Cologne Evolution Colloquium

SFB 680 Molecular Basis of Evolutionary Innovations

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Quantifying immune receptor diversity

Recognition of pathogens relies on the diversity of immune receptor proteins. Recent experiments that sequence the entire B- and T- cell repertoires provide a new opportunity for quantitative insight into naturally occurring diversity and how it is generated. The generation process is implemented via a series of stochastic molecular events involving gene choices and random nucleotide insertions between, and deletions from, genes. I will describe how we can attempt to quantify the diversity of the receptors formed in this complex process and point to the origins of diversity in these sequences. I will discuss the diversity in the junctional regions around CDR3, which is not possible to characterize by traditional alignment methods. The results suggest that antibody diversity is not limited by the sequences encoded in the genome and may reflect rapid adaptation to antigenic challenges. I show how we can describe the somatic selection pressures on particular sequences.

Wednesday, January 15, 2014, 17:00
University of Cologne, Institute for Genetics
Seminar Room 0.46

Hosted by Michael Lässig