



NEW ZEALAND GENOMICS LIMITED

# IMPACTS & OUTCOMES REPORT 2013

A large, stylized version of the NZGL logo graphic, consisting of overlapping, rounded rectangular shapes in yellow, red, green, blue, and purple, positioned in the lower right quadrant of the cover.

*Advancing  
New Zealand  
science  
through  
genomic  
infrastructure*



**New Zealand Genomics Limited**



**IMPACTS & OUTCOMES REPORT**  
**2013**

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Genomics



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## COMMENTARY FROM THE NZGL CHAIR

This year has been one of strong development from a governance perspective for New Zealand Genomics Limited (NZGL).

The Board, with representatives from our three collaborators and two independents, has worked hard at developing infrastructure for the New Zealand science community. Our chief executive, Tony Lough, has outlined in his report the specific developments this period.

From a Board perspective we have been focused on bringing the various components of NZGL envisaged in the original business case to life and ensure they operate for the benefit of our community.

We are seeking a balance between physical infrastructure, capacity building and an efficient, high quality production organisation. I would like to specifically thank our staff lead by our CEO Tony Lough, the members of our advisory groups who give freely of their time and knowledge and all those in our partner locations throughout New Zealand who are working very hard to provide our customers with the highest quality outcomes.

I would also like to record my thanks to staff at the Ministry of Business, Innovation and Enterprise (MBIE) for their contribution to NZGL.

During the year our inaugural chair, Hon Stan Rodger, stepped down. Stan worked very hard in the set up stages of NZGL and we appreciate all his input to the success of our organisation.

Looking forward we are focused on further developing, along with our collaborators, NZGL's business. We are continuing to work with organisations within our sector with a view to ensure we make best use of scarce resources.

Our challenge is to develop NZGL into a sustainable organisation contributing at a level sought by our science community. We look forward to meeting this challenge with your support.



**Graham Crombie**  
Chair  
9 August 2013

## COMMENTARY FROM THE NZGL CHIEF EXECUTIVE

New Zealand Genomics Limited (NZGL) was established as a genomics infrastructure service provider to the New Zealand science community. The Crown (\$40.6m) and Collaborating Universities (\$29.3m) – Otago, Massey and Auckland – agreed to co-invest to deliver a genomics infrastructure that was accessible to all researchers across New Zealand.

The first NZGL supported services were delivered in September of 2011 by way of investment in high capacity sequencing instrumentation. The following period to 30 June 2013 represented a continuous phase of service implementation. This included addition of low capacity sequencing, array technology and a Bioinformatics Consultancy Service with about 10 consultants delivering services.

NZGL is operational as a production level genomics service provider that is accessible to all. These services are integrated to the extent that a client researcher can have an end-to-end service including assistance with scoping the project through to data generation, storage and analysis using appropriate software inclusive of a bioinformatics consultancy service.

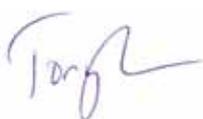
A significant NZGL investment over the past 12 months has been conclusion of an agreed arrangement for a dedicated genomics IT platform suitable for use by genomics researchers. This arrangement with Gen-i Ltd, Biomatters Ltd and Crown entity REANNZ was implemented in April 2013 with steady uptake of resources from that time.

It is important to note that NZGL operates within an integrated science ecosystem. While NZGL has significant genomic domain capability there has been recognition of the value of services provided by others. Significantly in this regard NZGL has contracted network support services from REANNZ. Together the first ScienceDMZ arrangement in New Zealand has been developed accelerating data transfer rates by as much as 8 to 16 times.

During the period to 30 June 2013 NZGL has delivered significant value to the research environment. Significant projects include service to the sheep and dairy industry (\$368,000); kiwifruit/PSA (\$29,000), the health sector (\$548,000) and native species, e.g. kiwi, tuatara (\$127,000). Collectively across all projects (167 during 2012 & 91 YTD June 2013) NZGL delivered a total of \$2.34m genomics services to fee-paying clients across New Zealand.

Capability development and human capital retention within the New Zealand research sector are viewed as key measures of NZGL success. NZGL service delivery includes support by way of genomics production services for up to 300 researchers and more than 110 research outputs (publication, reports, conference presentation and patents).

NZGL has now moved through the “start-up” phase of service implementation and over the coming period is focused on continuous service improvement and service uptake.



**Tony Lough**  
9 August 2013

## OVERVIEW

Genomics – the high-throughput technologies, which allow scientists to examine the structure and function of thousands of genes at a time – underpins economic development in New Zealand’s biological economy, through horticultural, agricultural and human health research endeavour.

The Government recognised the pivotal role genomics played across multiple sectors justified investment, alongside collaborating partners, in an infrastructure to provide genomics capability within New Zealand.



*Figure 1: NZGL and collaborators*

New Zealand Genomics Limited (NZGL) was established in 2010 as a genomics infrastructure service provider to the New Zealand science community.

Collaborating parties are: the Crown, University of Otago, Massey University and The University of Auckland. The parties agreed to work together to develop and operate a genomics infrastructure available to the research community and commercial clients (Figure 1).

NZGL is funded by a co-investment involving the Crown (\$40.6m) and the three university collaborators (\$29.3m). NZGL receives funding from Ministry of Business, Innovation and Employment (MBIE) and, through an agreed business case, supports service delivery from the university services providers.

### NZGL Services

All NZGL services, the Illumina MiSeq, GS Junior, Affymetrix and IonTorrent at Auckland, Illumina MiSeq at Massey, the Illumina HiSeq at Otago and a distributed Bioinformatics service had been successfully implemented in 2012. In the first quarter of 2013, NZGL and University of Otago supported the purchase of a HiSeq2500 instrument, which doubles HiSeq capacity from 1 June 2013. The NZGL Board approved incorporating existing Affymetrix capacity at Otago into NZGL services on 19 July 2013.

Much of the period since June 2012 has focused on the design and implementation of Bio-IT and data storage facilities through contracted arrangements with Gen-i, Biomatters and REANNZ. Utilisation of the platform is slowly increasing (30 Accounts using 10TB of storage) with a number of organisations either trialing the system or organising to do so. Most of the processing work relates to use by the Bioinformatics consultants on existing projects.

These services have been consistently utilised by the New Zealand genomics community, but there is still room to increase utilisation.

## NZGL Investment Case

The NZGL Investment Case (2008) anticipated several positive outcomes for New Zealand:

1. *Make a major contribution to innovation and economic development;*
2. *Leverage the current Research, Science and Technology investment in biological sciences and related technology development;*
3. *Expand its research capability and capacity;*
4. *Attract, nurture and retain world-class researchers in New Zealand;*
5. *Accelerate progress in research and the development of valuable commercial outcomes;*
6. *Be at the forefront of international science; and*
7. *Address critical scientific questions unique to New Zealand.*

**[Source: NZGL Investment Case, p5]**

The Investment Case also anticipated that the establishment of NZGL would enable New Zealand to be internationally competitive with regard to genomics capability – through research, training, outreach and the retention of genomics researchers in New Zealand.

*“The lack of advanced genomics facilities in New Zealand also means that the education of our students and future researchers will fall behind, making it more difficult for New Zealand to remain internationally competitive in the future.”*

**[Source: NZGL Investment Case, p11]**

Finally, it was anticipated that NZGL might have a positive impact on New Zealanders’ service delivery for research and industry-aligned activities, while also delivering positive outcomes for Māori and Pacifica communities. The Investment Case captured these expectations as:

- *In the biomedical field, it will be possible to study health problems unique to New Zealanders, such as those which disproportionately affect Māori and Pacific Islanders;*
- *In the biomedical field, it will be possible to develop and assess novel diagnostic treatments for a range of diseases that exhibit strong familial associations, or genotype-environment interactions;*
- *With livestock, it will be possible to define the relationships between the genetic make-up of animals and their real-life performance, such as health, productivity, product quality and metabolism;*
- *With pasture and horticultural and arable crops, it will be possible to define the relationships between performance and genetic make-up (e.g. productivity, fruit or grain quality, health-related attributes);*
- *In the area of biosecurity, it will be possible to characterise the genetic variation between species and populations, allowing rapid identification of intruders, and differentiation between related species; and*
- *In the area of conservation, it will be possible to define the amount of genetic diversity within a population, and therefore the vulnerability of that population.*

**[Source: NZGL Investment Case, p7]**

The purpose of this report is to illustrate the impact of NZGL against the expectations outlined in the NZGL Investment Case.

