient to maintain the original genetic diversity. However, a given founding effect, also epigenetic, modeled by the harsh working conditions, can be at the base of the physical potentiation that many African-America athletes demonstrate.

The genetic founding effect is evident in the transmission of certain diseases (Ankala et al., 2014). It is reasonable to accept the hypothesis of an epigenetic founding effect in relation to the physical excellence demonstrated by many athletes from the African diaspora.

Genetic background for physical performance

Failing the chance to see Usain Bolt as a hopeful monster, we will try to shed light on other paths that can elucidate his sportive excellence. We will try to understand Usain Bolt's physical excellence in the light of genetics and epigenetics.

Identifying candidate gene variants associated with sports performance is no easy task. Some genetic traits are products of epistatic interactions or additive effects of multiple recombined loci what makes it difficult to define «who is who» on the genetic determination. Sports performance relies on highly polygenic phenotypes having multifactorial determinants, both genetic and environmental, which contribute to differences among athletes.

Genes, made up of DNA, located in the cell nucleus, are the basic units of heredity. Every individual has two copies of each gene; one inherited from his father the other from his mother.

The human genome is much more complex than the sum of individual genes. Some non-coding regions are extremely important in gene regulation (enhancers, repressors, microRNAs, etc.). Beyond the more than 1.500 transcription factors that have been uncovered bind to 8% of the human genome, it harbours more than 70.000 promoter regions and more than 400.000 enhancer sequences that interact with other regions and factors to regulate the expression of the 20.687 genes currently recognized in the human genome (Pérusse et al., 2013). From studies with twins, it was suggested that genetic influence on physical performance could range from 30 to 80 percent. It is open for speculation the genetic percentage for Usain Bolt athletic success and if his physical quality is the outcome of a special genetic mixture of his parents, his grandparents, or his distant ancestors. Both, environmental and genetic factors play an important role in determining athletic performance. To elucidate this assertion concerning Usain Bolt, it would be necessary to trace Usain's genetic background through previous generations. It would be a difficult, almost impossible task, to trace Usain Bolt's genetic background, the parents' contribution to his physical excellence, knowing the genetic complexity of human inbreeding and the polygenic nature of each trait. For instance, a recent study found over 400 genes linked to variation in human height (Wood et al., 2014).

The capability of human skeletal muscle to produce force and velocity, which are the most important characteristics in elite sprinters, is strongly determined by genetics and without an appropriate genetic make-up, a sprinter cannot succeed. As the main quantitative traits relevant to power/sprint performance are diverse – flexibility, muscle strength, muscle fiber distribution, anaerobic enzymatic profile, mechanically advantageous levers, etc., the genetic «orchestration» to control so many features is so far impossible to clarify. It is not a topic for speculation that Usain's athletic performance has strong genetic support but it is impossible to discriminate the percentage of genetics and environment in his physical excellence.

A complete picture of human genetic variation is difficult to achieve with the actual limitations.

If Usain's sport excellence is the result of a specific single nucleotide polymorphism (SNP) it will be certainly linked to skeletal muscle features. Human skeletal muscle contains three myosin heavy chain isoforms (I, IIa, IIx) that form three pure myosin heavy chain (MHC) fiber types (I, IIa, IIx) and three hybrid fiber types (I/IIa, IIa/IIx, I/IIa/IIx) (Pette and Staron, 2000). Type IIx fibers are characterized by brief, high-amplitude calcium transients and lower ambient calcium levels (less than 50 nM) while slow-twitch type I fibers show high levels of intracellular calcium concentrations (100-300 nm). Muscle innervation of low frequency (10-20 Hz) promotes slow fiber phenotype while neuron firing at high frequencies (100-150 Hz) characterize fast fiber phenotype (Bassel-Duby and Olson, 2006).

