Immune Mediated Diseases

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Immune-mediated diseases (IMDs) are complex pathologies that are strongly influenced by environmental and genetic factors. Associations between genetic loci and susceptibility to these diseases have been widely studied, and hundreds of risk variants have emerged during the last two decades, with researchers observing a shared genetic pattern among them.

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1. Introduction

Immune mediated diseases (IMDs) are a diverse group of pathologies with different etiologies, characterized by a dysregulation of the immune system. These diseases show different effects on the organism, including either systemic or local symptoms, which may overlap between the diseases[1]. This complexity makes their diagnosis a clinical challenge, as different IMDs are found to have shared comorbidities and may co-occur in the same patient. A common example is cardiovascular disorders, which are present in several of these diseases[2][3][4][5], as well as the presence of autoantibodies, which have great clinical and diagnostic significance[6][7].

Thus, the high rates of familial clustering and comorbidities observed across IMDs indicate that they share molecular mechanisms of disease pathogenesis[8]. In the last decades, large-scale genetic studies, such as genome-wide association studies (GWAS) and Immunochip studies[9][10] have been essential to our understanding of IMD genetics, allowing the identification of a considerable number of loci associated with each individual disease [11][12][13][14], but also suggesting the existence of a common genetic background in autoimmunity[8].

However, despite the success of GWAS, most of the polymorphisms associated with IMDs are located in non-coding regulatory regions of the genome and therefore their direct consequences on the disease are not clear[15][16]. In this regard, functional genomics is very useful in order to identify the mechanism of action of disease-associated variants and therefore the mechanisms underlying complex diseases, thus allowing progress in translating genetic findings to the clinic[17][18]. As shown in Figure 1, the process from the identification of a disease-associated variant to its characterization at the phenotypic level includes different functional assessments, which differ depending on the genomic location of the variant.

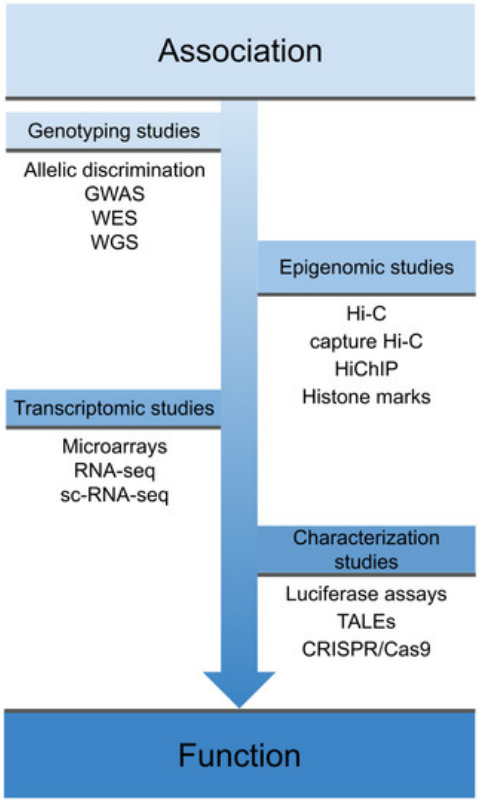

Figure 1. Overview of different techniques used in functional genomics. These techniques cover the spectrum from early association studies, through techniques that explore the physical interaction of these variants and their effects on the transcriptome, to phenotype characterization and gene function. GWAS: genome-wide association studies; WES: whole-exome sequencing; WGS: whole-genome sequencing; sc-RNA-seq: single-cell RNA sequencing, TALEs: Transcription activator-like effectors; CRISPR: clustered regularly interspaced short palindromic repeats; Cas9: CRISPR associated protein 9.

2. Shared Genetics across IMDs

In recent years, many efforts have been made in order to identify risk loci shared among IMDs by combining GWAS or Immunochip data across several diseases. This strategy allows a direct comparison of the genetic component of these diseases, as well as an increase in statistical power to detect associations with low-effect variants. To date, a considerable amount of pairwise cross-disease meta-analyses of GWAS data of systemic rheumatic diseases has been published[19][20][21], which has led to the identification of many risk loci shared between pairs of these diseases. Furthermore, five studies combining the GWAS or Immunochip data of multiple IMDs simultaneously have been published, thus identifying a total of 75 new shared risk loci with some degree of pleiotropy in autoimmunity, which could partially explain the comorbidity observed among IMDs[22][23][24][25][26]. Good examples of known shared risk loci in IMDs are *PTPN22*, *IL23R* and *TNFAIP3*, which have allowed the repositioning of anti-TNF and anti-IL-12/IL-23 therapies to be used in rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE), among others[1].