## THE IMPACT OF NZGL: ACHIEVEMENTS

A summary of the outputs and achievements of NZGL, from commencement of service delivery (September 2011) to 30 June 2013 are:

- **Contracts** – Agreed 262 service agreements with clients.
- **Human capital development** – NZGL has developed human capital through provision of services to 300 principal investigators, 80 postdoctoral students, 160 postgraduate students, 30 undergraduate students, and 30 other research staff (e.g. research fellows, science leaders and research technicians).
- **Data** – A large amount of high-quality sequence data has been generated and provided to the research community, based on about 800 machine runs or more than 22 Terabytes of data.
- **“Billed” value** – NZGL has delivered “billed” services worth \$2.32m to the research community, most of which were discounted from the full commercial rate as a result of government investment.
- **Species** – Projects span a wide variety of species, including kiwifruit, birds, bacteria, plants, human, invertebrates, cattle and sheep.
- **Sectors** – The sectors where projects have been applied include New Zealand native flora and fauna, agriculture, human health, biosecurity and the environment.
- **Basic and applied** – Outcomes are identifiable through both academic and industry aligned research. NZGL’s clients were derived from universities (64%) and private companies or other organisations (36%).
- **Outreach** – NZGL has participated in more than 41 outreach activities, including seminars, sponsored conferences and workshops.
- **Public relations** – Projects that received significant media coverage included: sequencing to determine the source of the PSA disease outbreak in New Zealand kiwifruit; sequencing of the scientifically-significant tuatara genome; research into kiwi breeding patterns; and debate on personal genomics in New Zealand.

NZGL’s impact can also be measured by the monetary value or number of agreed contracts related to significant projects. Table 1 indicates that \$1.072m was committed by various organisations to important agricultural, horticultural, native and human health projects.

*Table 1: Significant project areas to date (from Sept 2011 to 30 June 2013)*

Research area	Commercial Value of projects	Number of projects
Kiwifruit/PSA	\$29,000	4
Dairy/sheep	\$368,000	10
Human	\$548,000	42
Tuatara, kiwi and other indigenous animals	\$127,000	6

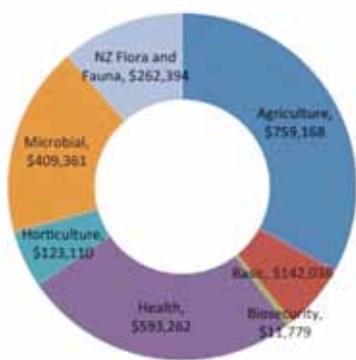
Figure 2 summarises delivered financial value and number of projects by sector or species. About two thirds of NZGL delivered service can be ascribed to agriculture and health. Service delivery to agriculture (\$548K or 7% of projects) is significant. While fewer in number, agricultural projects tend to be larger by delivered value, reflecting that Crown Research Institutes (CRIs) generally operate on larger projects than university researchers.

Figure 2: NZGL outputs by sector, species and delivered value (based on funding source input)

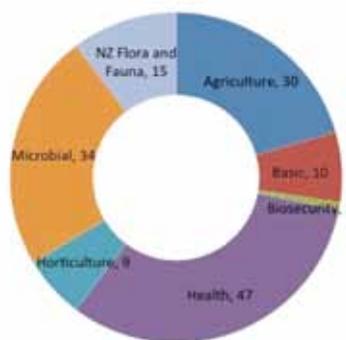
**NZGL Value Delivered**

(Outputs from service commencement September 2011 to May 2013)

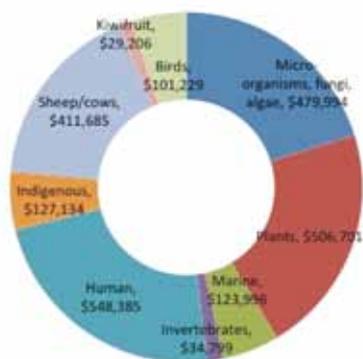
**Value Delivered by Sector**



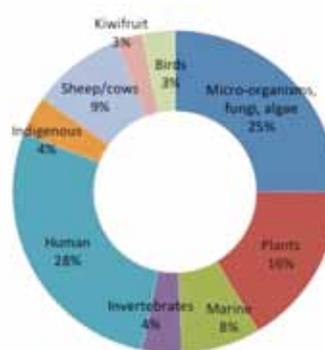
**Number of Projects Delivered by Sector**



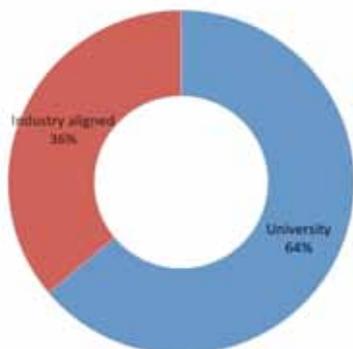
**Value Delivered by Species**



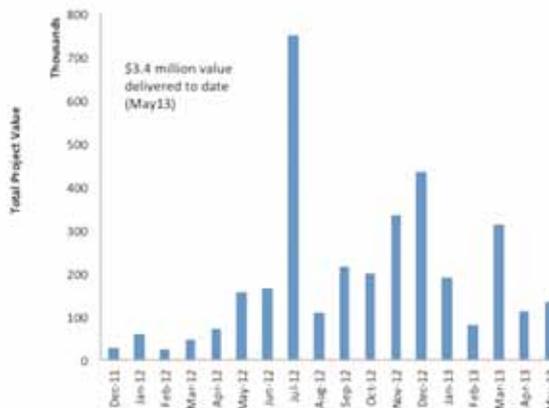
**Number of Projects Delivered by Species**



**Funding Source**



**Value Delivered**



# NZGL INVESTMENT CASE AND ANTICIPATED OUTCOMES

The following section details achievement of the NZGL Investment Case to 30 June 2013. It does so by reporting against the seven anticipated outcomes listed on page 5 of this report which come directly from the Investment Case that established NZGL.

## 1. Make a major contribution to innovation and economic development

NZGL delivers genomic services by way of Service Agreements with fee-paying New Zealand clients. Details of NZGL service contribution to innovation and economic development in New Zealand can be gauged from the projects listed in Table 3 and from the case studies including through this document and within Appendix I. Additionally, Table 10, page 28, summarises the value of NZGL projects to various sectors relevant to the innovation and economic development landscape and the Māori and Pacifica communities.

Figure 2, page 7, illustrates the split of projects by organisation of origin. From NZGL's commencement in September 2011, through until 14 May 2013, one third of NZGL's service delivery has been to CRI and private companies. The balance has been delivered to university clients. In general, service work delivered to CRI and private company clients is industry aligned.

**Table 2: Summary of NZGL contributions to innovation and economic development**

Institution or Company	Principle Investigator	Platform	Project Title	Description	Contracted End Date
Caldera Health Limited	David Musgrave	Illumina HiSeq	Identifying RNA biomarkers	Custom project including 1 lane of Illumina HiSeq	Delivered during 2012
Scion	Phillip Wilcox	Illumina HiSeq and MiSeq	Pine genome sequencing	20 lanes Illumina HiSeq/4 Illumina MiSeq	2013 – in progress
LIC	Andrew Scott	Illumina HiSeq	Dairy herd improvement	16 lanes Illumina HiSeq	Delivered during 2012
AgResearch	John McEwan	Illumina HiSeq	Genetic gain in the New Zealand sheep industry	21 lanes of Illumina HiSeq	Delivered during 2012 and 2013
ESR	Richard Hall	Illumina MiSeq	Pathologies of unknown diagnosis	43 flow cells Illumina MiSeq sequencing	Delivered during 2012 and 2013
University of Otago	Neil Gemmell	Illumina HiSeq	Transcriptomic – Johne's disease in deer	3 lanes of Illumina HiSeq	Delivered during 2012
University of Otago	Russell Poulter	Illumina HiSeq 2000	Identifying the source of the kiwifruit Psa outbreak	Half of 1 HiSeq lane	March 2012
Blis Technologies	John Hale	Bioinformatics analysis	Bioinformatic assessment of bacterial genetic similarity	80 hours of bioinformatics analysis	April 2013
University of Auckland	Peter Morrison-Whittle	GS Junior	Biogeography of yeast species associated with winemaking in New Zealand	1 GS Junior run	Delivered during 2012

## DEVELOPMENT OF A DIAGNOSTIC TOOL FOR PROSTATE CANCER

Auckland-based Caldera Health is contracting NZGL services to test the RNA-seq process as a diagnostic tool for prostate cancer

The project involves making RNA from a cell line that is already accepted as an international standard for prostate cancer cells, and prostatectomy tissue from cancer subjects, extracting RNA and using developed prostate cancer biomarkers and reference biomarkers as controls.

