**EDITORIAL**

# *Immunogenetics* special issue 2020: nomenclature, databases, and bioinformatics in immunogenetics

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In 2016, *Immunogenetics* published a special issue on the topic of evolution and origins of non-peptidic antigen recognition by T-lymphocytes (Zajonc and Flanik 2016). The contributions by leading experts in the field received wide attention and were well received by the journal's readership. Encouraged by this, the editorial team decided to embark on another enterprise of this nature. This time the focus was on MHC/KIR in health and disease (Bontrop 2017). Again, the various contributions provided a state-of-the-art overview of the most recent advances in the field. The manuscript on the role of MHC genes on contagious cancer in Tasmanian devils was downloaded many times (Caldwall and Siddle 2018). The next special issue concentrated on the biology and evolution of antigen presentation (Kasahara et al. 2019). This issue contains at least two classic contributions that we believe will be a tremendous resource for many young scientists in the field. The first article – by Peter Cresswell, a renowned leader in the discipline – is a personal historical perspective that reads like a novel (Cresswell 2019), while the second article is a comprehensive introduction to the genetics of antigen processing and presentation (Kelly and Trowsdale 2019).

The current special issue deals with *nomenclature, databases, and bioinformatics in immunogenetics*. We are keen to focus on these issues now because several years ago the HLA community realised that the different polymorphisms detected by alloantisera, often generated in various labs, may recognise similar or identical antigens. To investigate this, the community organised workshops (Bontrop et al. 2018), and the outcome was published traditionally as somewhat lengthy nomenclature reports (Marsh et al. 2019). These reports on annotated sequences are extremely useful not only to researchers in the field of immunogenetics but also to bioinformaticians, who are dependent on the quality of databases. Some other MHC societies adapted the approaches of the HLA field, but others simply chose not to follow. This has had serious consequences. For instance, the rat represents an extremely important animal model in biomedical research, but an official nomenclature report on rat MHC is lacking. The same situation is apparent for the chicken, which represents an important agricultural species. We are pleased to see published in this present special issue the first reports on the MHC nomenclature of rat and chicken (Walter 2019; Afrache et al. 2019).

The first nomenclature report on MHC sequences of Great Ape as well as Old and New World Monkey species appeared about a decade ago (de Groot et al. 2012). Since then, a large number of new annotated genes and alleles have been published, also from species that had not previously been analysed. The progress made has been summarised in an update of this report (de Groot et al. 2019). In a relatively short time, remarkable advancements have been made in the description and discovery of KIR genes/alleles of different macaque species (Bruijnesteijn et al. 2019). This update provides a welcome extension to a recently published nomenclature report on KIR sequences in different species (Robinson et al. 2018). Such well-annotated sequences need to be easily accessible, and this is only possible in dedicated electronic archives such as the immunopolymorphism database (Maccari et al. 2019). Most of the novel sequences for non-human species are stored and described in some of the nomenclature reports discussed here before eventually landing in the IPD database (https://www.ebi.ac.uk/ipd/).

From a functional point of view, MHC class I and II molecules can be considered as peptide receptors, and the complex may be recognised by the T-cell receptor. One of the

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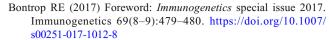
contributions in this special issue provides a historical overview of the Immune Epitope Database, which is an important tool for immunologists working in various disciplines (Martini et al. 2019). However, another team took an alternative approach and highlights a more recent database that describes T-cell receptor repertoires in relation to their antigenic specificities (Zvyagin et al. 2019). As one might expect, the combination of a particular peptide and its cognate MHC may sometimes trigger a disease. The most thoroughly understood example is provided by celiac disease. *Immunogenetics* was the first journal to publish the nomenclature and listing of celiac disease-relevant gluten T-cell epitopes restricted by HLA-DQ molecules (Sollid et al. 2012). This original report has been highly cited and greatly appreciated by the scientific community, and an updated version can be seen in this special issue (Sollid et al. 2019).

Owing to the introduction of novel techniques, immunogenetics, like other life sciences, is enjoying a very data-rich era, and the novel high-throughput data allow us to study complex entities of the immune system. However, to do this properly calls for an interdisciplinary approach in which bioinformaticians and computational biologists work in close collaboration with immunologists. Therefore, in this special issue, we present four reports that demonstrate the analysis of immunogenetics data. The first paper provides the outline of a next-generation sequencing approach that may serve as a typing system of MHC genes in Atlantic salmon (Sundaram et al. 2019), while another contribution describes the characterisation of the Ferret T cell receptor B locus (Gerritsen et al. 2019). Can Kesmir's group has analysed the whole VDJdb database (Ritmahan et al. 2019) for factors on T-cell receptor sequences that define the immunodominance of T-cell responses (Ritmahan et al. 2019). Finally, Eric Spierings' group describes an algorithm that can predict which of a donor's HLA epitopes can be presented by self-HLA molecules of the acceptor (and vice versa) in a transplantation setting (Geneugelijk and Spierings 2019).

By highlighting the topics of nomenclature, databases, and bioinformatics in this special issue, we hope to bring their importance and centrality in immunology into sharper focus. Our goal is to continue publishing outstanding research in these areas, which will serve as a guide to many immunologists in terms of where to find novel data and how to deal with them systematically and efficiently.

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