A first genome-wide association study in Dupuytren's disease.

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Abstract

Hypothesis: In order to understand the origin of Dupuytren's disease, a genome-wide association study (GWAS) will be performed to search for genes contributing to this disease.

Methods: In a large multicenter study in the Netherlands blood was collected for DNA isolation from approx. 1000 Dupuytren patients who visited the outpatient clinics of these hospitals. Patients are diagnosed by a qualified Plastic Surgeon. Genotyping of the samples will be conducted using Illumina CytoSNP-12 arrays. The genotyping data of 2000 individuals participating in a large population-based biobank ('Lifelines') will be used as controls. Cases and controls are of Caucasian origin.

Results: We are currently in the process of genotyping 1000 Dupuytren's disease cases. Control data has already been generated. Data analysis is expected to be completed by May 2010.

Summary: The first GWAS on Dupuytren's disease is currently ongoing. In order to confirm found genetic associations, replication is crucial. We are currently building a second cohort for replication studies.