While elite sprinters are characterized by a high percentage of type II fibers, elite long distance runners are characterized by a high percentage of type I fibers. A former world champion and still the world record holder in the 60-m hurdles and former world record holder in 110-m hurdles had a high percentage of pure MHC IIx (24%) and a total fast-twitch fiber percentage of 71% (Trappe et al., 2015). Contrary, elite distance runners display an elevated percentage (70%) of slow-twitch muscle fibers (Saltin et al., 1995). However, the data is not so clear because high-level endurance performance in running events is also associated with high percentages of isoforms corresponding to Myosin Heavy Chain IIa (Kohn et al., 2011). It seems that the

MHC IIa isoform is the interface for high performance in both sprint and endurance efforts.

MHC IIx fibers, the hallmark for sprinting, are highly responsive to intense exercise at the transcriptional level of the *Fn14* and *myostatin* genes with known action in muscle growth and remodelling (Trappe et al., 2015). After sprint, several skeletal muscle genes – *FOS, NR4A3, MAFF, EGR1, JUNB* were markedly upregulated (Rundqvist et al., 2019). This statement does not clarify the differences between athletes of different competitive levels.

Almost all genes are the same in all people. However, some genetic loci – alleles – can be different and encode different characteristics. This variation usually affects less than 1% of genes. These slight variations contribute to the physical features of each person. If the variation in a specific locus in the DNA sequence occurs in at least one in 100 people, we are in the presence of polymorphism. The most common type of polymorphism involves variation in a single base pair. Called a single nucleotide polymorphism (SNP), it determines specific phenotypes. A key challenge is to identify, among the multiple alleles, those variants that affect molecular function, phenotypes, and reproductive fitness to recognize their deleterious, neutral or benign action for protein structure and function (Kiezun et al., 2013).

Several genes with multiple physiological roles have been associated with sprint performance. The most studied polymorphisms associated with muscle strength and power athlete status are located in alfa-actinin-3 (*ACTN3*) and angiotensin-converting enzyme (*ACE*) genes.

Alfa-actinin-3 (*ACTN3*)

The *ACTN3* gene encodes the á-actinin-3 protein, which stabilizes the contractile apparatus predominantly at the Z-line in skeletal muscle fast fibers. Alfa-actinin-3 is one of the actin-binding proteins predominantly present on fast, glycolytic muscle fibers (Yang et al., 2003). A common polymorphism in this gene is R577X (rs1815739), where a C-to-T base substitution results in the transformation of an arginine base (R) to a premature stop codon (X) (Pickering and Kiely, 2017). Deficiency in the production of alpha-actinin-3 protein characterize X allele homozygotes and is linked to a lower fast-twitch fiber percentage (Vincent et al., 2007). While some authors found a weak association between the XX allele and endurance performance (Yang et al., 2003) other fail to find that association (Kikuchi et al., 2006). Muñoz et al. (2021), in table tennis players verified the predominance of the XX polymorphism. These authors have strangely related this predominance to favourable conditions for muscle strength and power. Other studies contradict this statement.

The R allele is associated with a high proportion of fast-twitch fibers that characterize strength, power, and sprint athletes (Del Coso et al., 2019). Some studies point to the association between the 577XX genotype and increased metabolic efficiency with a positive effect on endurance performance (Amorim et al., 2015).

A common null polymorphism in the ACTN3 gene, R577X (replacement of arginine (R) with a premature stop codon (X) at amino acid 577), in the fast muscle protein á-actinin-3 is common in approximately 1,5 billion people worldwide. This genetic trait (complete deficiency on á-actinin-3 that leads to the production of an abnormally short á-actinin-3 protein that is quickly broken down) relates to several functional traits as aging, bone health, and inherited muscle disorders (Houweling et al., 2018).

Some individuals present this anomaly in both copies of the gene that leads to a complete absence of á-actinin-3. This genetic trait appears to reduce the proportion of fast-twitch muscle fibers whereas increases the proportion of slow-twitch fibers. Some studies related this genetic variant with higher performances in endurance events. However, the results are conflictual because other studies do not support this relationship.

