Complementarity-Determining
Regions of Antibodies

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When I was at Cornell University Medical College, I read two very interesting articles by Elvin A. Kabat of Columbia University College of Physicians and Surgeons analyzing the amino acid distributions of light chains of immunoglobulins. Since I knew very little about immunology, I wrote to Elvin asking whether I could spend some time in his laboratory.

After learning that I was also trained in engineering and applied mathematics and was interested in mathematical biophysics, Elvin suggested instead that we should meet once a week to analyze the known sequence data on antibodies in more detail, initially by writing them on long strips of paper and later by using computers. We reasoned that the variable region of light chains of immunoglobulins could have random amino acid substitutions just like other proteins. However, at the antibody-combining sites many more substitutions would be needed to accommodate the vast number of different antibodies. Such amino acid variations were previously noted by Elvin as well as by Hilchmann and Craig, Putnam, Edelman, Frankel, Milstein, and Pink, and others. We defined a quantitative measure, variability, and this is the subject of this paper. A brief review of the most important work on the variability of immunoglobulins is presented.

Complementarity-determining regions (CDRs) were identified by Kabat and co-workers in the mid-1980s. These regions are involved in antigen recognition and are conserved among different antibodies. The CDRs are typically located at the tips of the antibody combining site, where they interact with the antigen.

The identification of CDRs has important implications for understanding the diversity of the immune response. CDRs are the areas of the antibody that are most susceptible to mutation, and they are critical for the binding of antibodies to antigens. By understanding the variability of CDRs, we can gain insights into how antibodies are able to recognize such a wide range of antigens.


