Presentation title:

An exploratory study of serum proteomics comparing subjects with treatment-resistant hypertension to controlled hypertension.

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Key Words:

Proteomics, Treatment-Resistant hypertension, Systemic inflammation, endothelial dysfunction

Introduction:

The mechanism of treatment-resistant hypertension (TRH) is not fully understood. This study aimed to identify any measurable differences in protein abundance between TRH and controlled hypertension (CH) subjects using serum proteomics, which may indicate a possible mechanism.

Methods:

The study samples were obtained from an existing observational study cohort involving CH and TRH; venous blood samples were previously stored at -80°C with appropriate consent and ethical approval. TRH was defined as blood pressure (BP) of ≥140/90 mmHg on ≥3 antihypertensive agents or controlled BP (≤140/90 mmHg) taking ≥ 4 agents. CH was defined as BP ≤ 140/90 mmHg on ≤3 agents. The study was conducted in two phases: the Discovery Phase, where 60 samples of matched group's (CH n=30, TRH n=30) were depleted from the highly abundant proteins before undergoing trypsin digestion. Liquid Chromatography Mass Spectrometry analysis was used. The Validation Phase included 140 candidates (CH n=82, TRH n=58). Data were corrected for batch effect, and the results were statistically analysed using an independent T-test; P value <0.05 was considered statistically significant. Gene Ontology (GO) description was used for the functional description of the proteins.

Results:

The two groups showed a significant difference in the expression of 15 proteins: Alpha 1B glycoprotein, Alpha 1 antichromotrypsin, Leucine-rich alpha 2 glycoproteins, Inter alpha trypsin inhibitor heavy chain H3, Lumican, Complement component C9, Coagulation factor XII, Contactin-1, Lysozyme C, Fibulin, Glutathione peroxidase, Insulin-like growth factor (IGF) binding protein 3, IGF binding protein complex acid-labile subunit, Vitronectin and Vascular cell adhesion protein 1. GO analysis suggests that some of the above proteins are involved In inflammatory process pathways and cell adhesion.

Conclusions:

This study showed significant differences in protein expression between TRH and CH using serum proteomics which may indicate a role for endothelial dysfunction and inflammation in the pathogenesis of TRH.