Yang et al. (2003) demonstrated that the frequency of the ACTN3XX genotype was reduced in Australian power athletes and was absent in female power athletes. Others drive the same conclusion replicating this study, but it is important to state that other studies showed no association between the ACTN3 R577X polymorphism and power athlete status (Maciejewska-Skrendo et al., 2019).

In humans, á-actinin-3 deficiency can decrease sprint and power performance as well as muscle mass and strength. Neither reduced muscle mass nor reduced strength are favourable features for sprinters and even too for endurance performance mainly for high-level endurance athletes.

In a cohort of male Caucasian sprinters, Papadimitriou et al. (2016) showed that the sprinters with the *ACTN3* 577RR genotype had faster best 200-m sprint time that their 577XX counterparts. Through genetic modelling (DNA isolated from buccal

epithelium or white blood cells), they found that the ACTN 577R allele justified 0.95% of sprint time variance. The expression of this variance should make us approach the results of this study very carefully.

The systematic review and meta-analysis made by Ma et al. (2013) showed an association of the ACTN3 R genotype and power events. Also, the review made by Eynon et al. (2013) points to the strong association between the ACTN3 R577X polymorphism and sprint performance. Besides strength improvement, the R allele of the common polymorphism R577X is associated with reduced muscle damage induced by eccentric contractions and sports injury (Pickering and Kiely, 2017). Contrary to these statements, Grenda et al. (2014) did not found any association with swimming sprint performance and the ACTN3 R577X polymorphisms. Scott et al. (2010) studied the association between the ACTN3 distribution and sprint athlete status in elite Jamaican and US African American sprinters. Athletes were compared to controls from the same population. They verified that athletes did not differ from controls and both showed the same low frequency for the ACTN3 XX genotype. The conflictual nature of the various studies should raise some doubts about the association of this polymorphism with performance in sport.

Angiotensin-Converting Enzyme (*ACE*)

ACE is the gene that converts angiotensin I into II a key element in the renin-angiotensin system with a direct influence in blood pressure regulation. The *ACE* insertion/deletion (I/D) polymorphism is characterized by the presence or absence of a 287-bp *Alu* repeat (Rigat et al., 1992). The insertion (I) variant of the human *ACE* gene is associated with lower ACE levels that the deletion (D) variant (Myerson et al., 1999). The *ACE* D allele seems to display higher angiotensin II levels and a higher proportion of type IIx fast muscle fibers (Zhang et al., 2003).

The D allele is associated with sprint performance while the I allele is associated with endurance performance (Myerson et al., 1999). Papadimitriou et al. (2016) verified that the sprinters with the *ACE* DD genotype had faster best 200-m sprint time than their ACE II counterparts. Soccer players showed also a trend towards the prevalence of *ACE* DD genotype (Galeandro et al., 2017). The mixed (aerobic-anaerobic) characteristic of soccer effort makes it difficult to validate the importance of the *ACE* DD polymorphism. Scientific research carries contradictory results. So, in ultra-marathoners supposedly benefited by the *ACE* I allele, the best results are associated with the D polymorphism of the *ACE* gene (Chiu et al., 2019). The systematic review and meta-analysis made by Ma et al. (2013) showed an association between *ACE* II genotype and endurance events. However, Padimitriou et al. (2018), showed no association between *ACE* I/D polymorphisms and endurance performance in a large cohort of Caucasian athletes. In addition, Grenda et al. (2014) did not found any association with swimming sprint performance and both ACE polymorphisms. Reinforcing this data, in elite US African-American and Jamaican sprinters Scott et al. (2010) showed they did not differ from controls in genotype ACE I/D. It seems that the ACE genotype is not a determinant for elite sprint performance. The conflictual results showed among the different studies must make us be careful towards definitive conclusions.

Peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1α)

PGC-1α is the main regulator of mitochondrial biogenesis and fat metabolism (Jacques et al., 2019). At first glance, this has nothing to do with the fundamental capabilities of a sprinter. Mitochondria and fat metabolism are issues related to marathon runners, not sprinters. See what the literature tells. After acute exercise, Barrès et al. (2012) showed a marked hypomethylation of PGC-1α, PDK4 (pyruvate dehydrogenase kinase, isoenzyme 4) and PPAR-ä (peroxisome proliferator-activated receptor delta). All these genes control mitochondrial function. Mitochondrial function is not crucial for sprinting. The meta-analysis carried out by Tharabenjasin et al. (2019) to estimate the association between *PPARGC1α* Gly482Ser polymorphism and athletic performance showed that while the Ser allele has no positive effect on the athletic ability the Gly allele was associated with endurance and power, differently favouring power performance. Complementary studies showed that functional Gly482Ser polymorphisms in the PGA-1α are associated with both endurance and sprint capabilities (Eynon et al., 2010). In transgenic mice overexpression of PPARGC1α upregulates the expression of various genes encoding mitochondrial proteins and proteins involved in angiogenesis regulation. These changes increase the rate of lipid oxidation during exercise, VO2max, and running time to exhaustion (Calvo et al.,

2008). In addition, Maciejewska et al. (2012), replicating a study with Russian athletes found in Polish athletes that 482Ser allele was underrepresented comparing with unfit individuals. It seems that *PPARGC1α* 482Ser allele impairs aerobic capacity while *PPARGC1α* Gly482 allele is positively associated with endurance performance. These adaptations are far from those required for elite sprinters.

So far, data are scarce to establish a clear association between any polymorphism of the PGC-1α gene and the ability to power/sprint performances.

Other polymorphisms associated with strength/power performance

A complete picture of human genetic variation is difficult to achieve with the actual limitations. As we saw before, sprint performance has been associated with specific SNP linked to skeletal muscle features. Some isolated studies showed the association between some polymorphisms and strength/speed performances. Naumov et al. (2014) showed that a rare polymorphism in the dystrophin gene (DMD rs939787 T allele) was overrepresented in strength/power athletes. Grishina et al. (2019) showed that the rs12055409 G-, rs4626333G-, and rs2273555 A-alleles are associated with higher levels of strength, muscle mass, and muscle fiber size. These results were not confirmed later by other studies. With the actual limitations, it is difficult to establish a clear link between one or several genetic features and the performative excellence in sprint.

Gene function may be modified either by altering the DNA sequence or by epigenetics changes.

Epigenetic background for physical performance

Environmental factors as light quantity and spectral quality, temperature, substrate chemistry or texture, relative humidity, day length, quality and quantity of food availability, the concentration of atmospheric carbon dioxide, oxygen, and other benign and pathological molecules as well as social interactions and population density can interact with all living systems inducing developmental plasticity (Sultan, 2003). Laboratory research has so far been unable to demonstrate the unique influence of the genetic matrix in developmental biology without environmental influence. Ortega Y Gasset philosophically claimed, «I am I and my circumstance; and if I do not save it, I do not save myself». This statement sets the tone for the mutual implications between individual organisms and their environment. The introduction of ecological influence on developmental biology opens new rational frontiers, which can highlight both the developmental causes and the ecological consequences of phenotypic variation (Sultan, 2003). The phenotype cannot be seen as a closed and mechanic print of the genotype. Development is not a pre-determined process; it is a Markovian process (a random process in which the future is independent of the past) whereby internal and external determinants interact and influence ontogeny. Individuals can differ under the influence of environmental heterogeneity. The same genetic template can result in different phenotypes through the influence of environmental heterogeneity. This phenotypic plasticity was seen in different living organisms from plants to mammals.

More than a rigid blueprint, genotype must be seen as a sensitive matrix to the environmental changes (Sultan, 2003). The environment influences the genome and can alter some of its expressions. Genotype-by-environment interaction act together to coin each phenotype. Each human being is a unique type of evolutionary novelty.