Prostate cancer is the most commonly diagnosed cancer in men in New Zealand and Australia. Based on data from countries that record cancer statistics by type, more than 1 million men worldwide are diagnosed each year with prostate cancer and at least 200,000 will die from the disease or associated causes.

Digital rectal examination and the Prostate Specific Antigen (PSA) blood test are the commonly used tools for detecting prostate cancer. However, many studies have repeatedly shown that the PSA test is unreliable – frequently reporting either false negative or false positive results.

Caldera Health Chief Scientist Dr Jim Watson says Caldera's technology addresses the medical problem that prostate cancer is not a single disease in men. "The phenotype of disease varies from one patient to another, due to variations in the genetic and environmental status of each patient and the complexity of genetic modifications that are unique to each cancer."

**Client:** Dr Jim Watson, Caldera Health

**Services:** Three proof of principal experiments, custom library preparation, three lanes of HiSeq2000 sequencing and bioinformatics



### REBECCA LAURIE

Manager, University of Otago Genomics Facility

*"It was extremely rewarding to be involved with the development of a new RNASeq diagnostic methodology for prostate cancer. Caldera's objectives were very clear, so it came down to us to make it work – and it had to be an assay that was highly reproducible. We were able to modify a robust method used in metagenomic studies and apply this to RNASeq and HiSeq sequencing with success."*

**Caldera Health used NZGL services to develop a new diagnostic tool for prostate cancer.**



## 2. Leverage the current Research, Science & Technology investment in biological sciences and related technology development

NZGL has significant and successful service provision relationships with CRIs who constitute around 36% of our contracts. Collectively, CRIs are important clients to NZGL and AgResearch is the single largest client institution for NZGL and has worked with them on many different types of projects.

Professor Warren McNabb says, “AgResearch has engaged with NZGL on several occasions over the last year to contribute in helping us deliver high quality science to our stakeholders and end-users.”

*[Source: letter to NZGL from Professor Warren McNabb, Research Director, AgResearch, 21 August 2013]*

NZGL monitors the source of funding that supports a client’s project. This provides an opportunity to demonstrate how government investment is leveraged to generate genomics research outputs. NZGL clients of university origin receive the highest level of discounting available as a reflection of the ‘public good’ aspect of the research undertaken.

Figure 3 shows the various types of entities that contract with NZGL for their genomics research while Table 3 shows how all these various types of entities access NZGL services at either the discounted ‘public good’ or commercial rate.

**Figure 3: Funding Source Supporting NZGL Delivered Services (September 2011 to June 2013)**

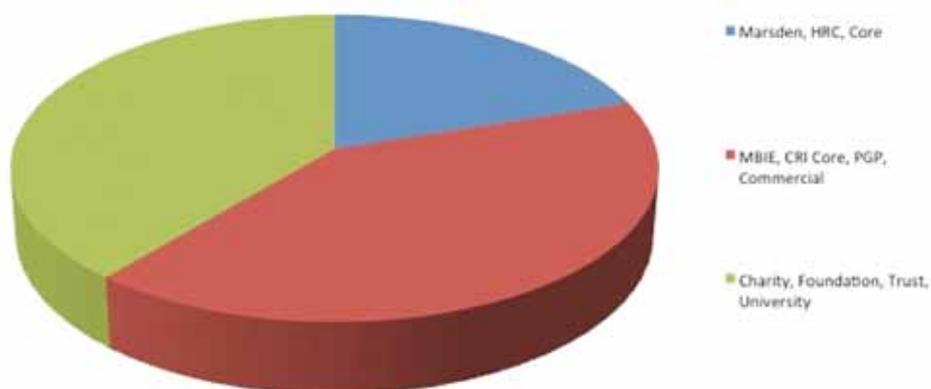


Table 3 summarises leveraged support in terms of value (\$) and number of projects.

**Table 3: Funding source applied to NZGL service contracts (September 2011 to June 2013)**

Funding source	NZGL clients of University origin (\$ billed)		NZGL clients of CRI or private company origin (\$ billed)		Total	
	\$	(n, % of total)	\$	(n, % of total)	\$	(n, % of total)
<b>Basic research:</b> Marsden, HRC, Centre of Research Excellence	317,663	38 / 13%	168,943	17 / 7%	486,606	55 / 20%
<b>Industry aligned:</b> MBIE, CRI CoRE funding, PGP, commercial	81,120	13 / 3%	924,642	50 / 38%	1,005,762	63 / 41%
<b>No overhead:</b> Charity, Foundations, Trust, University internal	916,290	139 / 38%	34,739	5 / 1%	951,029	144 / 39%
<b>Total</b>	<b>1,315,073</b>	<b>190 / 54%</b>	<b>1,128,324</b>	<b>72 / 46%</b>	<b>2,443,397</b>	<b>262 / 100%</b>

## GENETIC GAIN IN THE NEW ZEALAND SHEEP INDUSTRY

AgResearch work that utilises NZGL's services is seeing the introduction of new, commercially important traits to the New Zealand sheep industry.

Application of these traits is essential to ensure continued added value to farmers and the industry. NZGL provides cost-effective next-generation sequencing data generation that is then processed through research pipelines to target sheep breeding programmes.

Recent advances in next-generation sequencing technology have increased the output and lowered the cost to a level that it is now viable for genotyping-by-sequencing (GBS) to be undertaken in livestock, plant crops and aquaculture species.

GBS has the potential to be a cost effective, reproducible and high-throughput SNP genotyping method. Varying the number of samples and the "size" of the reduced genome per lane on an Illumina HiSeq2000 allows for differing magnitudes of SNPs to be genotyped and interrogated. This development has been funded to date by the FarmIQ PGP (Primary Growth Partnership) project.

AgResearch scientists Dr Shannon Clarke and John McEwan have explored GBS in sheep by combining restriction site associated DNA sequencing with a PCR specific primer approach to generate a method that can be fine tuned to return varying genome coverage. The method for reducing the complexity of the genome, as well as the sequencing and bioinformatics pipeline for GBS in sheep, is hoped to be the basis of rapid and low-cost genotyping of thousands of individual sheep to underpin elite animal breeding programme on an annual basis.

A further project is the development and utilisation of a high-density ovine SNP chip to add value to the New Zealand sheep flock and industry, again as part of the FarmIQ PGP project. This work includes the International Sheep Genome Consortia. The AgResearch team are using Illumina HiSeq2000 for re-sequencing large numbers of animals from the New Zealand sheep flock and this work resulted in a recently-validated 600K SNP chip.

**Client:** Dr Shannon Clarke and John McEwan, AgResearch

**Services:** HiSeq data delivered progressively during 2012 and 2013



### LES MCNOE

Sequencing specialist, University of Otago Genomics Facility

*"Genotyping by sequence (GBS) is a technique that allows cost effective sequencing analysis of genotypes from many individuals. This has huge implications for both commercial and academic sectors. To accommodate this new technology, we worked with AgResearch scientists and Illumina to modify our sequencing processes. The outcome is good quality data and a better understanding of HiSeq sequencing chemistry. We are now accepting client-prepared GBS sequencing libraries to be run on the HiSeqs from around New Zealand."*

**NZGL Next-generation sequencing data will assist AgResearch to improve sheep breeding in New Zealand.**

### 3. Expand its research capability and capacity

NZGL services a wide range of project types, spanning health, agriculture and aquaculture, through to indigenous species and environmental study.

NZGL's activity is strongly driven by the timing of funding body application deadlines and announcements, as demonstrated in Table 4 and Figures 4 and 5.

