



Fadi Joseph Charchar PhD FAHA

Robert HT Smith Chair in Cardiovascular Sciences.

Faculty of Science and Technology, Federation University, and Department of Physiology, University of Melbourne, Australia.

Department of Cardiovascular Sciences, University of Leicester, UK.

The World of HyperOmics

Advances in the Omic fields are bringing personalized medicine within reach in many fields of medicine. Many researchers have investigated the genomics of blood pressure regulation, hoping to find answers to hypertension's molecular mysteries.

Some studies have struck gold with findings such as the potassium (K(+)) channel KCNJ5 gene in adrenal aldosterone-producing adenomas and rare hereditary hypertension. But for the common or garden variety of hypertension, the genetic picture is far from complete. We have come a long way in understanding the genome itself in the last few decades. In the late 80s and early 90s genetic association studies relied on a few hundred mutations (markers in the genome) and a few hundred subjects.

We can now utilize a few hundred thousand mutations and studies are conducted in thousands of subjects. In 2011 a landmark meta-analysis study described 16 novel regions in the genome associated with BP regulation¹. Recent large meta-analysis studies found 662, 303 and 314 blood pressure-associated loci respectively. Interestingly, although the sample sizes are very large the identified loci still explain a small percentage (<10%) of the blood pressure variance. There is no denying that the findings present a good basis for studying novel blood pressure pathways and molecules, but for many researchers in the field we are left wondering where to now? Holding my crystal ball, which is often as accurate as a young Harry Potter's wand, here are my predictions.

- 1) Mega genome-wide association studies. Many in the field question whether these studies would reveal more loci.
- 2) The functional validation of many of the loci, which is not a small task. With the advent of gene editing this task is much more realistic.
- 3) Over the last 10 years, next generation sequencing (NGS) technologies have revolutionized genome analysis; we can now sequence the whole genome of an individual

within a couple days for less than \$5,000. NGS could be used to create hi-fi association studies. NGS also promises to characterize hypertension and translate the power of genomic research into the clinic.

- 4) Our group and others have shown the importance of non-coding RNA5 and epigenetic regulation of blood pressure. In particular microRNA which are potent cellular regulators. These molecules remain understudied in blood pressure regulation so I expect to see a lot more on these in the future.
- 5) Proteomics will follow in the footsteps of genomics and, in combination with other omics techniques will provide deeper information into the cause of hypertension.
- 6) Surprise discoveries about our genome, open to the imagination.

-Fadi Charchar

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