Emerging evidence indicates that both ancestral and parental experiences, including nutrition, environmental toxins, nurturing behavior, and social stress, can have powerful effects on the physiological, metabolic, and cellular functions of an organism. In certain circumstances, these effects can be transmitted across several generations through epigenetic (i.e. non DNA sequence based rather than mutational) modifications. Recent research stated the effects of diet on chromatin structure. These effects are usually stable and can be passed to offspring (Katada et al., 2012) by epigenetic processes.

Epigenetics is the study of changes in gene function that cause mitotically and/or meiotically heritable changes in gene expression that do not entail a change in the DNA sequence» (Indrio et al., 2017). Research on molecular processes of cell differentiation and development led to the recognition that post-translational alterations in chromatin structure can affect genetic expression and are inheritable. Epigenetics clarifies as genotypically identical cells turn into phenotypically different cells. There is sufficient evidence that parental environment-induced epigenetic changes are transmitted through both progenitors' germlines with differential effects at various levels. The connection between biology and culture gave rise to new

phenotypes. Biological selection developed the conditions for culture emergence, and culture acts as a selective factor promoting alterations in the biological matrix (Portin, 2015). From LUCA, environmental challenges led to natural selection and shaped human DNA, which is remarkably stable. New environmental alterations are susceptible to modulate new genetics features, which did not modify the base pairs sequence in the DNA strand but can modify DNA expression.

More than exclusively genome-focused, evolution must be seen through the environmental impacts that affect genome and the Lamarckian form of inheritance (Galera, 2017). Environmental acquired epigenetic traits are heritably transferring to the next generation through egg and sperm as germline cells (Gapp et al., 2014). However, not all epigenetic marks yield heritable changes. Some are retained and others are transient and disappear during meiosis, at fertilization, or in the post-zygotic stage. Mechanisms by which this happens are now being elucidated (Grossniklaus et al., 2013). Ontogenetic evolution may play a role in epigenetic marks through the endocrine system extremely influenced by environment changes (Zhang and Ho, 2011).

It is important to emphasize that the mutation rate for the human genome is extremely low, around 1.1 x 10^{-8} per site per generation (Roach et al., 2010). The epigenome is much more modifiable and can change in response to different environmental conditions. Epigenetic alterations can alter the timing and level of gene expression. There is sufficient evidence that epigenetic changes can cause disease without affecting gene sequencing. Genetic blueprint is extremely stable while epigenome is susceptible to changes in the environment. Alterations in gene expression induced by epigenetic influence can be passed throughout generations (transgenerational inheritance). This signifies that their descendants can inherit a change in the parents' gene expression (Bohacek and Mansuy, 2013). This is clearly and scientifically demonstrable for certain diseases; it can be speculated that some physical conditioning traits can also show inheritable influence. If some epigenetic modifications associated with cancer, diabetes, cardiovascular disease, and obesity can be transmitted to the next generations, it can be speculated that favourable characteristics can also be transmitted.

Aware that athletic performance has a strong genetic determination we will look to some epigenetic factors that can be eventually associated with Usain's physical capacity.

Adaptations exercise-induced are mediated by transcriptional, translational, and post-translational regulators (Hargreaves, 2015). These epigenetic alterations include DNA methylation, histone modification (acetylation, phosphorylation, ubiquitination, and methylation), and small non-coding RNAs (Levenson and Sweatt, 2005; Hargreaves, 2015). Two main epigenetic features are closely related – DNA methylation and histone modification. These epigenetic alterations play an important role in chromatin dynamics and in the regulation of several biological processes (Li and Zhang, 2014). It seems that, in part, athletic proficiency is achieved by post-transcriptional changes in DNA and nuclear proteins that elicit modifications in chromatin structure and alter genetic programming. The main drivers for these modifications are training and nutrition.

DNA methylation

DNA methylation is a chemical alteration that adds a methyl group to the 5-carbon position of a cytosine base; it is catalysed by a DNA methyltransferase. In mammals, DNA methylation is almost exclusively found in CpG dinucleotides (CpG islands) with the cytosines of both strands being usually methylated (Grazioli et al., 2017). In human somatic cells, methylated cytosine accounts for 70-80% of all CpG islands in the genome. DNA methylation is an epigenetic mark that is associated with gene silencing. The presence of DNA methylation on gene regulatory sequences, such as promoters and enhancers, represses gene expression (Dor and Cedar, 2018).