**Table 4: Funding application and announcement cycles**

Funding body	Closing date for full proposals	Results announced
Marsden	June	October
HRC – Emerging Researcher	October	April
HRC – Programmes	October	May
HRC – Projects	November	May

Table 4 and Figures 4 and 5 show three trends:

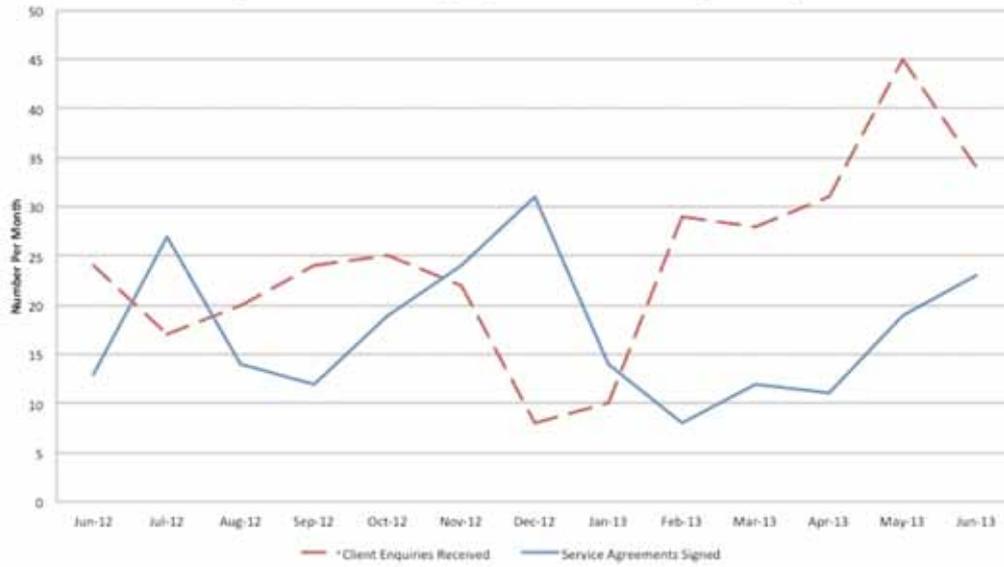
1. There is a clear lag of about two months between cycles of enquiry and Service Agreement signing;
2. There are noted spikes in enquiry during May-June and October-November, in keeping with grant application due dates; and
3. The commitment to Service Agreement and invoicing is particularly marked mid-year, reflecting HRC announcements and the financial year end.

Table 5 summarises NZGL performance by service and collaborator.

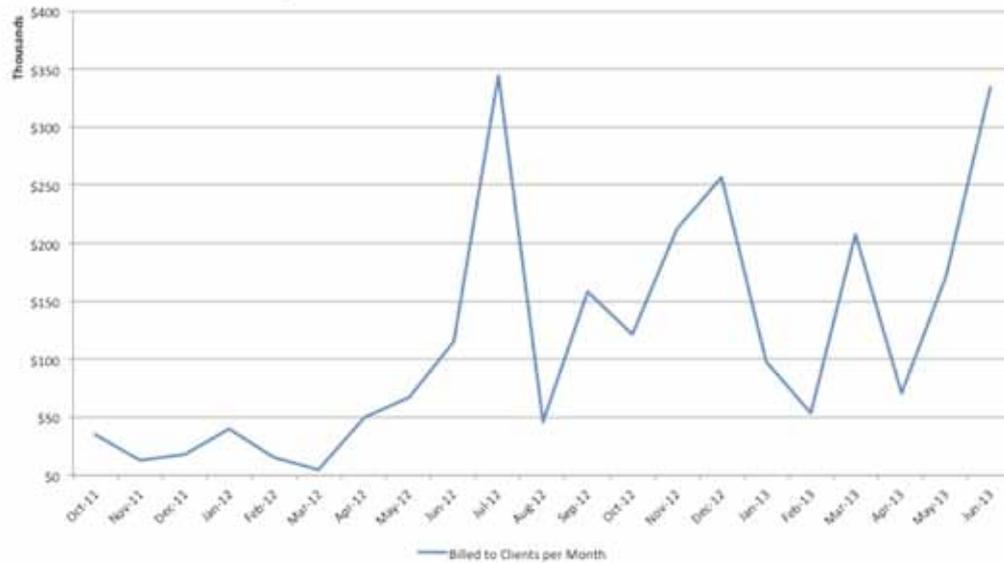
**Table 5: NZGL input metrics to the NZGL research system**

Metrics	2011 - 2012	2013 YTD	Total
<b>Agreed contracts (n)</b>	<b>174</b>	<b>88</b>	<b>262</b>
<b>Services supported:</b>			
<b>Bioinformatics consultancy</b>			
Contract value (\$)	164,175	186,972	351,147
Billed to client (\$)	52,385	82,496	134,881
<b>Sequencing Hiseq; Miseq, Ion Torrent &amp; Array</b>			
Contract value (\$)	2,517,905	1,292,567	3,810,472
Billed to client (\$)	1,444,891	863,625	2,308,516
<b>Total</b>			
<b>Contract value (\$)</b>	<b>2,682,080</b>	<b>1,479,539</b>	<b>4,161,619</b>
<b>Billed to client (\$)</b>	<b>1,497,276</b>	<b>946,121</b>	<b>2,443,397</b>

**Figure 4: Client Enquiry and Contracting Activity**



**Figure 5: NZGL Services Billed to Clients**





### REBECCA LAURIE

Manager, University of Otago  
Genomics Facility

*“It has been extremely fulfilling for the team to be involved with the scoping and sequencing design for this project. Associate Professor Print challenged us to find appropriate methodologies to work with some difficult clinical samples and we have been able to deliver some very encouraging results from the small pilot study. This project was the first of its kind for both our facility and NZGL – and our new-found expertise can now be applied to further clinical sequencing projects.”*

**NZGL worked closely with researchers from The University of Auckland on cancer research.**

## UNDERSTANDING COLON CANCER AND NEURO-ENDOCRINE TUMOURS

Researchers from the University of Auckland are using NZGL services to help them identify cancer-causing molecular pathways in colorectal cancer and neuroendocrine tumours.

Principal investigator Associate Professor Cristin Print says a unique feature of the research project was a researcher-funded planning exercise, which involved NZGL technicians and commercial sequencing experts working alongside the university researchers.

“The close work between University of Auckland researchers and NZGL allowed DNA and RNA sequencing methods to be optimised, greatly extending the range of stored tumour samples and corresponding non-tumour material that could be investigated using genomics in New Zealand. As a result, high quality sequencing data was obtained from these historical pathological specimens.”

The project also involves multi-modal analysis, which is providing a unique depth of understanding of the tumour types and the potentially druggable molecular pathways that underpin their growth.

NZGL has been contracted to generate a web-based database to house this new data alongside extensive data from overseas studies. This will allow automated generation of prognostic genomic profiles for individual patients, based on the genomic profiles and clinical outcomes of patients already in the database. This real-time combination of historical genomic profiles and new patient data is unique.

Associate Professor Print says the work would not have been possible using overseas genomics service providers, given the face-to-face planning meetings and iterative project scoping. “After a period of optimisation, the data quality obtained from relatively low quality tumour specimens has been excellent – in many cases exceeding the data quality obtained by overseas collaborators.”

**Client:** Associate Professor Cristin Print, The University of Auckland

**Services:** Four lane Hiseq pilot study, MiSeq pilot, 106 Affymetrix microarrays and bioinformatics services



NZGL delivers genomics services to research organisations across New Zealand (Table 6). The integrated end-to-end nature of service delivery, including access to expertise pre-contract, encourages a wide variety of organisations to request services.

