

The 2009 DNA Sequencing Research Group General Survey: Second Generation Sequencing Instruments and Services in Core Facilities

Bintzler, D.¹, Detwiler, M.², Dewar, K.³, Escobar, H.⁴, Kieleczawa, J.⁵, Perera, A.⁶, Schweitzer, P.⁷, Singh, S.⁸, Steen, R.⁹, Zianni, M.¹⁰

¹ DNA Analysis, Inc., ² Roswell Park Cancer Institute, ³ McGill University and Genome Quebec Innovation Centre, ⁴ University of Utah, ⁵ Wyeth Research, ⁶ Stowers Institute, ⁷ Cornell University, ⁸ University of Minnesota, ⁹ Harvard Medical School, ¹⁰ The Ohio State University

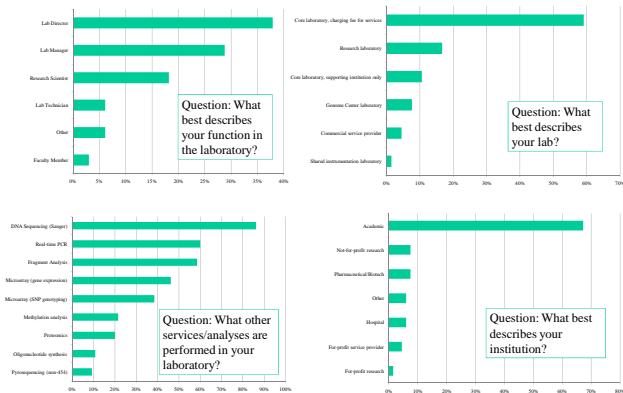
Abstract

The ABRF DNA Sequencing Research Group (DSRG) has conducted a general survey to collect data on the current state of second generation sequencing instrumentation (often termed “massively-parallel” or “next generation” sequencers) and services offered by core facilities. The DSRG has monitored trends in sequencing platforms in core facilities by conducting surveys periodically. However, this survey was the first to focus on second generation sequencers since their introduction. The information gathered this year provided data about the widespread availability of this equipment and these services in core facilities. The future acquisition and expectations for such instruments were also assessed. For comparison, the survey gathered information on Sanger (first generation) sequencing operations to determine how these technologies are affected by the second generation technologies. The importance of this survey lies in the fact that it serves as an initial “snapshot” of the status of second generation sequencing services in core facilities while they are in their infancy, and therefore is a baseline for surveys in years to come.

Survey Method

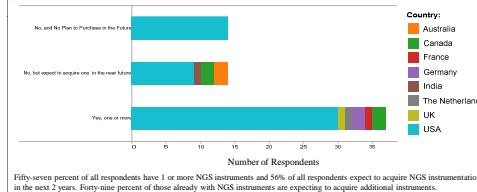
The 2009 DSRG survey was designed and conducted using the SurveyMonkey website (www.surveymonkey.com). The survey was collected over 29 days after being posted on the ABRF Discussion Forum and featured in an article distributed by *In Sequence* (GenomeWeb). The survey consisted of 39 questions, though designed in such a way that, depending on the responses to answers during the survey, the respondent would be presented with from 17 to 39 questions. Sixty-nine valid responses were obtained and used for analysis.

Results

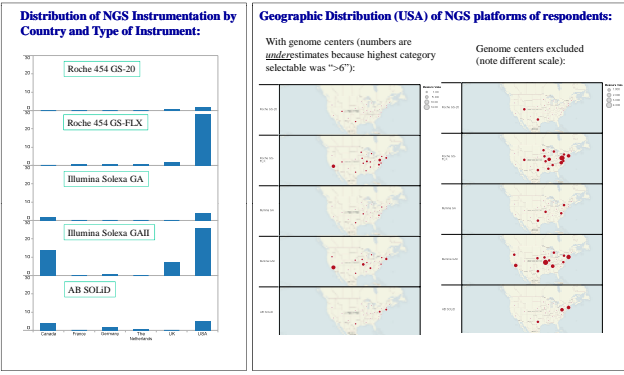


Results

Question: Do you currently operate a Next Generation Sequencing (NGS) platform in your laboratory?

