GenPro publishes EpiMarker feasibility study revealing distinct epigenetic signature of Parkinson's Disease in blood.

At a functional level, we can trace patterns in differential methylation back to pathways and genes that support hypothesis- level ideas about potential roles of DNA methylation in altered molecular, cellular and physiological activities of PD. These “signals” are evident in blood even though they convey a distinct neurodegenerative signature. Even with a small pilot cohort, we statistically recover epigenetic profiles that discriminate between healthy and PD blood profiles, with a functional relevance in many of the comparative differences. The quantitative sensitivity and repeatability (across patients) of the DNA methylation metrics presented here are substantial enough to warrant further exploration with larger patient cohorts and with the goal of trying to establish a blood-based marker screening test for early age Parkinson’s Disease.

Overall, the results of this profiling work reveal a large number of differentially methylated CpG sites that can be identified with high statistical confidence. With a larger subject cohort, these results would support the design and development of a targeted panel assay of select CpG sites using qPCR measurement platforms. Ultimately, targeted panels for detecting shifts in site-specific CpG methylation could make it possible to diagnose early onset stages of impending diseases or disease risks by identifying pre-symptomatic genomic changes via epigenetic mechanisms. The paper, *"Epigenetic DNA Methylation Profiling with MSRE: A Quantitative NGS Approach Using a Parkinson's Disease Test Case"*, is an open access publication and available at Frontiers in Genetics 2016:00191.

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