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**CATERPILLER and Plexin: Genomic identification of new gene families
in the immune system**

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In the past few years, we used two genomic approaches to identify new pathways in the immune system, and identified a host of new genes. The CATERPILLER (also known as nucleotide-binding domain, leucine-rich region containing, NLR) gene family was identified based on the structural analysis of CIITA, the master regulator of MHCII genes. CIITA contains an N-terminal acidic domain, a mid-terminal nucleotide-binding domain and a C-terminal leucine rich region. A scanning of the human and mouse genomes identified 20-30 genes encoding NBD-LRR structure. This gene family is preserved in sea urchins and plants, and in the latter constitutes an important family for host defense against pathogen-derived molecules. A discussion of this family as positive and negative regulators of inflammatory and immune responses will be discussed.

In scanning for new genes that are regulated by CIITA, we identified the Plexin-A1 protein as a transcriptional target of CIITA. The regulation of Plexin-A1 and MHCII by CIITA is achieved by somewhat different modes, although CIITA directly regulates the Plexin-A1 promoter. The function of Plexin-A1 lies in DC-T cell interaction, and the ablation of Plexin-A1 expression in DC disrupted the activation of T cells, the mobilization of actin in DC and the activation of Rho. This shows a non-MHCII gene that is the target of CIITA and plays a crucial role in antigen presenting cells.

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