**Table 6: Client institution of origin, from Sept 2011 to June 2013**

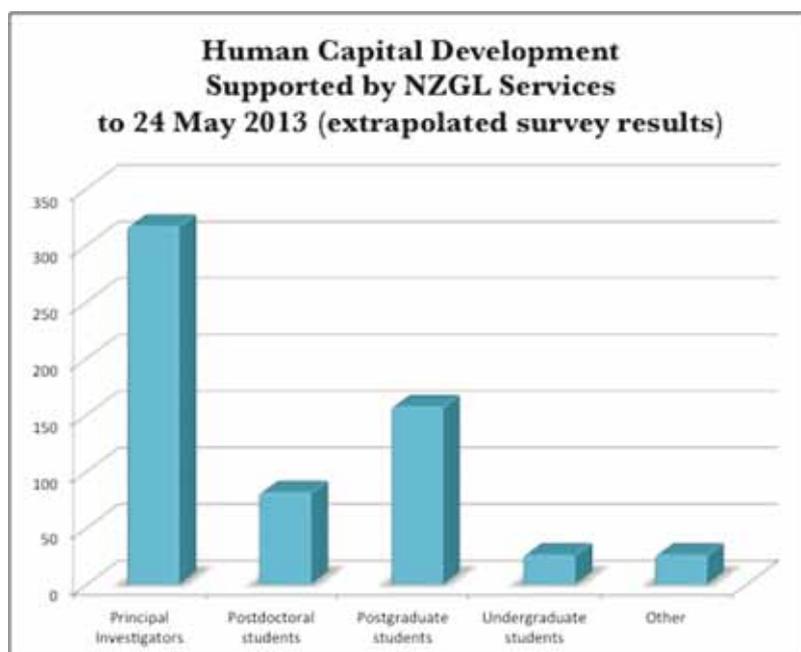
Client Institution	NZGL Service supplier			Total
	Auckland	Massey	Otago	
Auckland District Health Board			2	<b>2</b>
AgResearch Ltd		3	16	<b>19</b>
Auckland University of Technology	1			<b>1</b>
Blis Technologies			1	<b>1</b>
Caldera Health			5	<b>5</b>
Cawthron	1	3		<b>4</b>
Environmental Science & Research	1	10	3	<b>14</b>
Forestry Commission Research			1	<b>1</b>
LandCare Research			7	<b>7</b>
Lincoln University	2	5	2	<b>9</b>
Livestock Improvement Corporation			2	<b>2</b>
Massey University	6	28	14	<b>48</b>
Pacific Edge			2	<b>2</b>
Plant and Food Research	3	1	8	<b>12</b>
Scion (NZ Forest Research Inst. Ltd)			6	<b>6</b>
Three Harbours Health Foundation <sup>1</sup>	1			<b>1</b>
Unitech Institute of Technology			1	<b>1</b>
University of Auckland	48	2	12	<b>62</b>
University of Otago	4	9	44	<b>57</b>
University of Technology (Sydney)			1	<b>1</b>
Victoria University of Wellington	2	1	4	<b>7</b>
<b>Grand Total</b>	<b>69</b>	<b>62</b>	<b>131</b>	<b>262</b>

<sup>1</sup> Research conducted by Waitemata District Health Board and The University of Auckland.

#### 4. Attract, nurture and retain world-class researchers in New Zealand

From September 2011 activity to 30 June 2013, NZGL has delivered a total of 262 service contracts to New Zealand genomics researchers. This represents service delivery to 19 different organisations and 139 project-initiating principal investigators. In June 2013, an email survey distributed to 136 of the principal investigators was used to establish how effectively NZGL is developing the capability of human capital. This survey yielded 52 responses (38.2% response rate).

Figure 6 shows the extrapolated results from the June 2013 email survey. In summary, NZGL supported the development of: 121 principal investigators; 31 postdoctoral students; 60 postgraduate students; 10 undergraduate students and 10 other types of staff not specified elsewhere (e.g. research fellows, science leaders and research technicians).



*Figure 6: Human capital development promoted through NZGL service delivery (Sept 2011 to 24 May 2013)*

If the results of the survey were extrapolated to all of the service contracts delivered to 24 May 2013, the estimated human capability development through NZGL service delivery translates to: 300 principal investigators; 80 postdoctoral students; 160 postgraduate students; 30 undergraduate students, and 30 other types of research staff (e.g. research fellows, science leaders and research technicians).

Note: The extrapolated figure of about 300 principal investigators is indicative of the fact NZGL's contract management system records only one principal investigator per contract, yet research teams usually involve several lead principal investigators.

One way that NZGL has directly contributed to growing the capability of genomics researchers in New Zealand has been to run competitions with resulting projects receiving considerable free support in bioinformatics services and consumables. This both develops the research capability for the winning project teams, but also contributes to the amount of research data available in New Zealand and the 'public good' through projects being undertaken that otherwise may not have proceeded due to lack of funding. NZGL has run two competitions for MiSeq services – one in 2012 and one in 2013. The following case study outlines the intent of Dr Mikael Boulic's project, which was one of the winners of the 2013 MiSeq competition. See also the additional case study *Microbial Responses to Environmental Change* in Appendix I, page 35, which was also a MiSeq competition winner.

## AIRBORNE BACTERIAL COMMUNITIES IN JUNIOR CLASSROOMS

Does increasing the ventilation rate and warmth in New Zealand classrooms reduce the bacteria level and improve school children's health?

Massey University's Dr Mikael Boulic was one of two successful NZGL-Illumina MiSeq competition winners and has received financial support to progress his work.

Dr Boulic is involved in a two-year interventional project which could reduce classroom bacteria levels and improve children's health. NZGL services are providing critical detailed knowledge around the bacterial communities found in New Zealand junior classrooms.

Dr Boulic describes New Zealand primary classrooms as grossly under-ventilated, damp and having excessively high levels of bacteria for much of the school year. "It is known that dampness creates an ideal environment for bacteria. This, coupled with primary school children's under-developed immune system, makes school children most at risk of succumbing to respiratory infections."

This fact was reinforced during the 2009 influenza pandemic, when school-aged children had by far the highest rates of infection. Furthermore, Acute Rheumatic Fever (ARF) – an auto-immune response to infection with Group A Streptococcus bacteria – is predominant in children in the 5-14 age range. ARF can lead to rheumatic heart disease and lifelong damage to the heart valves. The incidence of ARF in New Zealand is not seen at similar rates in other OECD countries and is largely avoidable. Given children spend their second largest amount of time in classrooms, the contribution of cold and damp classroom on the communication of Group A Streptococcus bacteria and other respiratory infections needs research.

To date, there have been only two studies which have investigated the total bacteria level in New Zealand schools. Both studies found that 85% of the junior classrooms studied had a level of total bacteria similar to levels usually only found in the vicinity of sewage treatment plants.

**Client:** Dr Mikael Boulic, Massey University

**Services:** 1 MiSeq flow cell of data, delivered March 2013

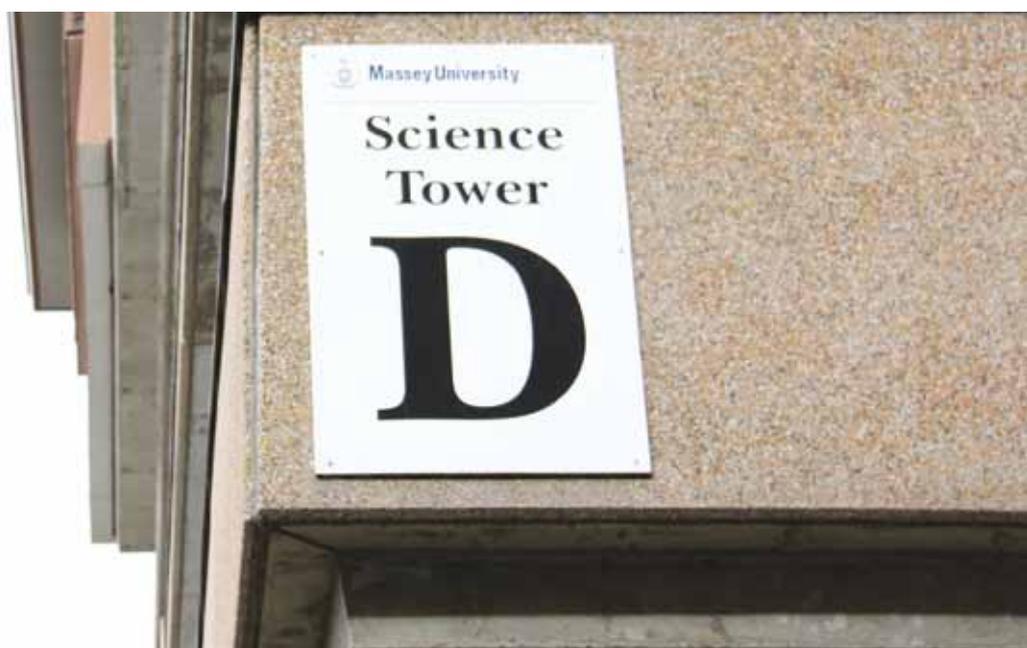


### PATRICK BIGGS

Massey University Genome Service

*"We worked with the client to put together a project plan, before carrying out the sequencing on the MiSeq. Additional client consultation was carried out to provide assistance regarding sample quality and to determine what method of library preparation will provide the best results. The data generated in this project will be used to assemble fragments of genes that can then be used for taxonomic identification, as well as functional analyses using the software package, MEGAN."*

**NZGL MiSeq competition winner Dr Mikael Boulic is investigating health issues in New Zealand schools.**



## 5. Accelerate progress in research and the development of valuable commercial outcomes

The case studies included throughout this report and within Appendix I describe the breadth of research activity and the impact on research, economic, health and the environment. These two stories are examples of how NZGL contributes to outcomes that are both of benefit to the community in terms of health and the economy as well as conducting new research that attracts world attention.



