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Genetic Studies are an Important Aspect of Modern Medicine to Optimize the Therapeutic and Rehabilitation Process

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Abstract

Due to the multiple origin of the lesions, identifying risk factors and assessing an athlete's susceptibility to experience an injury and the manner in which it will develop is difficult to predict. The value of each individual's genetic component as a probable source of injury predisposition has been debated in recent years. The goal of this paper was to write a review of the genetic studies on connective tissue injuries that have been done to date, as well as to suggest future research lines that would allow for the development of more personalised training programmes and specific preventive therapies to reduce injury risk. The complex nature of injuries makes identifying risk variables more difficult (extrinsic and intrinsic factors). These factors, combined with their interaction, predispose an athlete to injury. In recent years, the importance of each individual's genetic component as a possible source of injury predisposition has grown.

The purpose of this paper was to propose a review of published genetic studies on connective tissue repair or regeneration in order to pave the way for future Sports Medicine research. This information could be extremely beneficial in tailoring injury prevention efforts and optimising the therapy and rehabilitation process following an injury. Applied biology is already advancing knowledge by developing new biomarkers that will provide information and improve understanding of an individual's vulnerability to particular types of harm. Genetic analysis can provide us with a valid and objective predictive parameter that, when paired with current analysis methodologies, can help us improve athlete performance and management.

Keywords: Genetic polymorphism; Connective tissue; Sport injuries; Lesions

Introduction

The biological and mechanical qualities of the tissues influence physical and athletic performance. Due to the high degree of physical and psychological demands and loading involved, exposure to high levels of competition carries a significant risk of injury. Injuries have far-reaching consequences that go beyond the injured athlete or player [1]. The coaches, the team, the sponsors, and the clubs are all affected.

One of the goals of sports medicine is to scientifically label real risk variables and establish regimens using fatigability indexes [2, 3]. Fatigue is diagnosed using a variety of approaches. The use of global positioning systems (GPS) systems augments blood testing [3]. GPS systems used in training and matches offer data on each individual player's physical output (and, in some cases, physiological burden) during each session. Information on the number of sprints, movement patterns of acceleration and deceleration, the number of high-intensity movements, and cardiorespiratory data can all be useful. Extrinsic factors (EF) such as the playing field, ball qualities, sports equipment, and inadequate planning combine with intrinsic factors (IF) such as previous injuries, muscle imbalances, and lack of flexibility to cause injury. The IF makes us more susceptible to harm, yet it does not guarantee an injury. The interaction of an IF with a group of EF increases susceptibility to harm, but only when a trigger element is contacted [4]. Finally, the sum of IF and EF indicates the likelihood of harm risk. A high number of non-contact injuries (injuries that do not occur as a result of blows, external trauma, or collisions) jeopardises a player's ability to perform or may prevent them from competing. He has immediate implications that have a detrimental impact on not only the person but also the collective unit, as well as the ability to achieve defined individual and group goals and objectives. Non-contact injuries can be reduced by implementing and monitoring various injury prevention measures, as well as focusing on the prevention rather than cure mentality. Prevention plans must be established to lower the effect of various risk factors, reduce the incidence of injuries, and/or aim to reduce their severity at the same time. Historically, injury history, biochemical and metabolic markers, tomographic, anthropometric, and dietary data have been prioritized. These, on the other hand, have been ineffective in reducing the amount of non-contact injuries, particularly muscular injuries. In today's world of sport, progress is being made in the study and use of genetics, and genetic analysis of athletes can provide us with a valid and objective predictive parameter that, when paired with current analysis methodologies, can help improve athlete performance and management.