Contrary, non-methylated sites are linked to gene expression and many promoters in the mammalian genome are marked by unmethylated CpG islands (Suzuki and Bird, 2008). Studies show the association between mutation rates of the genome and DNA methylation and nucleosome positioning (Cavalli and Heard, 2019). DNA methylation seems to be important in long-term memory function. Two DNA methyltransferases (DNMT3A and DNAMT3B) catalyse the addition of a methyl group to cytosine while maintenance of the methyl groups during cell division is catalysed by DNMT1 (Li and Zhang, 2014). DNA methylation is a dynamic and reversible process. Ten-eleven translocation (TET) enzymes can remove methylation. Demethylation of DNA seems to be essential for embryonic development (Jones, 2012). DNA methylation changes after a given training period

seem to be retained although they are residual. Changes after training are smaller than after acute exercise (Jacques et al., 2019).

Acute and chronic exercises both influence DNA methylation in a highly tissue manner. However, observational studies showed a weak correlation between physical activity and global or gene-specific DNA methylation (Voisin et al., 2015).

Histone modifications

Histones are basic proteins in which DNA is coiled forming nucleosomes given the chromosomes a more compact shape. The nucleosome is a part of DNA that is wrapped around a set of histones (an octamer of two copies of each histone – H2A, H2B, H3, and H4) what gives DNA a more condensed shape (Cavalli and Heard, 2019). Histone modifications are controlled by a set of enzymes including histone acetylases (HATs), histone deacetylases (HDACs), histone methyltransferases (HMTs), histone demethylases (HDMs), histone kinases, and histone ligases (McGee and Walder, 2017).

Histone changes are closely linked to DNA methylation/demethylation (Jones, 2012). The N-terminal tails of these histones are modified through different biochemical processes: methylation, phosphorylation, acetylation, sumoylation, and ubiquitination (Szyf, 2009). The addition or removal of epigenetic marks are post-translational modifications that contribute to activating or silencing gene expression. Histone acetylation exposes DNA for transcription while histone deacetylation concurs with DNA methylation to the formation of a compacted chromatin inducing gene silencing.

Physical exercise is a strong inducer of epigenetic alterations, namely histone changes. Systematic training induces metabolic changes in the muscle that are epigenetically regulated. Increased gene transcription is associated with DNA hypomethylation and histone hyper acetylation (McGee and Hargreaves, 2019).

Different signalling pathways are associated with exercise-induced skeletal muscle phosphorylation – AMP-activated protein kinase (AMPK), mitogen activated protein kinase (MAPK), protein kinase A (PKA), protein kinase C (PKC) and the calcium/calmodulin protein kinase II (CaMKII) (Hoffman et al., 2015). Several studies showed the association of these signalling pathways with histone alterations (McGee and Hargreaves, 2019). Acetylation and deacetylation of muscle fibers are crucial for the regulation of their metabolic features. Histone acetylation is the most widely studied histone change in epigenetics namely the epigenetics of exercise (McGee and Walder, 2017). Patterns of histone modifications differ between slow- and fast-twitch skeletal muscles (Lim et al., 2020). In fast oxidative fibers enhancement of glycolytic metabolism is linked to deacetylation. However, acute adaptation to endurance exercise increases H3K36 acetylation and produces no change in H3K9 and H3K14 acetylation (McGee and Walder, 2017).

Regulation of transcriptional response to exercise involves numerous histone modifications. While the few existing studies have focused on changes in histones induced by endurance exercise, no one has been carried out on adaptations induced by sprint training.

