Reduced DNA methylation the human kidney is associated with increased blood pressure

Ingrid Wise[1] Maciej Tomaszewski[2] Fadi Charchar[3*]
1 & 3. Faculty of Science & Technology, Federation University, Victoria, Australia. Contact: +353-276-098.
* Corresponding author

Background and aims: There is increasing evidence that epigenetic modifications such as DNA methylation (addition of a methyl group to DNA (5mC) that leads to altered gene expression) is important to the development of common complex cardiovascular diseases. A recent study found that DNA methylation of blood cells is associated with blood pressure (BP) (1). So far there has been no studies of epigenetic changes in the kidney, which is a key organ in BP regulation and the development of hypertension. The aim of this study was to examine associations between BP and the global methylation profiles of the kidney and blood.

Methods and results: We used 93 human renal tissue samples from the TRANScriptome of RenaL HumAN TissueE (TRANSLATE) Study. All samples were collected from healthy, unaffected by cancer pole of the kidney after elective unilateral nephrectomies. DNA was extracted using the DNeasy Qiagen kit according to the protocol from blood and kidney samples. Global methylation was measured by ELISA assay to determine the percentage of 5mC in all DNA samples. A significant negative relationship was found between renal 5mC percentages and systolic (SBP) and diastolic (DBP) blood pressure (SBP r = -0.25, P = 0.018, DBP r = -0.32, P = 0.002). This correlation was also evident when BP is corrected for effects of antihypertensive medications (adjusted SBP P = 0.046, adjusted DBP P = 0.009). Comparatively, there was no significant relationship between 5mC percentage and BP in DNA extracted from peripheral blood leukocytes.

Conclusions: We found a significant negative correlation between the percentage of 5mC and BP in the renal DNA samples indicating that reduced DNA methylation leads to increased blood pressure. No such relationship was established in the leukocyte DNA, indicating that blood may not be a good template for analysis of epigenetic modifications in the hypertensive population.

1. Kato, N.; et al. *Nat Genet* **2015**,