Implementation of ISO15189 accredited Next Generation Sequencing for NSCLC on the novel Ion Torrent



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Genexus[™] in a clinical diagnostic laboratory.

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Introduction

The proposal to establish a Next Generation Sequencing (NGS) service for non-small cell lung carcinoma (NSCLC) in this clinical diagnostic Pathology laboratory with no previous experience of NGS was due to the following main drivers:

- Targeted therapy has increased clinical demand for timely solid tumour sequencing¹.
- Compliance with national and international best practice guidelines for lung cancer diagnostics^{2,3,4,5}.
 Limited tissue availability; NGS allows multiple genes to be assessed on a single specimen⁶.
 Research & Clinical Trials requiring investigation with comprehensive NGS panels.
- Verification on formalin fixed paraffin embedded (FFPE) real world clinical samples including surgical resections, biopsy and cytology cell blocks, commercial reference material (FFPE), and genomic DNA/RNA (n=181) (Fig. 2).



- AcroMetrix controls 100% specificity and 100% sensitivity across genes in OPA assay (Fig. 5).
- Extensive coverage and concordance of 11 key NSCLC variants included in validation.
- Reproducibility 6 runs, different days/operators; results within range (Fig. 6).



Aims

- Evaluation of automated NGS methodology and workflows for sample preparation, sequencing, and analysis of clinical lung tumour samples.
- Introduction of an accredited, NGS service in a clinical diagnostic laboratory with no previous NGS experience, utilising the novel Ion Torrent Genexus[™] sequencing platform.
- 3. Optimisation and verification of a targeted commercial panel (Oncomine Precision Assay) on clinical tumour samples **from sample to report**.
- 4. Reduce **turnaround times (TAT)** of NGS results to clinicians, in line with best practice guidelines.

Materials and Methods

A multifaceted project, over **12 months**, from initial concept to ISO15189 accreditation.

- Workflow evaluation based on:
 - Turn Around Time.

Figure 2. Range of NSG verification reference material spanning multiple specimen types.

 Assessment parameters include determining analytical sensitivity, specificity, positive percent agreement and positive predictive value (PPA/PPV), accuracy, reproducibility, Inter-lot, Inter-operator and Inter-run variability.

Results

 Automated Ion Torrent Genexus[™] novel sequencing workflow established with OPA and Oncomine Reporter selected as optimal solution for NSCLC samples in this diagnostic laboratory (Fig. 3).

Sample Preparation	Nucleic acid purification and quantitation	Library preparation to variant interpretation	NGS Integrated Report
 Pre-processing of material Tumour Annotation / Neoplastic Cell Content % FFPE lysate preparation 	Ion Torrent "Genexus" Punification Instrument (GPI) GPI concordant with KingFisher DuoPrime + Qubit	Integrated Sequencer Integrated Sequencer	Ion Torrent" Oncomine Reporter"
Duration: approx. 2.5 hrs.	Duration: approx. 5.5 hrs.	Up to 32 Samples per run	Manual Street St

Figure 6. HD789 Horizon multiplex control reproducibility assays, AF consistent & within range.

 Performance metrics established over 20 optimisation runs collated from run reports and data analytics from Genexus software (Fig. 7).

GENEXUS OPA RUN PERFORMANCE METRICS			
Target			
10-12M			
98-99%			
87-92%			
99.90%			
99.90%			
> 500K (>800 for 5% LOD)			
> 100K			
>90%			
>1000(>2,500 for 5% LOD)			
97-99% (>90% for 90%)			
>90%			
>500			
> 5% / 0.05			
<0.5 (0.18-0.24)			
>5/7			
85-100			
70-100			
97-99%			

- Complexity i.e., User expertise including bioinformatics.
- **Tissue requirements** i.e., sample input volume.
- Cost per assay i.e., penalty for small NGS run.
- Instrument selected Ion Torrent Genexus[™] sequencer with integrated Purification Instrument (Fig. 1); a novel sequencing instrument that automates specimen to report workflow.



Figure 1. Ion Torrent Genexus[™] sequencer and Genexus[™] Purification Instrument in-situ with close-up of reagent deck.

Figure 3. NGS Genexus sample to report automated workflow established at optimisation.

Sequencing Performance:

0.4

0.2

- Tissue requirements for OPA NGS; minimum input as low as 10ng/μl DNA/RNA were utilised.
- Commercial reference samples (n=56) tested on OPA assay over 20 runs. Oncospan DNA Reference Standard HD832 (Fig. 4) concordant with allelic fraction (AF) for each variant detected versus expected AF, all results within range 0.016 - 0.31.



Fig. 5 Acrometrix Oncology Hotspot standard, variants detected & AF.

Figure 7. Performance metrics established at optimisation.

- Irish National Accreditation Board (INAB) assessment Results : Attained ISO15189 INAB accreditation; no non-conformances.
- Turnaround Time (TAT) audit at 6 months post implementation: > 47% reduction in TAT of NGS results to clinicians.

Conclusions

- Optimal performance with OPA panel on the Genexus[™] using a wide range of specimen types, including NSCLC biopsies, excisions and cytology cell blocks in small **cost effective** runs.
- Successful implementation of an accredited NGS service utilising novel technology with a fast TAT currently unavailable in any other pathology laboratory in Ireland.
- Successful integration of Oncomine Reporter software to streamline reporting without in-

- Assay evaluated Targeted pan cancer panel,
 Oncomine Precision Assay (OPA) encompassing 78 variants, including mutations (45), CNVs (14), and fusion variants (19), across 50 key genes.
- 11 genes selected for NSCLC specific validation; ALK, BRAF, EGFR, ERBB2, KRAS, MET, NTRK1, NTRK2, NTRK3, RET, ROS1.
- Optimisation and establishment of laboratoryspecific performance metrics for use with OPA on NSCLC samples, including; limits of detection (LOD), minimal depth of coverage, minimum read counts, minimum mapped reads, uniformity and variant allelic fraction (AF).
- Reporting software Oncomine Reporter[™] verified to allow for sample to report integrated workflow.

house bioinformatics expertise.

Expansion of NGS to other cancer types ongoing.

References

- 1. Morganti, S.et al. 2020. Role of Next-Generation Sequencing Technologies in Personalized Medicine. In: PRAVETTONI, G. & TRIBERTI, S. (eds.) P5 eHealth: An Agenda for the Health Technologies of the Future. Cham: Springer International Publishing
- Lindeman et al 2018. Updated Molecular Testing Guideline for the Selection of Lung Cancer Patients for Treatment With Targeted Tyrosine Kinase Inhibitors: Guideline From the College of American Pathologists, the International Association for the Study of Lung Cancer, and the Association for Molecular Pathology. The Journal of Molecular Diagnostics, 20, 129-159.
- 3. Mosele et al., 2020. Recommendations for the use of next-generation sequencing (NGS) for patients with metastatic cancers: a report from the ESMO Precision Medicine Working Group. Annals of Oncology, 31, 1491-1505.
- 4. Matthijs et al., 2016. Guidelines for diagnostic next-generation sequencing. European Journal of Human Genetics, 24, 2-5.
- Li, M. M et al., 2017. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn, 19, 4-23.
 Deans, Z. C. et al., 2017. Integration of next-generation sequencing in clinical diagnostic molecular pathology laboratories for analysis of solid tumours; an expert opinion on behalf of IQN Path ASBL. Virchows Archiv, 470, 5-20



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