### GREGORY GIMENEZ

NZGL Bioinformatics  
Team Leader

*“The broad range of skills within the NZGL bioinformatics team allowed this project to be completed by team members with extensive experience in bacterial genome assembly and annotation. Fellow team member Elizabeth Permina and I split the work between us, performing comparative genomic and phylogenetic analyses to identify similarities and differences in metabolism across multiple strains of bacteria. Regular meetings with the BLIS researchers meant that the work could proceed rapidly, and be tailored to meet the specific needs of the project.”*

**NZGL delivered  
Bioinformatics analysis to  
support the safety profile  
of Blis probiotics.**

### BIOINFORMATIC ASSESSMENT OF BACTERIAL STRAIN SIMILARITY

BLIS Technologies (BLIS) contracted NZGL to carry out bioinformatic analysis on the genomes of two probiotic bacterial strains: *Streptococcus salivarius* BLIS K12 and *Streptococcus salivarius* BLIS M18.

Dr John Hale of BLIS says the purpose of the work was to analyse the similarities and differences between the company’s own two probiotic strains and then compare these with other published *S. salivarius* genomes. The project was carried out to support the safety profile of the probiotics.

“While only recently completed, BLIS has already compiled the data and is using it to increase its market penetration in existing countries of sale, as well as new ones.

“Furthermore, BLIS is using this data to support the expansion of its delivery formats – by leveraging existing safety data through this bioinformatic approach to petition respective regulatory authorities of countries, through regulatory applications to further accept our product as safe for human consumption.”

BLIS Technologies publishes its research and is currently preparing a manuscript, based on the results generated by the NZGL project, for submission to an internationally peer-reviewed scientific journal.

**Client:** Dr John Hale, Blis Technologies Limited

**Services:** 80 hours of bioinformatics consultancy service



## WHOLE GENOME SEQUENCING OF *Pinus radiata*

In the past year, NZGL has undertaken several major sequencing projects on *Pinus radiata* for Scion.

Projects included sequencing transcriptomes for discovery of DNA sequence differences between genotypes and the generation of a whole genome sequence data for the first ever assembly of the *Pinus radiata* genome.

Researcher Dr Phillip Wilcox says the projects would not have been possible without NZGL's subsidised sequencing services.

“The sequencing services have facilitated transitioning Scion’s research from pre-genome (data limited) to the post genome (data rich) era. The information is providing the New Zealand forest industry and the Radiata Pine Breeding Company with the confidence to work with Scion in co-developing genomic selection for radiata pine. This includes a MBIE partnership proposal. Data from the above projects are being used to develop marker panels for genomic selection and other tree breeding applications.”

He says the services also allowing Scion to be at the forefront of assembly of the *Pinus radiata* genome, including participating in an international collaboration to develop informatic resources for this species that will accompany the actual sequence.

“In the longer term, we expect the NZGL-generated data to provide the basic information for leading-edge research in areas such as disease resistance and biomaterials, further enhancing sustainability of New Zealand’s plantation forest industry.”

**Client:** Dr Phillip Wilcox, Scion

**Services:** Four MiSeq flowcells and 20 HiSeq2000 lanes of sequencing data



### LORRAINE BERRY

Facility Manager, Massey University Genome Service

*“This was a collaborative project with the Otago University Genomics Unit. The Massey University Genome Service carried out the Illumina MiSeq genomics, while Otago put together the project plan and prepared the Illumina TruSeq DNA library. The Massey work involved determining the integrity and quality of the libraries and carrying out a series of assays to determine concentration and levels of both RNA and protein contamination.”*

**Genomics research into *Pinus radiata* is enhancing the sustainability of New Zealand’s plantation forestry industry.**

## 6. Be at the forefront of international science

The impact of NZGL support for human capital development is also measurable in terms of research outputs associated with student and staff research activity.

Using information gathered in the June 2013 email survey, Table 7 summarises the output data relating to 111 items over the period September 2011 to 24 May 2013. Output categories are defined in the investment case. Several researchers indicated that as their projects had only recently been completed, they were still in the analysis phase of their research and outputs were six to 18 months away. Given that the total number of principal investigators supported by NZGL could be as high as 300, actual research outputs are substantially greater than those captured by the survey.

*Table 7: Research outputs supported by NZGL service delivery (Sept 2011 to 24 May 2013)*

Research Output Category	Number
Publications (peer reviewed and non-peer reviewed)	5
Industry or Ministry reports	4
Conference or other oral presentations	40
Poster presentations	11
Patents granted or pending	4
Publications or oral presentations pending	30
Grant application data	4
Other types of outputs such as postgraduate research theses or new data additional to existing public genome databases	13



## SEQUENCING THE TUATARA GENOME

The international biological science community is eagerly awaiting the sequencing of New Zealand's tuatara – recently identified as one of the most evolutionarily significant animal genomes in the world.

Professor Neil Gemmell says that, because of New Zealand's unique geographical position in the world, there is always a lot of interest in the country's species, but particularly the tuatara. It's not from the order containing lizards and snakes. It's a reptilian order all of its own and that's special."

In 2011 – working alongside Northland-based iwi Ngatiwai, which holds kaitiaki (guardianship) to one of New Zealand's largest populations of tuatara – Professor Gemmell and fellow scientists were provided with blood samples from a large male tuatara on Mauimua Island (Lady Alice Island) of the Hen and Chicken's group and they began sequencing of the tuatara genome.

"The tuatara genome will be one of the biggest genomes ever assembled, making it a challenging project."

Professor Gemmell says that sequencing the tuatara genome within New Zealand would not have been possible without NZGL and the Illumina technology.

"But there's another element to this. During this project, we may develop new approaches around sequencing methodology and it is not inconceivable that New Zealand scientists may attract attention for their expertise in the complex field of genomics technology. Certainly, we already punch well above our weight in this field, with our prowess well established through our agricultural, horticultural and forestry endeavours. Here, we have the opportunity to make a contribution to our understanding of life on earth through the sequencing of an organism unique to New Zealand, which is not only a taonga (treasure) to Māori, but to the world – due to its critical importance to our understanding of the evolution of many vertebrate lineages, including ourselves."

**Client:** Professor Neil Gemmell, University of Otago

**Services:** 18 lanes of Hiseq data delivered and an additional six lanes of sequencing scheduled for September 2013



### REBECCA LAURIE

Manager, University of Otago Genomics Facility

*"We recognised that this was going to be an extremely challenging project for Professor Gemmell and a project of significant value to New Zealand science. The project has required multiple sequencing libraries and types, and the implementation of new protocols for mate-pair and PCR-free libraries. Due to the success of the tuatara mate-pair libraries, this has now been added as a standard service by the facility."*

**Research into the tuatara genome is expected to also draw attention to the expertise of current and future New Zealand scientists in the field of genomics technology.**

## 7. Address critical scientific questions unique to New Zealand

A review of projects reveals the impact of activity in terms of scientific questions unique to New Zealand (Table 8).

