Results: Twenty-one SNV were genome-wide significant ($P < 5x10-8$), of which six are unreported in literature to date. Three SNV highlight novel BP loci: rs9678851 (missense, SLC4A1AP), rs7437940 (AFAP1), and rs1055144 (7p15.2). In addition, we identified three potentially independent BP-associated SNV (rs13303 (missense, STAB1), rs3416322 (missense, SYNPO2L), rs2729835 (missense, LACTB)) at known loci. Two of the new loci and three SNV at known loci are associated with expression levels of nearby genes, and SNV at four loci are associated with other traits.

Conclusions: These new findings yield further new candidate genes for hypertension. Follow-up studies to define the causal variants and genes underlying these associations may highlight novel proteins and pathways to target to lower BP and reduce cardiovascular risk.

P – 2 MicroNRA miR-199a-5p is a marker of blood pressure in premature cardiovascular disease patients homozygous for the methylenetetrahydrofolate reductase (MTHFR) C677T polymorphism

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Introduction: MicroRNA are small, non-coding ribonucleic acid RNA which are potentially valuable markers of cardiovascular disease (CVD) risk, including hypertension. This novel investigation aims to profile circulating serum concentrations of microRNAs in premature CVD patients to identify microRNAs that correlate best with hypertension.

Methods: Serum samples from an existing cohort of 75 premature CVD patients were analysed for expression of 68 CVD-related microRNAs. Patients had been screened for the methylene tetrahydrofolate reductase (*MTHFR*) gene polymorphism C677T, a risk factor for hypertension. Samples had been collected at baseline and following intervention with riboflavin, co-factor for the MTHFR enzyme, as part of a placebo-controlled double-blind, randomized trial. The associations between miRNA expression and blood pressure at baseline and post-intervention were investigated. Comparisons of data between homozygous normal CC and homozygous variant TT *MTHFR* genotype groups, and in response to intervention, were assessed using analysis of variance (ANOVA), Pearson's correlation and corrected t-test statistical analyses.

Results: MicroRNA expression was successfully detected and quantified in all samples. At baseline miR-199a-5p expression was inversely correlated ($r = -0.51$; $P < 0.001$) with blood pressure in patients with the *MTHFR* TT genotype only. The decrease in blood pressure in those TT genotype patients who responded to riboflavin intervention was inversely correlated with miR-199a-5p expression ($r = -0.55$; $P < 0.05$). *In vitro* and *in silico* analysis of miR-199a-5p function was also performed.

Conclusions: This is the first study to identify miR-199a-5p as a potential serum biomarker of blood pressure in a cohort of at-risk CVD patients. We propose that serum profiling of microRNA could aid early prediction of CVD and may lead to improved treatment regimes.

P – 3 Ambulatory blood pressure monitoring (ABPM) in healthy adults stratified by methylenetetrahydrofolate reductase (MTHFR) genotype

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Introduction: The C677T polymorphism in the gene encoding the folate metabolising enzyme methylenetetrahydrofolate reductase (MTHFR) is associated with hypertension. Supplementation with riboflavin (the cofactor for MTHFR) can lower blood pressure (BP) in homozygous individuals (i.e. *MTHFR* 677TT genotype) as demonstrated previously in randomised controlled trials conducted at this centre (McNulty *et al*, 2017). To date, however, studies investigating the association between this genetic risk factor and BP have relied on clinic BP measurements. The aim of this study was to evaluate 24-hr blood pressure patterns and related parameters using ambulatory blood pressure monitoring (ABPM) in adults stratified by *MTHFR* genotype.

Methods: Adults with the homozygous variant TT genotype were age-matched to those with homozygous normal CC or heterozygous CT genotypes. All participants ($n = 167$) had clinic BP and ABPM measured, in accordance with NICE clinical guidelines (CG127).

Results: Clinic systolic BP was significantly higher in participants with the TT v CC/CT combined genotypes 134.6 mmHg vs 126.1 mmHg, $P = 0.001$. ABPM parameters were also significantly higher in participants with the TT v non-TT genotypes: 127.5 mmHg vs 124.4 mmHg, $P = 0.05$ for mean daytime systolic BP; 111.6 mmHg vs 107.1 mmHg $P = 0.006$ for nighttime. Daytime mean arterial pressure ($P < 0.001$) and heart rate ($P = 0.044$) were also significantly