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"Exploring allergy with structural biochemistry: from plant allergens to antibodies"

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Auditorio principal de la UPDCE

Semblanza
Prof. Adela Rodríguez Romero is, since 1986 a reaseacher of the Insitute of Chemistry of the UNAM. She has notoriously participated in the implementation and consolidation of the protein crystalography not only in the UNAM but in the country. Currently she is a full researcher type C and is level 3 of the Conacyt's National Reseach System. Prof. Rodríguez received her Ph.D. in Chemistry from the Autonomous Metropolitan University and was twicely Guest Researcher at the Center for Advanced Research in Biotechnology, NIST, Maryland, USA, where she made her research on antibodies cristalographic studies and enzymes of industrial interest. From 1997 she has been responsible of the National Lab of Structure and Macromolecules- IQ, former University Lab of Proteín Sctucture. As pioneer on protein cristallography in Mexico her research group is focused in diverse projects of structural biology with international impact.

Keywords
Allergy, allergen, antibody, crystallography, epitope, structural biology.

Abstract of the conference
Human type 1 hypersensitivity or allergic diseases, such as rhinitis, are mediated by allergen-specific IgE antibodies produced in susceptible individuals after allergen exposure. IgE antibodies bound to high affinity receptors on the surface of effector cells trigger an allergic response by interacting with recognition sites (conformational epitopes) on the allergen surface. This type of epitopes is important for inhaled allergens, which reach the respiratory system mostly in their original globular structure. An efficient treatment for allergic diseases is specific allergen vaccination; therefore, the development of harmless vaccines would enable a more general use of the treatment. One of the problems that we have addressed is the structural study of allergenic proteins from different sources, such as rubber tree latex, maize and fruits. In general, these proteins participate in the defense mechanisms of plants and they are also involved in cross-reactivity reactions. Knowledge of the three-dimensional structure of these allergens and allergen-antibody complexes facilitates epitope mapping and enables a rational approach to the engineering of molecules with reduced IgE binding. We recently determined the crystal structure of the complex between the Hevea allergen profilin (Hev b 8) and the Fab fragment of an IgE monoclonal antibody at 2.9 Å resolution. We also determined the KD of the complexes IgE-profilin (100 nM) and Fab-profilin (1.7 M) using biolayer interferometry and we found that the KD of the fragment is two orders of magnitude lower than the complete antibody. Moreover, in vitro investigations using the murine IgE and rat basophilic cells showed that binding affinity and dimerization are important to triggering the allergic response. The use of this data can pave the way for the use of recombinant allergens, well characterized natural allergens or antibodies in diagnosis and immunotherapy tools.

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