**Table 8: Summary highlighting project contributions unique to New Zealand**

Institution or Company	Principle Investigator	Platform	Project Title	Description	Contracted End Date
University of Otago	Neil Gemmell	Illumina HiSeq	Tuatara genome sequencing	8 lanes Illumina HiSeq	Delivered during 2012
Victoria University	Kristina Ramstead	Illumina HiSeq	Little spotted kiwi and the rowi; genetic differences impacting on breeding numbers	4 lanes Illumina HiSeq	Delivered during 2012
University of Canterbury	Ian Hawes	Illumina MiSeq	V4 profiling of microbial mat communities in an Antarctic lake; microbial responses to environmental change	1 MiSeq flow cell	Due to be delivered during 2013
University of Otago	Martin Kennedy	Illumina HiSeq	Exome sequencing; investigating the link between Takutsoba syndrome/broken heart syndrome and the CHC earthquakes	1 Lane Illumina HiSeq	Delivered during 2012
University of Otago	Tony Merriman	Illumina HiSeq	Gout in the NZ population including Maori and Pacifica	13 lanes Illumina HiSeq	Delivered during 2012
University of Otago	Michael Knapp	Illumina HiSeq	Experimental sequencing of ancient DNA from New Zealand Haast's Eagle	2 lanes Illumina HiSeq	Ongoing
Landcare Research	Thomas Buckley	Illumina HiSeq	Whole genome sequencing of Weta	8 lanes Illumina HiSeq	Ongoing
Massey University	Alastair Robertson	GS Junior	Mating systems of native kowhai and tree fuschia and the potential for declines in bird pollination	1 GS Junior run	Delivered during 2012

### THE ROLE OF GENETICS IN LOW KIWI REPRODUCTION RATES

While none of New Zealand’s five species of kiwi exist in plentiful numbers, populations of the two rarest species – the little spotted kiwi and the rowi – are worrying low.

There are 1600 little spotted kiwi, spread over eight isolated locations throughout New Zealand, and 350 to 400 rowi, which all live in South Westland’s Okarito Sanctuary.

The Department of Conservation (DOC) is working hard to increase kiwi numbers through practical interventions and predator control. At the same time, Dr Kristina Ramstad – a postdoctoral fellow at Victoria University’s Allan Wilson Centre for Molecular Ecology and Evolution – is investigating how genetics might play a part in why some individual kiwi produce no chicks each season.

“A full third of adult rowi do not breed and, of those that do, half the eggs left in the wild do not hatch. We need to know why. Rowi numbers were down to only 150 or so birds in the mid 1990s and, in a population that small, mating among relatives could be common and lead to inbreeding depression. So it might be genetic differences that explain why some birds always breed and others do not, and why some eggs hatch and others do not.

“Without NZGL, we would have gone through a much smaller and far less powerful process to try and do something similar. We would have been lucky to find tens or hundreds of genes in total and even luckier to find 10 or 20 genes related to reproduction – may be fewer. Because the Illumina sequencing technology provided by NZGL is so powerful, discovering 5000 to 10,000 genes in less than a year is not unrealistic. The technology is now convenient as well. There’s no longer a need to go overseas, which adds many practical hurdles that together can quickly become insurmountable.”

**Client:** Dr Kristina Ramstad, Victoria University of Wellington

**Services:** Four lanes of Hiseq data delivered early 2012

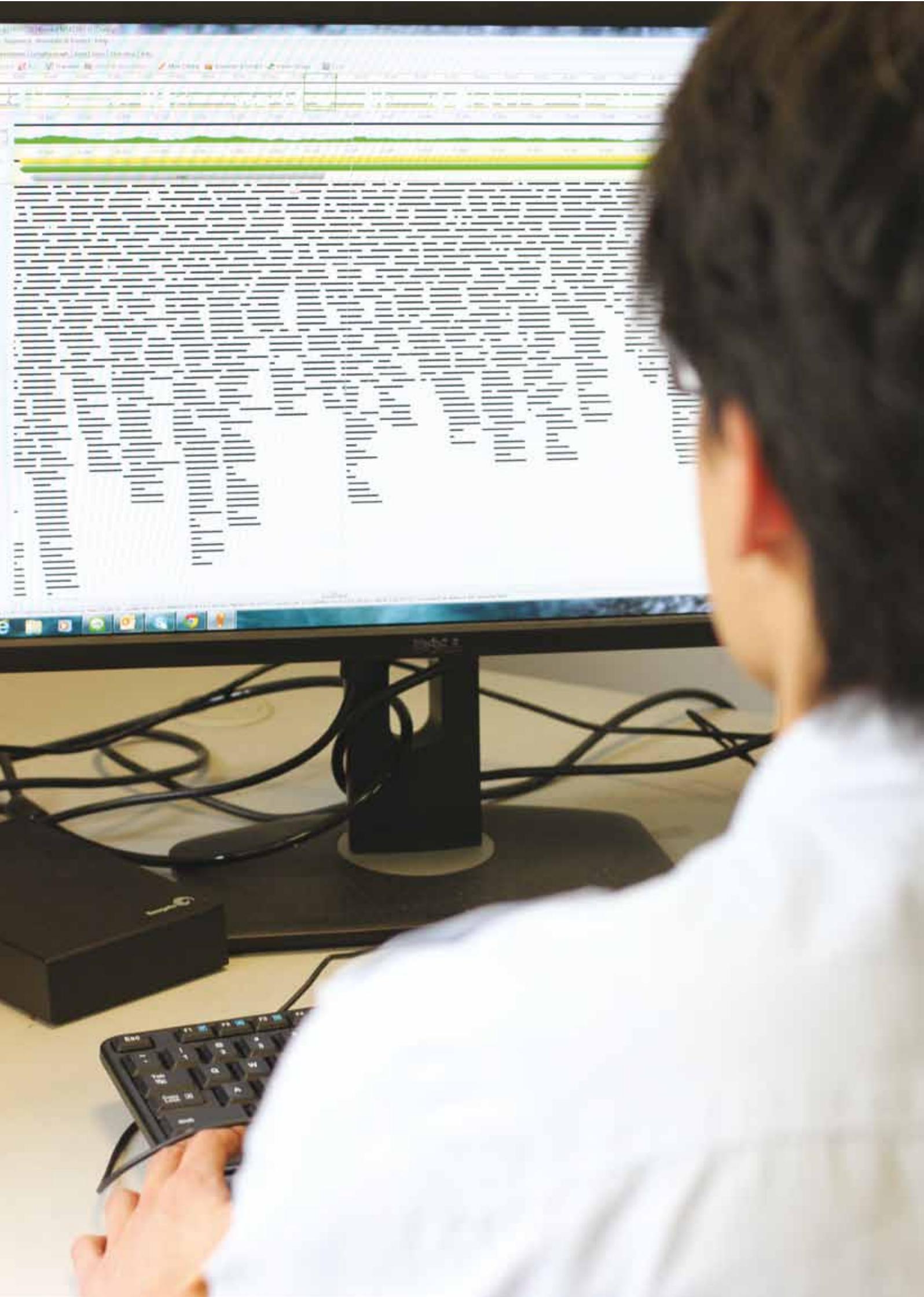


#### LES MCNOE

Sequencing specialist, University of Otago Genomics Facility

*“It is always exciting to be involved in the sequencing of an iconic New Zealand species and the opportunity to work with Dr Ramstad and Illumina on this project was very rewarding. Dr Ramstad required a rapid turnaround of data and, after overcoming several technical problems, we were able to meet these requirements.”*

**Access to genomics capability within New Zealand is speeding up research into the poor reproduction rates of some kiwi species.**



# NZGL'S ROLE WITHIN THE RESEARCH LANDSCAPE

This section summarises NZGL's involvement with other Crown service delivery investments.

## REANNZ

NZGL has contracted network management services (Network Access Agreement, signed 25 March 2013) from the Crown-owned Research and Education Advanced Network New Zealand Ltd (REANNZ). The agreement is for REANNZ to manage the network connecting NZGL to KAREN (Kiwi Advanced Research and Education Network) and the internet.

This network connects the NZGL data centre at Gen-i (Tennyson St, Dunedin) to all major research institutions across New Zealand. In this way, NZGL utilises a "trusted" high-speed network and avoids the constraints imposed by institutional firewall restrictions.

NZGL is the first entity in New Zealand to implement this network arrangement, called a Science DMZ. A DMZ, or Demilitarized Zone, is an area of an organisation's network that is close to the 'edge' of the network that has its own security policy. The Science DMZ refers to a network that allows organisations to connect specific systems and operate on a trust basis to provide more reliable and faster file transfer, which is essential to the NZGL Bio-IT operations. It is being exemplified by REANNZ as best practice for network services within New Zealand. The direct impact of the Science DMZ is enhanced data transfer rates for New Zealand genomics researchers.

