Kill or Be Killed
Edward M. Behrens and Randy Q. Cron

J Immunol 2015; 194:5041-5043;
doi: 10.4049/jimmunol.1500774
http://www.jimmunol.org/content/194/11/5041

Supplementary Material
http://www.jimmunol.org/content/suppl/2015/05/15/194.11.5041.DC1

References
This article cites 38 articles, 10 of which you can access for free at:
http://www.jimmunol.org/content/194/11/5041.full#ref-list-1

Why The JI? Submit online.
• Rapid Reviews! 30 days* from submission to initial decision
• No Triage! Every submission reviewed by practicing scientists
• Fast Publication! 4 weeks from acceptance to publication

Subscription
Information about subscribing to The Journal of Immunology is online at:
http://jimmunol.org/subscription

Permissions
Submit copyright permission requests at:
http://www.aai.org/About/Publications/JI/copyright.html

Email Alerts
Receive free email-alerts when new articles cite this article. Sign up at:
http://jimmunol.org/alerts
Kill or Be Killed
Edward M. Behrens* and Randy Q. Cron†

emphagocytic lymphohistiocytosis (HLH) refers to a group of rare genetic disorders characterized by a massive proinflammatory cytokine storm resulting in coagulopathy, CNS dysfunction, increased hemophagocytosis, pancytopenia, multiorgan failure, and death (1). Defects in cytolytic function are typical in the immune cells of these infants, and without early aggressive immunosuppression and bone marrow transplantation, familial HLH (fHLH) is a uniformly fatal condition that affects 1 in 50,000 live births (2). Even with bone marrow transplantation, 5-y survival rates are ~50% (3). Most of the familial cases of HLH are associated with autosomal recessive disorders. The first of these genes to be identified as a cause of fHLH was perforin (4).

In 1999, Stepp et al. (4) connected two important facts, that defects in cytotoxic function had been regularly associated with fHLH, and that the 10q21–22 locus had been consistently linked to multiple families with fHLH in their pedigrees. They hypothesized that the missing link connecting these two associations was that the gene encoding perforin, a critical effector molecule of cytotoxic function, mapped to the 10q21–22 locus. In their landmark paper (4), they went on to more finely map perforin to the centromeric end of the 10q21 locus, and then showed that eight of eight unrelated fHLH patients studied with 10q21–22 linkage had mutations in their perforin genes. To demonstrate that perforin-mediated cytotoxicity was indeed defective in these patients, they used a Fas-deficient target cell in combination with a Fas-blocking Ab in an anti-CD3 Ab-mediated cell killing assay to eliminate the possibility that Fas–Fas ligand interactions might confound killing measurements. T lymphocytes from patients harboring a nonsense mutation mediated no killing in this assay, and cells from patients with a missense mutation had dramatically reduced killing, suggesting that the genetic alterations in perforin in these patients did indeed result in loss of perforin-mediated killing. The authors then went on to demonstrate loss of perforin protein in these patients by immunofluorescence, showing no, or greatly reduced, perforin staining in granzyme B+ vesicles. Thus, the genetic lesions in perforin were linked to both protein level and function in these patients, supporting loss of perforin as a functional cause of fHLH in these patients.

The impact of the identification of perforin deficiency as a cause of fHLH can been seen in clinical medicine, as well as in fundamental immunology. Although defective NK cell cytotoxicity had been previously associated with fHLH (5), establishment of perforin deficiency as a causative genetic defect provided a mechanistic rationale for using NK cell cytotoxicity for clinical testing. This knowledge also provided a basis for the identification of other fHLH causative genes by offering clues to search for genes involved in perforin release when other genetic loci associated with disease in perforin-sufficient families were identified (6–9). These perforin-mediated cytolytic pathway gene products include other causes of fHLH (Munc13-4, Syntaxin 11, Munc18-2), as well as some immuno-deficiencies (e.g., Rab27a mutation in Griscelli syndrome type 2) (10). Consequently, the perforin-dependent cytolytic pathway employed by CD8+ T cells and NK cells has been further explored via natural mutations in the associated genes.

Armed with the concept that perforin deficiency must be linked with pathogenesis, a multitude of murine studies linked a CD8+ T cell–intrinsic perforin defect with excessive IFN-γ production and disease pathogenesis (11–14). The exploration of a perforin defect in NK cells has also demonstrated their role in HLH, and NK cell cytolytic activity and protection against HLH appear to be IFN-γ-independent (15). Most recently, it has been shown that defects in perforin-mediated killing of target cells by NK cells and CD8+ T cells and NK cells has been further explored via natural mutations in the associated genes.

Recognition that the rheumatic disease–associated macrophage activation syndrome (MAS) was similar in phenotype to fHLH has led to investigations that suggest depressed perforin function may also be found in this disorder (17–21). In addition to perforin deficiency, murine models of HLH have been explored in a variety of other mice deficient in various proteins in the cytolytic pathway (e.g., Munc13-4, Munc18-2). Indeed, there has been a recent suggestion that the degree of cytolytic dysfunction in both mice and humans correlates with the severity of HLH (22). Intriguingly, there appear to be single copy mutations in the gamut of fHLH genes in a substantial percentage of children and adults with the much more common disorders of secondary HLH and MAS (10, 23). This is blurring the genetic distinction between fHLH and both secondary HLH and MAS (10, 24).
Disclosures

The authors have no financial conflicts of interest.

References