Genetic variation and detection methods: The modification of responses to environmental stimuli is caused by nucleotide polymorphisms in the genetic code. These differences, known as polymorphisms, affect about 1% of the population and can take several forms, including tandem repeats (microsatellites), deletions, insertions, duplications, and single nucleotide polymorphisms (SNPs). SNPs are the most prevalent variations in the genome, accounting for 90% of all alterations and occuring every 100-300 base pairs. Hey are changes of a single base in the DNA sequence that occur infrequently in populations but are relevant enough to be investigated since they may or may not alter the phenotypic of people, giving rise to a clinically useful biomarker. Because genetics has an impact on athletes'

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phenotype, using genetics as a supplement to the criteria researched thus far is critical and very useful. These SNPs can be discovered in both the promoter (sections composed of specific DNA sequences positioned just where the transcription starts) and exon (regions encoding a specific protein) regions of the genes. SNPs can also be discovered in the intronic (non-coding DNA) or intergenic (coding DNA) regions of a genome (nucleotide removed during RNA splicing). Any of these scenarios could lead to a change in the final genetic product. This occurs either as a result of a change in the protein's final confirmation or as a result of an increase or reduction in messenger RNA (mRNA) levels, resulting in more or less elevated protein levels [5]. SNPs can also be discovered in the intronic (non-coding DNA) or intergenic (coding DNA) regions of a genome (nucleotide removed during RNA splicing). Any of these scenarios could lead to a change in the final genetic product. It occurs either as a result of a change in the protein's final confirmation or as a result of an increase or reduction in messenger RNA (mRNA) levels, resulting in more or less elevated protein levels [5]. To determine the existence of SNPs, the individual's DNA must be obtained. Sampling for future DNA extraction and purification can be done in a variety of methods, including biological samples. Blood or saliva is examples of fluids. Following the collection of the sample, the DNA is extracted according to pre-established procedures. There are a number of methods for detecting SNPs, but the most popular is the use of restriction enzymes or the allelic analysis technique. Assays for discriminating Restriction enzymes are enzymes that identify nucleotides. Identify a sequence within a DNA molecule and cut it at that place (restricted goal) This approach has a significant flaw in that it yields a large number of false positives, causing problems with interpretation the outcomes It is more exact and accurate to use allelic discrimination tests. It is feasible to distinguish between them with only a small bit of DNA. Wild-type, heterozygous, and homozygous populations are the three sorts of populations in support of the SNP In most cases, fluorescently labelled samples are used in the study. TaqMan probes that have been labeled. The method is based on real-time data. The polymerase chain reaction (PCR) is a technique for detecting the released DNA each amplification cycle's fluorescence. Is it because of the fluorescence. It's feasible to distinguish between the three types of populations we're dealing with been previously discussed [5].

Recent research has demonstrated the importance of the individual genetic component, referred to as an IF, in non-contact injuries [6-9] in the soft tissues. All of these research show that there is a substantial link between the two. Genetic influence on the nature of injuries (greater than 50%) happening. According to other research, the occurrence of these differences. Although there is a link between DNA and connective tissue injury majority of these research have been conducted in non-sporting environments population [10].

Conclusion

Epidemiological studies have shown to be the most effective approach for learning about and learning about the occurrence of soft tissue injuries to date. They aid in the detection of risk variables that may be implicated in these injuries so that preventive strategies can be developed and implemented. Genetics has recently enlightened and driven the search for novel biomarkers that could help identify more objective risk factors. Genetic studies are an important aspect of modern medicine, and they should be employed in sports medicine, particularly in the areas of injury risk biomarkers and treatment responses. To progress, homogeneous populations are required in order to conduct extensive monitoring in order to correlate and validate genetic studies with reality of the sport practice.

Applied biology and genetics are already contributing new knowledge by developing biomarkers that will aid in the provision of information and a better understanding of an individual's susceptibility to certain types of injuries, their ability to be considered good or bad responders to a specific treatment, and the planning of a recovery protocol when modulating loads. The quality of connective tissue (defined by genetic profile) is a critical factor in the ability to accept and sustain training and competition loads.

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Note applicable.

Conflict of Interest

Author declares no conflict of interest.

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