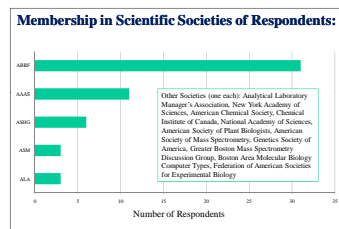
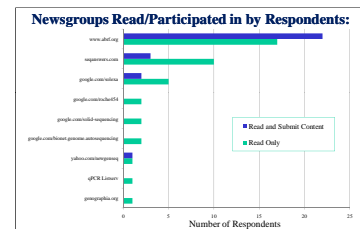
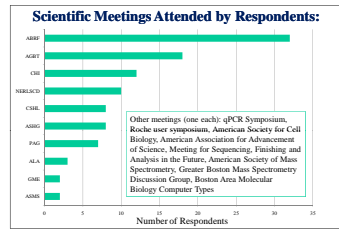
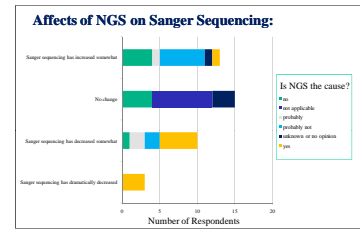
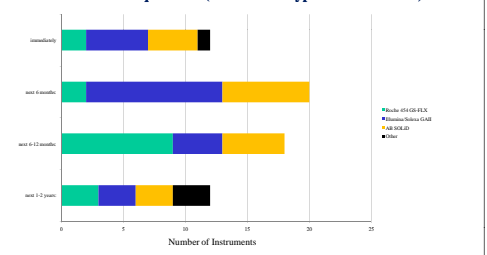


Fifty-seven percent of all respondents have 1 or more NGS instruments and 56% of all respondents expect to acquire NGS instrumentation in the next 2 years. Forty-nine percent of those already with NGS instruments are expecting to acquire additional instruments.

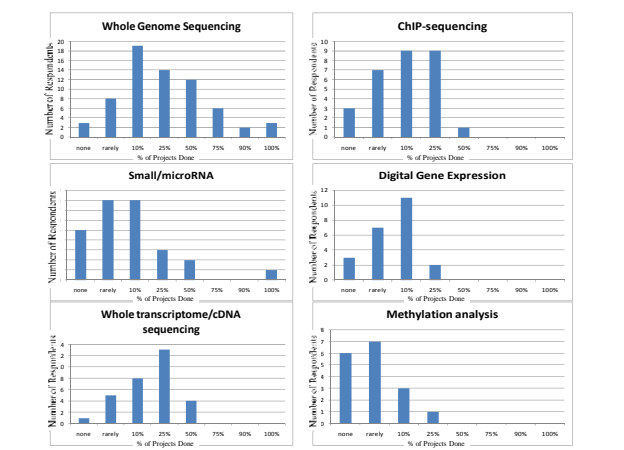


Results

Planned Future Acquisitions (number and types of instruments):



Types of Sequencing Projects done using NGS Instrumentation (includes outsourced projects):



Several labs perform exclusively one type of analysis (3, whole genome sequencing; 1, small/microRNA), and the predominant projects performed are whole genome sequencing, ChIP-sequencing and transcriptome/cDNA sequencing are the next-most performed analyses. Digital gene expression and methylation are the least-performed types of analyses.

Discussion

The 2009 DSRG general survey on second generation sequencing instruments and services in core facilities (and other sequencing labs) serves as an initial “snapshot” of the status of these relatively new technologies while they are in their infancy. Data was collected on the number of instruments in use, the types of projects performed, the potential future acquisitions of second generation sequencing instruments, the scientific affiliations, and newsgroups lab members read. The effects on Sanger sequencing was also assessed; data was also collected on the current state of Sanger sequencing operations (data to be presented elsewhere).

The majority of responses were obtained from lab directors and lab managers from fee-for-service core facilities at academic institutions, but data also was obtained from genome centers and research labs, among others. The majority of respondents were members of the ABRF who read and participated in the ABRF discussion forum, which is not surprising since the primary announcements were made in that discussion forum. Also, the majority of respondents (57%) have one or more second generation sequencers, probably due to this survey being advertised as a “NGS sequencing survey.” Therefore, data from laboratories without these instruments (and perhaps planning acquisitions of such instruments) may be underrepresented.

This survey will serve as a baseline for subsequent surveys in years to come, and additional data from this survey, not presented in this poster, will be prepared for submission to the journal of the Association of Biomolecular Resource Facilities, the Journal of Biomolecular Techniques.

