

Cost analysis of standard Sanger sequencing versus next generation sequencing in the ICONIC study

Patel Nishma¹, Ferns R. Bridget², Nastouli Eleni², Kozlakidis Zisis³, Kellam Paul⁴, Morris Stephen¹

1. Department of Applied Health Research (P Nishma MSc, M Stephen PhD), and 3 Division of Infection and Immunity (K Zisis PhD), University College London, London, UK; 4 Division of Infectious Diseases, Imperial College London, UK (K Paul PhD); and 2 Clinical Microbiology and Virology, University College London Hospitals NHS Foundation Trust, London, UK (F R Bridget PhD, N Eleni MD)



Introduction

HIV and hepatitis C virus (HCV) are a major cause of morbidity and mortality, and both viruses contain high genomic variation. To date, viral gene sequencing has been handled by standard Sanger sequencing (SSS) for the detection of specific drug-resistance determinants for HIV and HCV. However, SSS-derived information is limited. By contrast, full-length viral gene sequences when linked to clinical data might influence the monitoring of drug resistance to optimally guide treatment, identify sources of viral transmissions within health-care settings, and track emerging epidemics. The ICONIC (Infection Response through Virus Genomics) study aims to introduce a novel method called next generation sequencing (NGS) within UK health-care settings, testing potential implementation in routine practice. With use of samples within established diagnostic laboratory workflows, NGS has the potential to produce higher informational content than SSS and report in a timely fashion. However, economic evidence for this emerging method is scarce.

Aims

To use the examples of HIV and HCV to compare the cost of NGS versus SSS.

Methods

We performed a bottom-up cost analysis using published, genomic-testing, costing templates to estimate the mean cost per sample for SSS and NGS methods over a 1 year period at a major London hospital. Data on resource use associated with genomic testing were based on estimates from individual sample data, routinely collected from a UK population.

Results

With SSS, mean cost per sample, including operating costs, was £178 for HCV (2080 samples) and £79 for HIV (520). Mean cost per sample with NGS was £119 (2207 samples, including operating costs), generating a cost saving of £59 for HCV and a surplus of £40 for HIV.

Conclusions

Although this method is still research based and prices vary widely, our results demonstrated a broad NGS and SSS cost equivalence.

