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Antibody engineering from hybridoma-derived monoclonal antibodies

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Antibody engineering requires the identification of antigen binding domains (variable regions; VRs) unique to each antibody. This determination can be achieved by sequence analysis of the antibody transcript obtained from the hybridoma as each clonal hybridoma cell line produces in principle a single antigen specific monoclonal antibody (MAb). However, the polyploidy nature of hybridoma cells often results in the added expression of aberrant immunoglobulin-like transcripts or even production of nondescript antibodies. The occurrence of these transcripts confounds identification of the VRs of immunoglobulin heavy and light chains that correspond to the antigen specific antibody. It is the VRs that define the unique antigen binding properties and proper sequence identification is essential for functional performance of a recombinant engineered antibody. To address this problem, we have identified and complied a database of aberrant Ig-like transcripts found in myeloma cell lines (SP2/0-Ag14 and P3X62A8U.1) frequently used in the generation of hybridomas and developed a PCR-based method for the selective amplification of heavy and light chain VRs from a given antigen specific immunoglobulin isotype combined with molecular cloning and DNA based sequence analysis. These methods should increase the certainty regarding the VR sequence structure when evaluating the functional performance of a recombinant antibody. This work serves to facilitate antibody engineering applications with broad interest to biotechnology and pharmaceutical industries.

Biography

Lmar Babrak is currently a Post-doctoral Research Scientist in the laboratory of Dr. Robert Hnasko at the Agricultural Research Service located in Albany, CA. Her research has focused on the development of immunoassays used for the detection of disease causing pathogens, toxins and other agricultural contaminants. She has completed her PhD in Microbiology in 2015 from Oregon State University.

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