

## Translating Aboriginal genomics — four letters Closing the Gap

TO THE EDITOR: Rare diseases (RD) are typically complex, chronic, often multisystem, and frequently genetic disorders associated with significant morbidity and mortality. They affect up to 6–8% of the population and 30% of Australians with RD waited between 5 to 30 or more years for a diagnosis.<sup>1</sup> There are now game-changing clinical genomic approaches that are reducing these diagnostic odysseys. However, parallel to hitherto unachieved improvements in RD diagnosis is the known and recently demonstrated risk<sup>2</sup> that Indigenous Australians will not enjoy the same diagnostic opportunities as non-Indigenous Australians.

This health care gap is due to the absence of Indigenous genomic reference information. Genomic references provide a context for understanding the normal variation in the four biological letters — A, C, T and G — of our DNA code. They are fundamental to determine whether genetic variants identified in an individual are disease causing (pathogenic) or otherwise. Rare variations are often population specific and rare genetic variants are disproportionately important as the cause of rare and other diseases.<sup>3</sup> Therefore, reference genomic data representative of the population to which the individual belongs are crucial for separating real from spurious findings.

In response to a delay in diagnosing an RD in an Aboriginal family in remote Western Australia — due to the lack of a suitable genomic reference — an initial solution was to deal with this urgent clinical need. Whole exome sequencing had been performed in Aboriginal people in WA, from locally relevant regions, on research cohorts unselected for RD. In these studies, which proceeded with deep culturally appropriate community engagement and governance,<sup>4</sup> participants agreed to deposition of their genomic data in a public database. In accordance with participant consent, and to prevent a potential diagnostic delay and health care inequity, applications can now be made to access these data for clinical diagnostic work in the health system. This has been applied to clinical genomic test interpretation in WA.

This rapid clinical translation is a first step to closing the clinical genomic gap and must be followed by the generation of further Indigenous reference data that include other Australian regions. ■

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doi: 10.5694/mja16.00513

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References are available online at [www.mja.com.au](http://www.mja.com.au).

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