Some families seem to be afflicted with more than their fair share of chronic illness — and sometimes more than one. Why does a particular disease develop in some members of a given family, whereas other members fall victim to apparently unrelated conditions? A simple model is that exposure to environmental risk factors in a genetically susceptible host leads to disease. A particular combination of genetic and environmental risk factors (together with chance and bad luck) leads to one disease, and another combination of factors leads to a different disease. Because members of the same family have exposure to many of the same genes and environmental factors, they are more likely to have a related set of diseases, assuming that the diseases share common risk factors. Although this model is appealing, few bona fide examples of such shared risk factors have been documented to date.

In this issue of the Journal, Smyth and colleagues provide an answer to the question of why some families seem to have an undue susceptibility to two autoimmune diseases: type 1 diabetes mellitus and celiac disease.1 The study identified up to 15 genetic risk variants (or alleles) that contribute to both diseases and simultaneously demonstrated that 13 alleles were specific to one disease or the other. These observations support an emerging model of shared genetic risk factors for many common diseases, which may, in turn, identify previously unexpected biologic pathways that link diseases together.

In type 1 diabetes, which generally presents in childhood, the endocrine pancreas is attacked and destroyed by the body’s immune system. Celiac disease is also autoimmune in nature, but it is the small intestinal mucosa that is attacked, leading to a chronic enteropathy caused by intolerance to gluten.

For years, epidemiologic data have suggested that the two autoimmune diseases share a common cause.2 For example, the prevalence of celiac disease in children and adults with type 1 diabetes is higher than that in the general population by a factor of 5 to 10.3 However, it has been difficult to identify shared risk factors, whether genetic or environmental, to explain the observed increase in risk.

When Smyth et al. initiated their study, unequivocal associations had already been drawn between 8 alleles and a risk of celiac disease and between 15 alleles and a risk of type 1 diabetes outside of the major histocompatibility complex (MHC) region.4-6 However, only one allele had been shown to have a definitive association with both diseases (SH2B3 on chromosome 12q24). In their study, Smyth et al. asked two simple questions: Do alleles that are associated with a risk of celiac disease also confer a risk of type 1 diabetes, and do alleles that are associated with a risk of type 1 diabetes also confer a risk of celiac disease?

The answer was a resounding yes. Of the eight previously validated celiac disease alleles, at least four also contributed to a risk of type 1 diabetes (P<1.00×10−4), with one other allele demonstrating a highly suggestive association (P=0.002). Of the 15 previously validated alleles conferring an increased risk of type 1 diabetes, at least 2 contributed to a risk of celiac disease (P<1.00×10−4), with 5 showing highly suggestive associations (ranging from P=1.00×10−4 to P=0.05). If subsequent studies confirm the highly suggestive associations, then about half the genetic risk alleles that have been identified to date are shared between the two diseases. It is worth noting that two of the six shared alleles actually had opposite effects in the two diseases: the minor alleles of IL18RAP on chromosome 2q12 and TAGAP on chromosome 6q25 conferred protection against type 1 diabetes but susceptibility to celiac disease. One can begin to imagine how combinations of these alleles lead to celiac disease and other combinations lead to type 1 diabetes, with multiple possible combinations for both diseases.

Another finding of the study was the identification of a new risk allele for both type 1 diabetes and celiac disease: a 32-bp insertion–deletion variant in the CCR5 gene. This allele prevents the expression of the receptor on the surface of lymphocytes and other cells. Moreover, persons who
are homozygous for the mutant allele are highly resistant to infection with the human immunodeficiency virus (HIV). That is, the mutant CCR5 allele is protective against the development of both type 1 diabetes and celiac disease (two alleles are more protective than one allele) and also against HIV infection (but only when two copies of the mutant allele are inherited).

As this last observation highlights, the findings of Smyth et al. have implications beyond shared genetic causes of type 1 diabetes and celiac disease. Epidemiologic studies have suggested shared causes for other autoimmune diseases (e.g., systemic lupus erythematosus and rheumatoid arthritis), an observation that is supported by genetic data (e.g., the STAT4 gene). But epidemiologic data have also linked diseases that might not be considered similar at first glance. For example, type 2 diabetes is associated with a reduced risk of prostate cancer. Human genetics provides support for such epidemiologic observations, since an allele of HNFIB is associated with a risk of type 2 diabetes yet protection against prostate cancer.

Finally, what are the clinical implications of this research? The most important implication is likely to be the ability to define biologic pathways, many of which are unexpected, that cause disease. Over many years, such insight may lead to the development of novel therapies to treat, prevent, or even cure disease. In theory, a more immediate clinical application would be to screen for the presence of risk alleles in asymptomatic patients with one disease (e.g., celiac disease) to predict whether another disease (e.g., type 1 diabetes) is likely to develop. However, such screening is controversial, and the modest effect sizes of the alleles that were identified by Smyth et al. (an increase in risk of 10 to 20% per copy of the allele) are unlikely to add substantially to screening measures.

So there are indeed alleles that segregate in families and influence the risk of more than one disease. As we are beginning to understand, some combinations of alleles (together with environmental factors and chance) lead to celiac disease, and others lead to type 1 diabetes. There are going to be many combinations of these risk factors, and future research that is aimed at understanding these combinations and the underlying biologic pathways should lead to new insights into disease.

No potential conflict of interest relevant to this article was reported.

This article (10.1056/NEJMe0809719) was published at www.nejm.org on December 10, 2008.

From the Division of Rheumatology, Immunology and Allergy, Brigham and Women’s Hospital, Boston.


Copyright © 2008 Massachusetts Medical Society.