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Bibliometric Analysis was conducted to Identify Journals and Authors Working in this Field

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Description

The most numerous marine ecosystems are coral reefs. However, due to natural disturbances, climate change, and local anthropogenic drivers, coral cover has decreased worldwide. In recent decades, a variety of genetic methods and molecular markers have been developed to evaluate the genetic diversity, structure, and connectivity of various coral species' populations in order to determine their vulnerability. The purpose of this review is to identify the methods and molecular markers used in population genetic studies of scleractinian corals conducted in the past ten years. In order to locate journals and authors working in this field, bibliometric analysis was carried out. Based on data from 178 studies, we then calculated the number of genetic studies by species and ecoregion. The most widely used molecular markers are microsatellites, and coral reefs and molecular ecology were the most widely published population genetics studies. Among the ecoregions with the most population genetics data are South Kuroshio in Japan, the Australian Barrier Reef, and the Caribbean. In contrast, we discovered little information about the Coral Triangle, a crucial region for the conservation of coral reefs and home to the highest biodiversity.117 scleractinian coral species have genetic studies, which is noteworthy. This review focuses on the coral species that have been studied, the areas where more research is needed for coral conservation, and any remaining knowledge gaps. Prognosis and early treatment greatly benefit from identifying common shared pathways between upper and lower airway diseases. Adults with asthma who do not receive treatment for AR have a threefold increased risk. Lower airway disease may be better understood with the help of accessible, noninvasive nasal passage sampling. According to the previous discussion, there appear to be gene-level mechanisms that are common to upper and lower airway pathologic conditions for some disease phenotypes. Kicic and colleagues50 looked at similarities in transcriptomic profiles from the upper and lower airways regardless of airway symptoms. Although it is common knowledge that AR and asthma are linked, only a small number of studies have looked into the connection between CRS and asthma and unified airway pathology.

Tissue Remodeling, Arachidonic Acid Metabolism

To verify these early findings, additional research is required. Additionally, studies on asthma, AR, and CRS have shown that diseases that affect both upper and lower airway subsites share genetic variants. The genes that control innate and adaptive immunity, cytokine signaling, tissue remodeling, arachidonic acid metabolism, and other pro-inflammatory mechanisms are the most frequently identified genetic variations. In well-characterized diseases, larger replicable studies across diverse populations are required. The introduction of Massive Parallel Sequencing technology into the field of forensic genetics has provided new opportunities for forensic DNA genotyping. There are numerous advantages to MPS, including sequencing throughput parallel production of millions of DNA molecules simultaneous examination of many different markers as well as various sort of markers and a large number of samples collected during a single experiment. MPS allows for the genotyping of a novel kind of genetic marker, known as micro haplotypes, in addition to the genotyping of traditional forensic markers for identification, such as mitochondrial DNA, Single Nucleotide Polymorphism, and Short Tandem Repeat. Additionally, MPS makes it possible to investigate the potential of forensic transcriptomics and DNA phenotyping. This article discusses the various forensic MPS approaches, their applications, and the advantages and disadvantages. Even though the genus Capsicum has a variety of sources of LCVD resistance, it is always necessary to find new sources of LCVD resistance and incorporate them into economically important cultivars. In addition, no comprehensive studies have been conducted to ascertain the significance of POD, PPO, and phenolic compound concentration changes in resistant and susceptible cultivars and their offspring. Therefore, the purpose of this study was to determine the quantitative estimation of phenolic compounds, protein content, and given enzymes in the leaves of resistant and susceptible cultivars and their offspring in order to determine the role that these compounds play in LCVD resistance. Future chilli breeding programs will benefit greatly from the information gained in this area of research. Four hot pepper parental lines were crossed with one bell pepper cultivar to

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produce four distinct offspring for the experimental material. Biochemical analysis was also performed on the selected genotypes after they were screened for LCVD reaction and categorized as resistant or susceptible. According to the phenotypic classes provided by Sharma et al., the disease reaction was recorded under artificial screening conditions. Because there are only a few studies that describe the role of ant oxidative enzymes in the LCVD resistance mechanism in pepper, the present investigation revealed the genetics of newly identified LCVD resistant sources as well as information on their ant oxidative profile. There is a lack of information regarding the genetics of new LCVD resistant sources. The resistant offspring's elevated levels of antioxidant and defensive enzymes. Two significant changes from previous editions are included in the seventh edition.

Awareness of the Genetic Concepts and Determinants

The first is that the text will be published in 11 separate volumes. Prior to the introduction of the electronic version in the previous edition, the book had grown from two to three massive volumes. An attempt to divide the content into smaller, more digestible chunks can be seen in the decision to divide the book into multiple smaller volumes. The majority of these are organized around a common theme, typically based on particular body systems. Specialists who are interested in the application of medical genetics to their field but do not wish to invest in a larger volume that covers all aspects of medicine may find the book more useful as a result of this. Additionally, it demonstrates our awareness of the fact that genetic concepts and determinants now underpin all medical subspecialties. In today's high-tech world, the second change publishing the 11 volumes in prints rather than solely electronically may appear retrograde on the surface. However, both the experiences of the editors and our readers indicated that printing a smaller volume with two-page summaries was ineffective and that accessing the web version through a password-protected site was time-consuming. We have in this way gotten back to a full print rendition, albeit a digital book is accessible for the people who favour an electronic variant.