Lim et al. (2020) showed that resistance training (significant part of sprint training) increased expression of 153 genes (+ 9.6% versus pre-training, $p<0.05$). In this study, some epigenetic changes were observed: significant up-regulation of acetylated histone 3 (+ 235%) and H3 mono-methylated at lysine 4 (+ 290%), tri-methylated at lysine 27 (+ 849%), and down-regulation of H3.3 variant (-39%) were observed at transcriptionally after acute resistance training compared to basal level. Acetylation of H3 after resistance training increased 40%. In the future, studies will clarify the extent of chronic adaptations induced by consecutive acute changes.

Studies are scarce but technological advances will allow, in the future, a deeper and more accurate approach to the epigenetic mechanisms associated with sprint training. Research focus will be twofold: (i) the global changes in the nucleosome induced by exercise, and (ii) the basic profile of DNA methylation/demethylation and histone acetylation/deacetylation in elite sprinters. This being resolved, a better characterization of Usain Bolt's sporting excellence could be achieved.

Non-coding RNAs (ncRNAs)

Eukaryotic transcription from different genomic regions and RNA processing sites produce various ncRNA species with different biological functions but not the coding function. Studies revealed that 98% of the non-coding DNA could be transcribed into enhancer regions or transposon elements (Zhang et al., 2019). Some ncRNAs, e.g. microRNAs (miRNA), regulate post-transcriptional processes, whereas others are involved in transcriptional regulation.

MicroRNAs are small (~20-30 nucleotides) non-

coding RNAs that potentially regulate post-transcription mRNA expression inhibiting protein translation or enhancing mRNA degradation. More than 1.000 mi RNAs have been identified in mammals (Ogasawara et al., 2016). A small number of muscle-specific miRNAs have been identified and shown to interfere with myoblast proliferation and differentiation as well as embryonic muscle growth (McCarthy and Esser, 2007).

Exercise quickly and transiently mobilizes different miRNA eventually involved in the regulation of skeletal muscle regeneration, gene transcription and mitochondrial biogenesis (Russell et al., 2013). Ogasawara et al. (2016) identified 102 miRNAs with altered expression after chronic resistance training with 26 miRNAs differently regulated in high versus low responders.

Resistance training (usually part of the sprinter's basic training), in both low and high responders, altered the expression of several miRNAs whether after acute exercise or after chronic adaption (Ogasawara et al., 2016). Muscle hypertrophy, a hallmark of elite sprinters is controlled by a plethora of genetic loci and epigenetic marks. However, to date, there is no study to characterize the phenotypic expression of miRNAs in elite sprinters and the training-induced changes.

Conclusion

In the light of evolutionary biology, we cannot say that Usain Bolt is a hopeful monster. Evolutionary theories state that a human genetic variation commonly exhibits geographic structuring as a consequence of demographic history (such as population subdivision, migration, and admixture or replacement), as well as locus-specific forces such as selection, mutation, and recombination. Even accepting the hypothesis that Usain ancestors developed a special genetic trait since the migratory outbreaks from West Africa, we cannot say that this trait is the result of an evolutionary leap, thus rejecting the saltational hypothesis. Usain' sporting excellence is entirely consistent with the principles of modern population genetics and the phenotypic variability that characterizes the human race. It can be assumed that Usain Bolt is a special case of phenotypic novelty. The study of the genome sequencing and the respective phenotypic expressions of Usain Bolt, his parents and his African ancestors, an impossible thing to do, would give us clues to decipher the evolutionary basis of his sporting excellence.

Scientific research in genetics and epigenetics, although characterized by a progressive breadth and depth, is still unable to elucidate the genetic and epigenetic components of the performance of athletes specialized in speed and power events. The attempt to characterize Usain Bolt's excellence in the light of evolutionary biology is a challenged intellectual exercise but impossible to solve with the current level of scientific research. Sport performance is a construct of multiple factors whose basement lies on the individual genetic matrix with a strong influence of environmental conditions. High performative athletes surely display a special polygenic phenotype. However, it is currently impossible to discriminate the genes, alleles or epigenetic markers that are linked to extreme sport performances.

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