Tim De Pooter

Neuromics Support Facility
Genomic Service Facility
VIB-UAntwerp Center for Molecular Neurology
University of Antwerp

Education

BSc in Medical Laboratory Technologies, Karel de Grote Hogeschool Antwerp, 2002

Position

2002 Technician NBD group
2007 Technician GSF
2017 Expert Technologist GSF

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Science/Technology

In 2007 I joined the team of the Genomic Service Facility as senior technician. After five years of assisting research in the Neurodegenerative Brain Diseases Group of Professor Christine Van Broeckhoven, I gained a lot of experience in optimizing sequencing and genotyping reactions, analyzing the data and dealing with troubleshooting. This knowledge helps contributing to the aim of our facility, resulting in quick and reliable high quality sequencing data.

Whilst capillary sequencing is still of great importance for our facility, we are still updating our techniques for the future. Therefor we invested in next generation sequencing technology by Illumina. Since 2014 I am responsible for operating and maintaining the MiSeq- and NextSeq 500-systems. On the MiSeq-platform we mainly focus on the Multiplex Amplification of Specific Targets for Re-sequencing (MASTR-assays), for research and diagnostic purposes. The NextSeq 500 is for the moment mainly used for processing Whole Exome Sequencing and RNA sequencing (mainly Illumina Truseq Stranded mRNA and Lexogen QuantSeq 3'mRNA-seq). Besides these standardly offered applications, we are always interested in exploring and optimizing new possibilities in order to perfectly suit our customer's needs.

In January 2017, I was promoted to expert technologist within the Neuromics Support Facility, further focusing on NGS-applications. In order to maintain our competitive edge, we are always on the lookout for new and emerging technologies. Since 2017 we are building up in-house expertise with the Oxford Nanopore Technologies MinION and PromethION, offering us the possibility to sequence whole genomes and perform direct RNA-seq using the power of long sequencing reads. Preliminary test results highlighted the strong advantages of these new platforms and further disrupting the current NGS-sequencing field, moving onto long read sequences in order to have the possibility to detect (large) structural variants within the human genome.

The pipeline for processing samples and preparing libraries for these NGS-platforms platforms is highly automated by the use of a robotic platform (Biomek FXp). Quality control is streamlined by the usage of varying techniques (e.g. AATI Fragment Analyzer, Trinean DropSense16, Invitrogen Qubit 3.0).

Besides offering a wide portfolio on DNA-sequencing technologies, we are always open for optimizing and testing out new technologies and sequencing kits in close collaboration with third parties.

Expertise

- DNA techniques
  - PCR
  - Sanger Sequencing
  - Fragment analyses
  - SNP detection (e.g. Pyrosequencing, Sequenom platform)
  - DNA extraction from blood samples, lymphocytes and saliva
  - Plasmid extraction
  - DNA and RNA concentration and quality measurement (e.g. Invitrogen Qubit® 3.0 Fluorometer, Trinean DropSense 16, Trinean DropSense96, AATI Fragment Analyzer, Caliper Labchip GX)
  - Operation, maintenance and troubleshooting on Applied Biosystems 3730xl DNA Analyzer
  - DNA fragmentation using Covaris S220, Diagenode BioRuptor Pico and Diagenode MegaRuptor
  - DNA size selection using SageScience BluePippin

- NGS
  - Roche 454 Pyrosequencing
  - Applied Biosystems SOLiD 5500XL EZ Bead system
  - Applied Biosystems SOLiD 5500XL Wildfire Technology
  - Illumina MiSeq Illumina Nextseq500
  - Oxford Nanopore Technologies MinION
  - Oxford Nanopore Technologies PromethION
  - Robotic Platforms: Beckman Coulter Biomek NX and FXp

- Cell Culture techniques
  - Maintaining cell cultures
  - Preparing lymphocyte pellets
  - Transformation of lymphocytes and lymphoblasts with EBV
  - Preparing serum and plasma from blood samples

Selected publications:

Null mutations in progranulin cause ubiquitin-positive frontotemporal dementia linked to chromosome 17q21. Cruts M, Gijselinck I, van der Zee J, Engelborghs S, Wils H, Pirici D, Rademakers R, Vandenberghe R, Dermaut B, Martin JJ, van Duijn C, Peeters K, Sciot R, Santens P, **De Pooter T**, Mattheijssens M, Van den Broeck M, Cuijt I, Vennekens K, De Deyn PP, Kumar-Singh S, Van Broeckhoven C. Nature. 2006 Aug 24;442(7105):920-4. Epub 2006 Jul 16.

Promoter mutations that increase amyloid precursor-protein expression are associated with Alzheimer disease. Theuns J, Brouwers N, Engelborghs S, Sleegers K, Bogaerts V, Corsmit E, **De Pooter T**, van Duijn CM, De Deyn PP, Van Broeckhoven C. Am J Hum Genet. 2006 Jun;78(6):936-46. Epub 2006 Apr 10.

Linkage and association studies identify a novel locus for Alzheimer disease at 7q36 in a Dutch population-based sample. Rademakers R, Cruts M, Sleegers K, Dermaut B, Theuns J, Aulchenko Y, Weckx S, **De Pooter T**, Van den Broeck M, Corsmit E, De Rijk P, Del-Favero J, van Swieten J, van Duijn CM, Van Broeckhoven C. Am J Hum Genet. 2005 Oct;77(4):643-52. Epub 2005 Aug 30.

List of all publications