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NEXT Molecular Analytics Announces Publication of Pharmacogenomics Paper.

Chester, VA. NEXT Molecular Analytics (NEXT) announces the publication of a large pharmacogenomics clinical study involving Next Generation Sequencing (NGS) of CytochromeP450 genes from different ethnic populations. The work, lead by three scientist who now work at NEXT (Katie O'Hanlon, Greg Meyers and Tom Reynolds), represents one of the largest studies of its kind. The study, which was performed from 2013-2014 at a previous employer, is entitled "Next Generation Sequencing Reveals Disparate Population Frequencies Among Cytochrome P450 Genes: Clinical Pharmacogenomics of the CYP2 Family". It will be published in the upcoming issue of the International Journal of Computational Biology and Drug Design**.** The paper examines the distribution of genetic polymorphisms and the predicted effect for several key members of the Cytochrome P450 family of drug metabolizing enzymes from over 30,000 subjects from various ethnic groups living in the USA using NGS technology. The scientists led the overall effort, provided critical analysis and oversight of the work, and are authors on the publication. Greg Meyers, currently COO and Co-founder of NEXT, provided the design of the NGS assays, working directly with scientists at Life Technologies, creating the first NGS clinical assay for Pharmacogenomics. Meyers also oversaw the bioinformatics and laboratory processing of the clinical samples. Katie O'Hanlon, currently a Senior Scientist at NEXT, was responsible for developing and validating the NGS assay as well as processing a large portion of the samples. Tom Reynolds, currently the President and a Co-founder at NEXT, is senior author on the paper and was responsible for the original concept of the study and participated in the design, analysis, and writing/editing aspects of the paper. Reynolds, O'Hanlon and Meyers also previously presented the work at a number of conferences including ION World in October 2013, and as a poster presentation at The American Society of Human Genetics in October 2013. This work highlights that genetic variation of key medication metabolizing enzymes is common within and between ethnic populations. The paper alerts physicians to the concept that there is truly no such thing as a normal patient when it comes to drug metabolism highlighting the fact that each patient is unique in their ability to process different medicines.