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IN BRIEF

STRUCTURE

CD1d–lipid-antigen recognition by the semi-invariant NKT T-cell receptor.

Borg, N. A. *et al. Nature* **448**, 44–49 (2007)

In this paper, the authors resolve the first crystal structure of the semi-invariant T-cell receptor (TCR) typically expressed by natural killer T (NKT) cells in complex with the glycolipid α-galactosylceramide (α-GalCer) bound to CD1d. Their analysis reveals several striking differences in how TCRs recognize lipid versus peptide antigens. First, the semi-invariant TCR docks onto α-GalCer–CD1d in a parallel rather than diagonal orientation. Second, the semi-invariant TCR binds the extreme end of the CD1d-binding cleft, such that only the TCR α-chain, and not the β-chain, makes contact with the antigen, which explains why a particular α-chain is required for recognition. Third, the semi-invariant TCR shows little structural variation on ligation, thereby favouring a 'lock-and-key' type interaction. Finally, clues to the diversity of lipid-antigen recognition come from the orientation of the glycolipid α-galactose head group and a flexible complementarity-determining region 3 (CDR3) in the TCR β-chain.

T HELPER CELLS

BOB.1/OBF.1 controls the balance of TH1 and TH2 immune responses.

Brunner, C. *et al. EMBO J.* **26**, 3191–3202 (2007)

OBF1 (octamer-binding-transcription-factor-binding factor 1; also known as OCA-B and BOB1) is a lymphoid-specific transcriptional co-activator that is important at several stages of B-cell development, and is inducible by co-stimulation in T cells. To investigate the specific role of OBF1 in T cells, Wirth and colleagues analysed T-cell development and function in mice lacking OBF1. *Obf1*$^{-/-}$ mice showed increased susceptibility to *Leishmania major* infection. These mice had specific defects in both T helper 1 (T_H1) and T_H2 cells, such that T_H1-type cytokine expression was decreased, whereas T_H2-type cytokine production was increased. OBF1 regulates the expression of the transcription factor PU.1, which is probably responsible for indirectly controlling the increased T_H2-type cytokine production. These results show a new role for OBF1 in regulating the balance of T_H1- versus T_H2-cell-mediated immunity.

IMMUNOGENETICS

A genome-wide association study for celiac disease identifies risk variants in the region harboring *IL2* and *IL21*.

van Heel, D. A. *et al. Nature Genet.* **39**, 827–829 (2007)

Coeliac disease is a common inflammatory condition of the small intestine induced by dietary wheat, rye and barley. However, despite high heritability, no genetic risk factors have been identified, other than an association with the MHC loci. Here, genetic variation in a region encompassing interleukin-2 (*IL2*) and *IL21* is shown to be associated with coeliac disease. The authors carried out a genome-wide association study, testing more than 300,000 single-nucleotide polymorphisms in 778 individuals with the disease and in 1,422 controls, to reveal a genomic region (on chromosome 4q27) that is associated with this disease. This region contains four genes (one of unknown function); of these, *IL2* and *IL21* look to be the most likely candidates for the causal susceptibility gene, although further studies are required to determine how they may be involved in the disease.