EMIF Deliverable 3.6: 4 GWAS-identified SNPs for abnormal CSF abeta and tau and hippocampal atrophy

Executive summary

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The goal of this task was to identify single nucleotide polymorphisms (SNPs) associated with abnormal CSF Abeta and tau levels as well as SNP associated with hippocampal atrophy in MRI data generated by our project partners.

To investigate DNA sequence variants, we performed genome-wide SNP genotyping using the "Global Screening Array" (GSA; Illumina, Inc). The GSA covers includes ~700K genetic variants across the genome, including approx. 500 known AD-causing mutations; GSA-based genotyping and all subsequent data processing, QC and statistical analysis was performed at UZL.

The UZL-led GWAS subproject within WP3 provided in-depth genomic profiles for the EMIF-AD MBD study. In addition to replicating the well-known association between genetic variants within the APOE region on chromosome 19q, our GWAS analyses uncovered at least seven novel genomic regions associated with CSF- and MRI-based outcome phenotypes. These are currently subject to independent replication analyses. Current dissemination activities include preparing the above-mentioned genomics results for peer-reviewed publication. Subsequent analyses will focus on generating and disseminating multivariate results (especially by integrating genomics and epigenomics data) in these same EMIF-AD individuals.

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