

## T CELL RECOGNITION

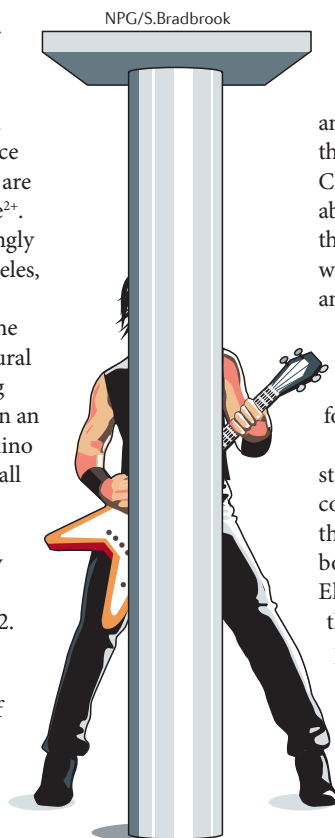
## A hidden heavy metal

Industrial workers who handle the metal beryllium commonly develop chronic beryllium disease (CBD), which is a lifelong CD4<sup>+</sup> T cell-mediated inflammatory lung condition. T cell recognition of this metal depends on Be<sup>2+</sup>-capturing peptides that bind MHC class II molecules, but exactly how T cell receptors (TCRs) recognize beryllium has been unclear. Now, Kappler and colleagues show that the TCR does not interact directly with the Be<sup>2+</sup> cation but instead recognizes changes to the surface of MHC class II molecules that are induced by internally bound Be<sup>2+</sup>.

Susceptibility to CBD is strongly associated with MHC class II alleles, such as HLA-DP2, that have a glutamic acid at position 69 of the  $\beta$ -chain ( $\beta$ 69E). Previous structural analysis with HLA-DP2-binding peptides showed that  $\beta$ 69E lies in an acidic pocket with two other amino acids ( $\beta$ 26E and  $\beta$ 68E) and that all three residues are important for Be<sup>2+</sup> presentation. In addition, the structure showed a relatively large gap (11 Å) between the peptide backbone and HLA-DP2.

Kappler and co-workers decided to test whether two conserved acidic amino acids of Be<sup>2+</sup>-capturing peptides might influence the ability of the MHC pocket to bind Be<sup>2+</sup>.

“the presence of Be<sup>2+</sup> led to conformational changes”



They examined two mutated forms of a complex between the Be<sup>2+</sup>-capturing peptide mimotope-2 (M2) and HLA-DP2: one complex in which the two conserved acidic amino acids of M2 were changed to nearly isomorphous amides, and another complex in which the HLA-DP2 glutamic acid at  $\beta$ 69E was changed to lysine, which is the amino acid found at position 69 in MHC class II alleles that are not associated with CBD. The wild-type and mutated complexes were tested for their ability to stimulate Be<sup>2+</sup>-specific CD4<sup>+</sup> T cells in the presence or absence of Be<sup>2+</sup>. The authors found that the T cells only responded to the wild-type HLA-DP2–M2 complex and only in the presence of Be<sup>2+</sup>. Thus, both  $\beta$ 69E in HLA-DP2 and the acidic side chains of the conserved amino acids of M2 were required for Be<sup>2+</sup> presentation.

Next, the authors solved the structures of the HLA-DP2–M2 complex in the absence of Be<sup>2+</sup> and the HLA-DP2–M2–Be<sup>2+</sup> complex bound by a Be<sup>2+</sup>-specific TCR. Electron density mapping showed that the side chains of the M2 peptide entered the acidic MHC pocket both before and after the addition of Be<sup>2+</sup>. The presence of Be<sup>2+</sup> led to conformational changes in the acidic pocket, which indicates that Be<sup>2+</sup>

was bound within the pocket. Furthermore, the electron density map suggested the presence of an additional large atom, so the authors included Na<sup>+</sup> in their structural model. The structure revealed two unexpected features of the complex: first, the Be<sup>2+</sup> cation itself is bound; and second, neither Be<sup>2+</sup> nor Na<sup>+</sup> are accessible on the surface of the complex. Thus, Be<sup>2+</sup>-specific TCRs must recognize changes in the surface of the complex that are induced indirectly by Be<sup>2+</sup> and Na<sup>+</sup>.

In summary, this study shows that metal ions, such as Be<sup>2+</sup>, can join the internal structure of a peptide–MHC complex and indirectly cause structural and biophysical changes to the surface of the complex that is recognized by the T cell. Interestingly, the immune response to beryllium not only resembles allergic hypersensitivity — due to the metal ion causing an allergic reaction — but also resembles autoimmunity, as the immune system mounts a response against a self-peptide. Furthermore, particular MHC class II alleles can confer susceptibility to autoimmune disease and this is also the case for CBD.

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