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Computers analyze environmental factors in diabetes

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Like many complex diseases, diabetes results from the interplay of genetic and environmental factors. To examine genetic risk factors, scientists pore over the human genome sequence. Environmental factors have been trickier to pin down because there is no way to evaluate them comprehensively.

Now, researchers at Stanford University present what they call an environment-wide association study (EWAS) or to systematically examine the contributions of hundreds of factors in the development of Type 2 diabetes. This "enviromics" approach, which mirrors genome-wide association studies, harnesses high-speed computers and publicly accessible databases.

The first-of-its-kind study, which was funded by the National Institutes of Health (NIH), appears in the May 20, 2010, issue of PLoS One. The article is titled An Environment-Wide Association Study (EWAS) on Type 2 Diabetes Mellitus.

The authors examined 226 separate environmental factors like nutrition and exposure to bacteria, viruses, allergens and toxins. They found that certain factors, notably a pesticide derivative and the environmental contaminant PCB, were strongly associated with the development of diabetes. Other factors, including the nutrient beta-carotene, served a protective role.

The scientists describe their work as a demonstration that computational

approaches can reveal as much about environmental contributions to disease as about genetic factors. They posit that the technique could be applied to other complex diseases like obesity, hypertension and cardiovascular disorders.

The authors acknowledge that many challenges remain, including the fact that, unlike the genome, "the environment is boundless."

Provided by National Institutes of Health

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