Plasma cell-free RNA profiling of Vietnamese Alzheimer's patients reveals a linkage with chronic inflammation and apoptosis: a pilot study

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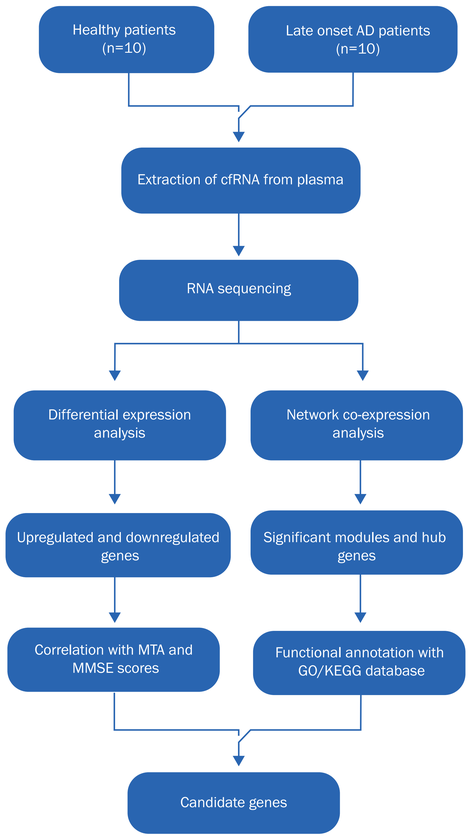
Plasma cf-RNA can address Alzheimer's diagnostic challenges

Circulating cell-free RNA (cf-RNA) is considered a potential biomarker for early diagnosis of Alzheimer's Disease (AD) as it can construe the genetic expression level, giving insights into the pathological progress at the outset.
By inspecting molecular changes in AD, these procedures can predict the pathology in advance, aiding the quality of life of Vietnamese in the rural area.

→ Goals

Identify the key drivers of expression changes in cfRNA between Alzheimer's patient and healthy controls
Examine whether the cfRNA transcripts significantly correlate with clinical indications of Alzheimer's disease

Transcriptomic profiling of plasma cf-RNA



Differential expression analysis shows contrast in transcriptomic profile of Alzheimer's patients

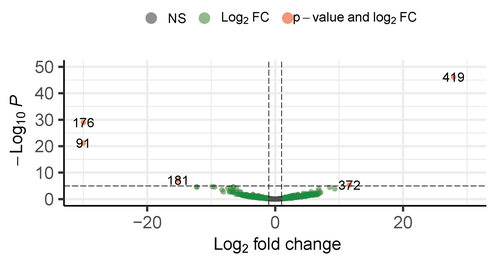


Figure 1: *Volcano plot of the correlation between the log2foldchange and the adjusted p-value of 533 detected genes (grey - p > 0.05, green - p < 0.05; orange - p < 0.0001 and abs(log2foldchange) > 20)*

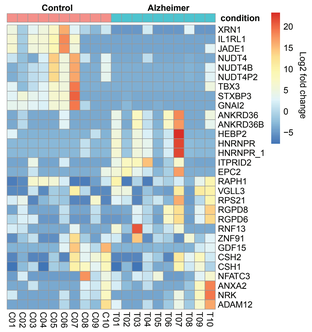


Figure 2: *Clustered heatmap of expression of the top 30 genes with the highest variance*

Co-expressed gene modules are associated with potential AD processes

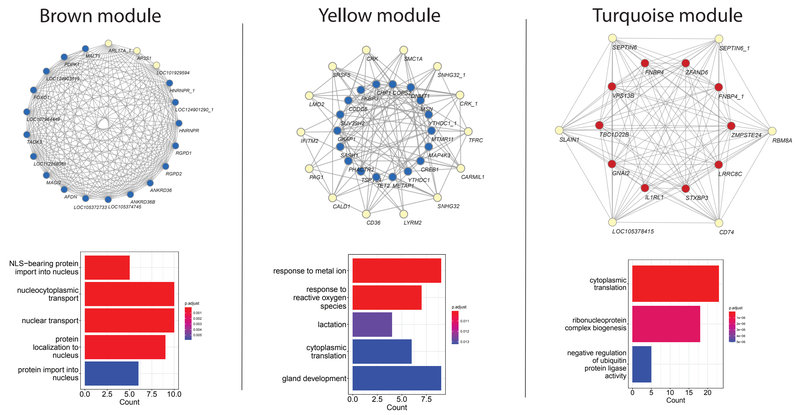


Figure 4: *Network visualization of key genes in each module and their associated Gene Ontology annotations.*

Significant genes are associated with immune response and neuronal death

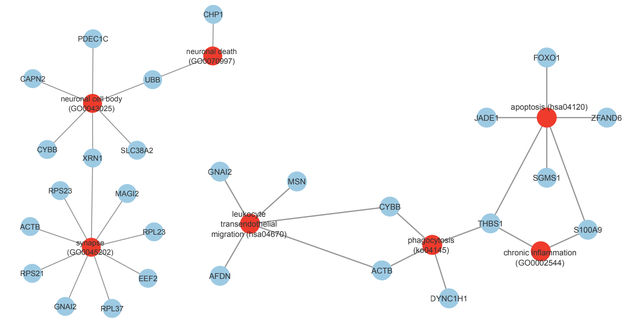


Figure 3: *Visualization of genes associated with neuronal activity and immune response*

Significant genes are correlated with Alzheimer's clinical indicators

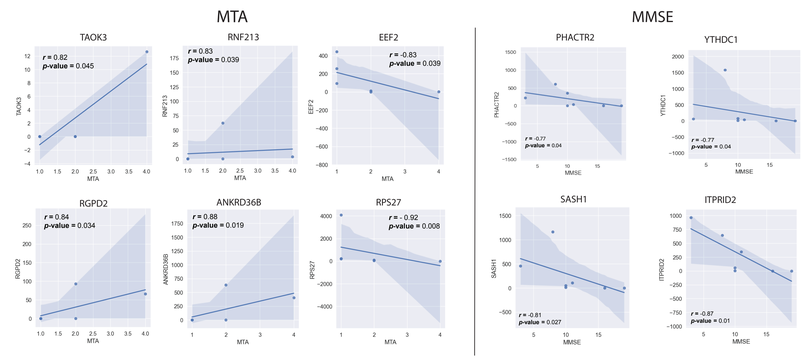


Figure 5: *Correlation between MTA-score and the normalised transcript counts (median of ratios)*

Figure 6*: Correlation between MMSE-score and the normalized transcript counts (median of ratios)*

Conclusions

(1) We have identified some gene clusters that are potentially related to the pathogenesis of Alzheimer's.
(2) We have identified some candidate genes (YTHDC1, SASH1, ITPRID2. ANKRD36B, TAOK3, EEF2, RNF213) that are highly correlated with Alzheimer's disease clinical indications.

Limitations & Future directions

Small sample size (n=20) -> Need to validate the identified candidate genes with a larger cohort of samples to ascertain their value in early diagnosis of Alzheimer's disease

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