APOE\textsubscript{e3} and APOE\textsubscript{e4} whereof the latter increases the risk of disease 4-15 fold in a dose-dependent manner whilst APOE\textsubscript{e2} appears to be protective. The biological mechanisms underlying the modified risk of disease in APOE\textsubscript{e2} and APOE\textsubscript{e4} carriers are not known. We previously showed that APOE\textsubscript{e4} carriers exhibit a prominent plasma apolipoprotein E (apoE) deficiency caused by a specific reduction of the apoE isoform. This apoE deficiency was not observed in cerebrospinal fluid. In cognitively intact APOE\textsubscript{e3}/e4 carriers an increased relative ratio of plasma apoE4 to apoE3 correlated to glucose hypometabolism and gray matter volume reductions in brain areas most often affected in AD. Hence, we speculate that peripheral apoE levels are linked to processes driving the risk of developing AD brain pathology. In order to determine the cause of the observed phenotype of plasma apoE deficiency in APOE\textsubscript{e4}-carriers we aimed to investigate the expression of different APOE alleles in liver biopsies from individuals with an APOE\textsubscript{e3}/e4 versus an APOE\textsubscript{e2}/e3 genotype. Methods: Liver biopsies from liver explants were received from n=3 APOE\textsubscript{e3}/e4 and n=3 APOE\textsubscript{e2}/e3 carriers who had undergone liver transplantation at the Karolinska University Hospital in Sweden. Total RNA (\geq 80\% in DV200 score) was isolated according to routine laboratory methods and used for RNA sequencing employing the high-throughput Illumina platform. Paired-end sequencing reads were aligned to the human reference genome (hg19), using TopHat, and gene counts for expression determined using HTseq-count. Differential expression between the genotype groups was calculated using DEseq2. Results: Preliminary analyses revealed differential expression of n=624 genes between individuals with an APOE\textsubscript{e3}/e4 versus an APOE\textsubscript{e2}/e3 genotype. Conclusions: In total n=624 genes are differentially expressed in livers from APOE\textsubscript{e3}/e4 versus APOE\textsubscript{e2}/e3 carriers. Further analyses will reveal the identity of the differentially expressed genes and whether there is a specific difference in the expression of APOE alleles that could explain the observed APOE\textsubscript{e4} related plasma apoE deficiency.

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**CALCULATING POLYGENIC RISK FOR INDIVIDUALS WITH SPORADIC EARLY ONSET ALZHEIMER’S DISEASE**

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**Background:** Sporadic early onset Alzheimer’s disease (sEOAD) exhibits the symptoms of LOAD but lacks the familial aspect of the early onset familial form. The genetics of AD shows APOE\textsubscript{4} to be the biggest genetic risk factor, however AD is a complex disease involving different genetic loci, with around 30 of these currently known. Polygenic risk scores (PRS) accumulate the total risk of a phenotype in any individual based on variants present in their genome. We determined whether sEOAD cases have a higher PRS compared to controls. **Methods:** PRSice is a program that generates scores for individuals in a target dataset based on variant information from a base dataset. The target dataset consisted of 408 cases and 436 controls, genotyped on the NeuroXchip. The base dataset was collated by the IGAP consortium, with significance values from 17,008 LOAD cases and 37,154 controls. PRS were generated at significance thresholds, in increments of one thousandth. The best threshold for generating scores was identified using Nagelkerke’s \textsuperscript{2}. Sensitivity, specificity, and area under the curve (AUC) were calculated to estimate predictive power. Sex, APOE\textsubscript{2} and APOE\textsubscript{4} genotypes were used.