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Whole genome or exome sequencing: An individual insight

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Focusing on parts rather than the whole, when it comes to genome sequencing, might be extremely useful, finds research in BioMed Central's open access journal *Genome Medicine*. The research compares several sequencing technologies in the same individual with Charcot-Marie-Tooth disease (CMT), and shows that sequencing the coding regions alone at high depth of coverage can identify the genetic variation behind this disease, and was also able to resolve previous ambiguities.

Next generation sequencing for understanding human DNA variation and genetic disorders is advancing in leaps and bounds. Whole genome sequencing reads all of an individual's DNA, whereas exome sequencing captures only the parts of the DNA which code for proteins. Exome sequencing is faster and cheaper, but concerns have previously been raised that it misses important information.

A team from Baylor College of Medicine led by Prof. James Lupski and Prof. Richard Gibbs compared several different exome and whole genome sequencing technologies on DNA from the same person with CMT. Prof. Jim Lupski explained, "Both methods were able to find the same 12 variants which affect cellular response to specific drugs such as betablockers, warfarin and the anti-cancer drug paclitaxel, and identify novel CMT-associated mutations in SH3TC2 that encodes for a protein with a role in peripheral nerve myelination."

Exome sequencing had fewer false positives, and a greater sensitivity due to the higher coverage achieved when focusing only in a small

fraction of the genome. Consequently it was able to correctly identify nucleotides which were ambiguous when using whole genome sequencing at lower coverage, and so clarify whether they were associated with CMT or not.

Prof. Richard Gibbs commented, "The higher coverage afforded by focusing on the exome at approximately 120x for clinical exomes allows greater precision of exome sequencing making this a superior approach, rather than a shortcut, to find which people might respond to a particular therapy or to define who has a specific disease."

Provided by BioMed Central