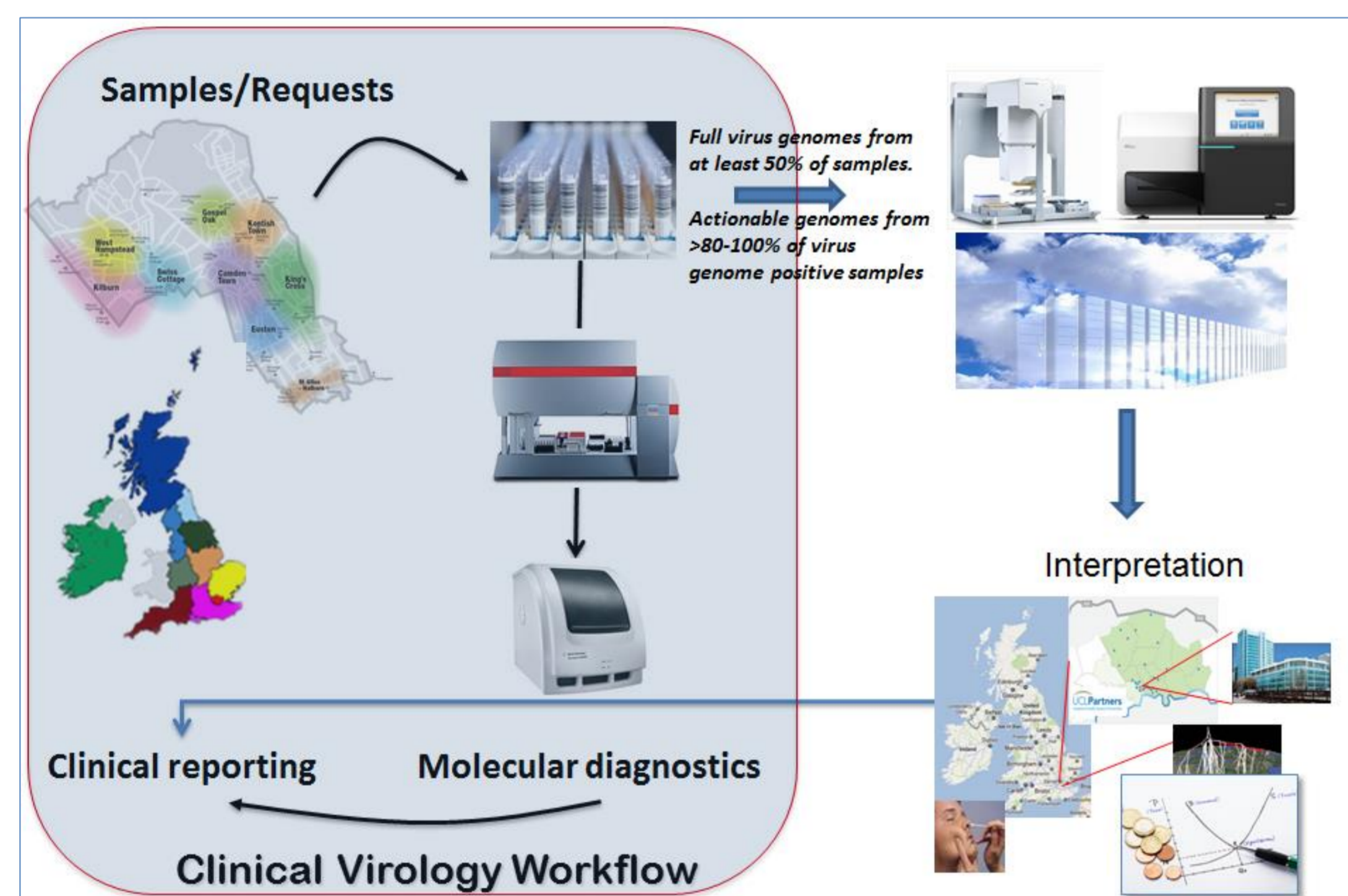


Figure 1: The ICONIC workflow in relation to the existing virology clinical pathway (shaded box).

Viral infections represent a significant burden to the NHS and a continuing threat to human health with national treatment and care costs for influenza pandemics for example in excess of £2billion. The effect of virus outbreaks is difficult to calculate because of the often very constraint time windows in which patients and their linked data need to be processed, interpreted and actioned upon and the high number of related patient co-morbidities.

Until recently the investigation of viral transmission during an outbreak was challenging as molecular typing models such as Sanger Sequencing (SSS) had low discriminatory power and their informative value on infection control measures was limited, resulting in reduced outbreak containment and increasing healthcare costs. This is set to change with Next Generation Sequencing (NGS) which provides the maximum possible discrimination between closely related viral strains. Here we present the preliminary results from the Infection Control through Viral Genomics (ICONIC) project, a flagship Health Innovation Challenge Fund project with the aim of introducing NGS processes into routine NHS operations for the effective detection and surveillance of viruses and improved stratification of patients.

Table 1: HCV and HIV bottom up cost per sample

Sample size	HCV cost category					HIV cost category				
	2080					520				
Stage	Equipment	Consumables	Staff	Miscellaneous	All categories	Equipment	Consumables	Staff	Miscellaneous	All categories
Clinical sample booking in (plasma, tissue, stool etc)	£4.51	£0.02	£0.04	£5.00	£9.57	£1.13	£0.02	£0.02	£1.25	£2.42
Clinical sample testing (Nucleic acid extraction both DNA and RNA)	£50.81	£3.08	£2.58	-	£56.47	£12.70	£3.08	£0.64	-	£16.42
Reverse transcription and genome amplification by targeted PCR to generate amplicon 3-6 hours	£4.18	£12.76	£2.58	£0.64	£20.16	£1.05	£16.77	£0.84	-	£18.66
Standard Sanger Sequencing run time 5-8 hours	£37.90	£12.16	£1.16	-	£51.22	£9.47	£12.83	£0.58	-	£22.88
Standard sanger sequencing data analysis 2 hours	£0.64	-	£1.55	-	£2.19	£0.16	-	£1.55	£0.16	£1.87
Total (before overheads)	£98.84	£28.01	£7.91	£5.64	£140.40	£24.51	£32.69	£3.63	£1.41	£62.24
% total cost	70%	20%	6%	4%	-	39%	£52%	6%	2%	-
Total (including overheads at 27.5%)	£125.01	£10.08	£35.72	£7.20	£178.00	£31.25	£41.68	£4.62	£1.80	£79.35

Supported by:



Department of Health

This publication presents independent research supported by the Health Innovation Challenge Fund T5-344 (ICONIC), a parallel funding partnership between the Department of Health and Wellcome Trust. The views expressed in this publication are those of the author(s) and not necessarily those of the Department of Health or Wellcome Trust. Correspondence: Nishma Patel (nishma.patel@ucl.ac.uk)