

Poster presentation

Visualising the immune repertoire

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Background

Antibodies play a central role in the adaptive immune defense of all vertebrates. Thereby, the specific recognition of antigen structures by antibody molecules determines the success of the immune response. Therefore, the repertoire of antigen binding sites within the immune system of an individual, but also, within a population, has been a main focus of immunological research within the last 3 decades. The first tool to analyse the DNA sequence of the antigen binding site of an antibody was DNAPLOT <http://www.dnaplot.de>. Associated with the Vbase database [1], the DNAPLOT search page was the first of its kind which allowed the analysis of the modular composition of these binding sites, the immunoglobulin gene rearrangements. The focus of this site was to identify and mark the genetic elements that are used for these rearrangements. In the meantime, several similar tools are available, including the current DNAPLOT version at the VBASE2 database [2] <http://www.vbase2.org>.

Results

We have now introduced a major extension to the functionality of DNAPLOT. The new features allow the systematic analysis and visualization of the expressed immune repertoire of an organism. Thus, DNAPLOT is now able to demonstrate the dynamics of the expressed repertoire, e.g., during the time course of the antibody response against a certain pathogen.

Looking at antibody structures, it is well known that mainly the so called complementary determining regions

(CDRs) contain the information of the interface between a given antibody and its antigen. The adjacent regions, the so called framework regions (FRs), build the antibody structure and provide a frame to expose the 3 CDR regions of each variable domain of the antibody. The new extended DNAPLOT version loads a list of variable domain DNA sequences, extracts the CDR regions and presents them as a color-coded string of amino acids. In this way, the essential information on the docking sites of a given antibody population is easily visible. Thus, by removing redundant information on the FRs, essential information about the antigen binding sites is displayed, and critical amino acids can be viewed at a glance. The new DNAPLOT extension is not only applicable for the analysis of naturally occurring immune repertoires but also for the analysis of artificial antibody populations isolated from phage display libraries.

Conclusion

The program DNAPLOT provides the base for systematic analyses of expressed immune repertoires and aids to detect patterns of changes in the CDR regions of a given repertoire.

References

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