

## Next Generation Sequencing Arrives in West Virginia

Next Generation Sequencing (NGS) proceeds by massively parallel sequencing reactions. This enables rapid and relatively inexpensive sequencing of large amounts of DNA or RNA, such as entire genomes or transcriptomes,

The Marshall University Genomics Core has installed an Illumina HiSeq1000 Next Gen sequence analyzer, and instrumentation for preparation of the target to be sequenced (purification, shearing, amplification and quality assessment). This Illumina System offers a short-insert paired-end capability for high-resolution sequencing as well as long-insert paired-end reads that can be used in many applications:

- (1) Genetic variant discovery by whole genome re-sequencing;
- (2) De novo sequencing and assembly of bacterial and lower eukaryote genomes;
- (3) whole transcriptome analysis or expression profiling (e.g. RNA Seq);
- (4) small RNA discovery and analysis;
- (5) genome wide profiling of epigenetic modifications and chromatin structure (Methyl-Seq, ChIP-Seq etc), and
- (6) novel species discovery and classification through metagenomic methods.

The large amount of sequence data generated creates large data

analysis needs. WV-INBRE is acquiring all the hardware and software necessary to perform NGS data analysis.

The Partek Genomics Suite has tools for analysis of the NGS applications described above and more. With visualization-intense statistical and discovery tools, Partek Genomics Suite can be used for microarray data analysis as well as NGS. Integrated analysis of microarray and NGS data is supported, for example using ChIP-Seq and expression microarray to identify regulatory binding sites and assess change of mRNA expression.

Investigators wanting to use NGS should contact the Genomics and Bioinformatics Cores to discuss experimental design and cost prior to initiating the experiment. Please contact Don Primerano in the MU Genomics Core at 304-696-7338 for additional guidance.

WV-INBRE-supported NGS projects include whole exome sequencing of patients with Familial Combined Hyperlipidemia (FCHL) and the following NGS pilot grant projects:

**Christopher Cuff** will use NGS of subgingival plaque samples from an elderly population to identify bacteria phylotype. Differences in the microbiome and cognitive function will be analyzed to assess which phylotypes contribute to the known relationship between poor oral health and cognitive degeneration.

**Philippe Georgel and Elaine Hardman** will use ChIP-Seq meth-

ods to establish the genes bound by MeCP2 and to map genome-wide methylation. By comparing omega-3 fatty acid exposed offspring to controls, epigenetic influences associated with decreased cancer risk will be assessed.

**Alexey Ivanov** will use ChIP-Seq to identify genomic binding sites for the transcriptional repressor Snail in epithelial cells undergoing epithelial-mesenchymal transition as part of the metastatic process.

**Travis Salisbury** will use ChIP-seq to discover where in the genome the AH receptor binds DNA. AH receptor antagonists inhibit adipocyte-stimulated breast cancer cell growth; this project will identify candidate genes or miRNAs that regulate growth.

**Wei-ping Zeng** will use NGS to perform analysis of DNase I hypersensitivity sites in the genome of regulatory T Cells and identify candidate cis gene regulatory elements involved in the activation of regulatory T cells.