On the other hand, a recent study identified shared germline variants that predispose patients to RA, SLE and primary Sjögren's syndrome (SjS) through whole-exome sequencing of 31 families, highlighting related T-cell-activating genes[27]. This familial aggregation suggests that a specific molecular pattern, leading to common pathogenesis in certain IMDs, could exist. Furthermore, Li et al. [22] quantified pairwise genetic sharing across 17 IMDs from the Immunobase resource, revealing a closer association among major systemic IMDs (including RA, SLE and systemic sclerosis (SSc)) than with other autoimmune disorders, such as psoriasis and inflammatory bowel disease. These studies support the idea that genetic pathways are shared among apparently clinically different IMDs and therefore a molecular reclassification of these diseases could lead to the discovery of new biomarkers for patient stratification and prognosis[28]. In line with this, a recent study stratified seven systemic IMDs into groups of molecular patterns, taking into account high dimensional molecular data including genome, transcriptome, and methylome data from whole blood samples, performing an unsupervised clustering analysis. Authors observed that systemic IMDs clustered in three different groups, representing "inflammatory", "lymphoid" and "interferon" groups, with specific molecular patterns independently from their clinical classification[29].

The emergence of GWAS and associated genotyping platforms led to an increase in the number of variants associated with complex diseases, allowing for the development of more accurate genomic risk score (GRS) calculations, a direct application of genomic data to the clinical setting. GRS measures the additive effect of single nucleotide polymorphisms (SNPs), calculating the relative risk of individuals suffering from a given disease [30][31][32]. GRSs have been applied to different IMDs such as SLE, RA, SSc and psoriatic arthritis (PsA)[33][34][35][36]. Furthermore, genomic data can be useful for making a differential diagnosis, which is especially interesting in the case of inflammatory arthritis, since these conditions present with similar symptoms in the early stages[37]. In addition, the different relevant symptoms of the disease can be used to increase the predictive power of GRS, such as the appearance of lupus nephritis in SLE[33], or the appearance of autoantibodies in SSc[35].

3. New Approaches for Drug Targeting

The identification of new targets is a critical step in the drug discovery process. In this sense, the recent massive accumulation of different genomic data, mainly through GWAS, and their annotation through different functional data, establish the perfect framework to elucidate the underlying pathogenic mechanisms of IMDs and thus prioritize potential new therapeutic targets[38].

In this regard, one of the main examples of the usefulness of genomic studies in the identification of potential new drug targets is a study published by Okada et al.[11]. Through the largest GWAS conducted in RA, the authors identified more than 100 loci associated with this disorder. Subsequently, using bioinformatic methods based on functional annotation, they identified a total of 98 biological candidate genes, some of which were targets of RA therapies, whereas others were targets of drugs potentially useful for the treatment of this disease. A more recent GWAS performed in SSc identified a total of 27 independent risk loci for this condition. The subsequent functional analysis, using HiChIP data, of the most probable causal variants allowed the identification of 43 robust target genes, highlighting *CD80* and *BLK* as potential drug targets[14]. Furthermore, meta-analysis of GWAS data, including different IMDs, also led to the identification of shared risk loci, as well as potential new drug targets through drug enrichment analysis[24]. It is worth mentioning that drugs with mechanisms based on genetic evidence have a higher probability to be approved through the drug development process [39].

On the other hand, the biological function of a genetic change can be easy to observe, thus making it easy to identify a potential drug target. For example, the knowledge of mutations and deletions occurring in the *JAK3* gene that cause severe combined immunodeficiency[40]was useful to develop drugs such as tofacitinib to treat inflammation in RA[41].

Additionally, genomic and epigenomic data, using functional genomic approaches, are being integrated in order to facilitate drug repurposing in IMDs[42]. In this regard, analysis of capture Hi-C data from B-cells and T-cells to identify causal genes for rheumatic diseases revealed many disease-associated genes to be targets of existing drugs. A recent study demonstrated an approach that integrates functional genomics and immune-mediated annotations with the evidence of physical interaction in order to prioritize drug targets, an approach which has been validated and applied in RA[43]. In this sense, the emergence of TNF as a highly ranked target confirms the utility of this approach [43][44].

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