VITALS

Major Finding: Patients with type 1 diabetes are 10 times more likely to have an enterovirus infection, compared with patients without diabetes.

Data Source: A meta-analysis of 34 case-controlled studies using molecular diagnosis of enterovirus.

Disclosures: The investigators reported that they have no relevant financial relationships.

tablished type and eventual type 1 diabetes) was the outcome. This systematic review of 33 prevalence studies, involving 1,931 patients and 2,517 nondiabetic individuals.

They identified 34 studies – 9 involving patients with prediabetes (198 cases and 733 controls) and 25 studies of diabetes patients (1,733 cases and 1,784 controls).

Thirty studies used RT-PCR or in situ hybridization to detect enterovirus RNA; immunostaining for the enterovirus capsid protein vp1 on autopsy pancreas specimens was used on four studies. Most studies investigated children and adolescents up to age 16 years, though some included adults up to age 53 years.

The summary odds ratio of identifying enterovirus in patients with prediabetes compared with patients without diabetes was 3.7 (*P* less than .001). All but one of the 25 studies of patients with type 1 diabetes had odds ratios greater than one for patients with diabetes testing positive for enterovirus, with a summary odds ratio of 9.8 (*P* less than .001).

They used sensitivity analyses to test the robustness of the results by country and study quality.

In all, 19 studies were conducted in Europe. "There was some evidence for geographical differences; in non-European studies the odds ratio was 13.5, compared with 8.6 in European studies, though there was considerably overlap in the confidence intervals," they wrote.

In addition, "the odds of having an enterovirus infection in people with established diabetes (OR, 11) suggest that persistent enterovirus infection is also common among patients with type 1 diabetes." ■

Insulin Regulator Gene Tied to Type 2 Diabetes

FROM JAMA

Patients with type 2 diabetes were more likely to have genetic variations for a key protein regulating cells' insulin receptors, according to a multinational case-control study.

The variants' presence could serve as an early predictive marker of insulin resistance and type 2 diabetes, particularly in patients with a family history of the disease, the study's authors noted.

The investigators examined variations in the high-mobility group A1 protein, or HMGA1, a key regulator of insulin receptor gene expression. The protein's most frequent functional variant was found in 7.2% of the study's 3,278 Italian patients with type 2 diabetes, compared with 0.4% and 3.3% of two Italian control groups (2,544 and 784 patients) without diabetes, significant differences resulting in adjusted odds ratios of 15.8 and 2.0, respectively.

In addition, the variant was found in 7.7% of 970 U.S. case patients, compared with 4.7% of 958 U.S. control patients (adjusted odds ratio, 1.6), a significant difference, and in 7.6% of 354 French case patients vs. 0% of 50 French controls, also a significant difference, reported Dr. Eusebio Chiefari of the University of Catanzaro (Italy) and colleagues (JAMA 2011;305:903-12).

Three other functional variants also were observed in the Italian population, although those variants were not studied in the U.S. and French populations because of the relatively small sample sizes.

Overall, when all four variants were analyzed, nearly 10% of Italian patients with type 2 diabetes were found to have HMGA1 defects, compared with less than 1% of controls.

The four variants of the HMGA1 gene were also shown to be associated with decreased insulin receptor gene and insulin receptor protein expression.

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–Sharon Worcester