NZGL is working with REANNZ to develop several initiatives that will benefit the wider research community. These include:

- **Cooperation** – NZGL and REANNZ meet regularly to explore joint projects with the potential to deliver good science outcomes to the New Zealand research community.
- **Case study and publicity** – NZGL, commercial network provider Juniper and REANNZ are participating in joint publicity to highlight the Science DMZ Science network arrangement and the associated advantages.
- **Network resiliency** – NZGL and REANNZ continue to work through connection redundancy, so NZGL connectivity is via multiple paths and therefore "robust".
- **Technical initiatives** – NZGL anticipates leveraging REANNZ expertise, as network specialists, to assist with the Science DMZ network (and other network-related activities (e.g. implementation of the cloud-based application, GLOBUS for data transfer efficiency. GLOBUS is a cloud based application that manages large file transfers between two systems. It simplifies complex operations so that the user can use point and click interface to achieve sophisticated operations.)
- **Additional cloud services** – Join forces with REANNZ and other REANNZ members to obtain favourable pricing for cloud-based services to Australia and the United States.

## NeSI

NZGL and Crown-owned NeSI are developing initiatives to benefit the research community, including participation in the recent eResearch Conference (2-4 July, Christchurch) to illustrate the Science DMZ network arrangement and efficacy. At the conference, NZGL also participated in a panel discussion on forward-looking strategic activities that might benefit the wider science ecosystem.

## EDUCATION AND OUTREACH

The NZGL Investment Case anticipated a significant role for NZGL and collaborators in terms of education and outreach:

*“The lack of advanced genomics facilities in New Zealand also means that the education of our students and future researchers will fall behind, making it more difficult for New Zealand to remain internationally competitive in the future.”*

**[Source: NZGL Investment case, p11]**

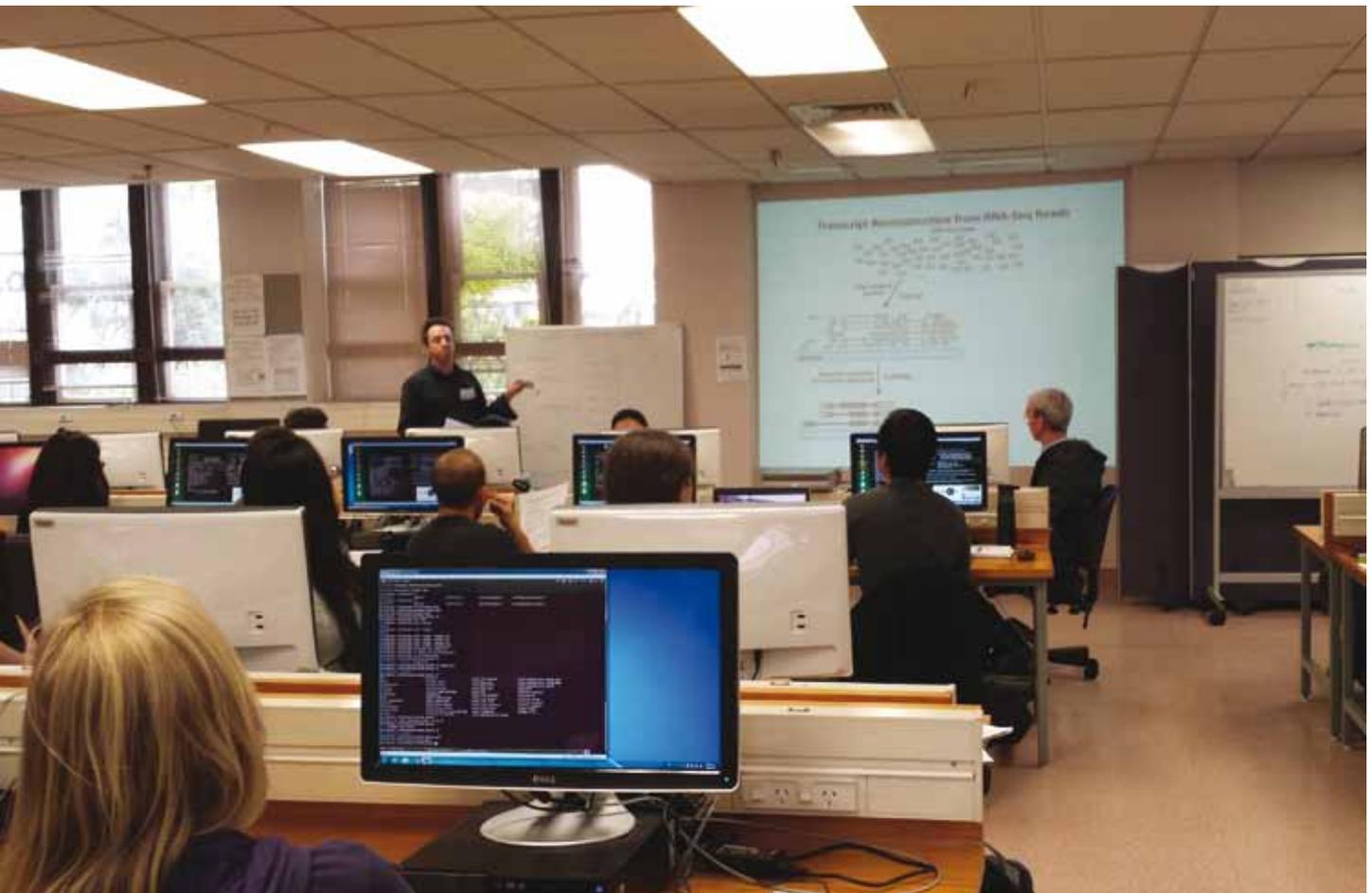
*“Future Researchers Programme: A significant benefit of NZGL will stem from its ability to provide research projects, internships, and a career path for graduates of New Zealand Universities. Hence, training is recognised as a vital component of NZGL activities.”*

**[Source: NZGL Investment case, p16]**

Table 9 details outreach initiatives to the research community. These will be the basis for further workshops – both introductory (outlining services) and specific to genomics applications – over the coming year.

**Table 9: Education and outreach initiatives for the year ending 30 June 2013**

Initiative	Results
<b>Workshops/training</b>	<ul style="list-style-type: none"> <li>Plant &amp; Food Research, Lincoln (July 2012)</li> <li>Massey University, Palmerston North (July 2012)</li> <li>Microbiology Dept, University of Otago (July 2012)</li> <li>University of Otago, Anatomy Dept x 2 (July 2012)</li> <li>Victoria University of Wellington (Aug 2012)</li> <li>University of Auckland, Medical School (April 2013)</li> <li>University of Auckland, School of Biological Sciences (June 2013)</li> <li>Sponsorship of Ensembl workshops (Sept–Oct 2013 at locations across New Zealand) conducted by outreach officer from the European Bioinformatics Institute</li> <li>NZGL 2013 series of training workshops at Auckland, Massey and Otago universities (August 2013 onwards), comprising three levels: Introductory (outlining NZGL Genomics, Bioinformatics &amp; IT Services), Advanced Bio-IT &amp; IT, and Q&amp;A Sessions</li> </ul>
<b>Seminars</b>	<ul style="list-style-type: none"> <li>CEO talk at Next Generation Sequencing Conference Otago (Aug 2012)</li> <li>CEO talk Queenstown Research Week (Aug 2012)</li> <li>CEO talk at University of Otago Microbiology retreat (Oct 2012)</li> <li>CEO talk at New Zealand Microbial Conference, Otago (Nov 2012)</li> <li>CEO talk at Ecological Society Conference, Lincoln (Nov 2012)</li> <li>NZGL chaired Session at NZBIO (Auckland) - Big Data: Tsunami or fantastic opportunity (March 2013)</li> <li>Panel discussion and Science DMZ presentation, eResearch Conference, Christchurch (2-4 July 2013)</li> </ul>
<b>Conferences</b>	<p>NZGL Sponsorship and attendance at:</p> <ul style="list-style-type: none"> <li>4th Next Generation Sequencing Conference, (Aug 2012)</li> <li>Queenstown Research Week, August 2012</li> <li>NcSi Symposium (July 2012 and July 2013)</li> <li>NZ Microbial conference (Nov 2012)</li> <li>NZ Ecological Conference (Nov 2012)</li> <li>NZ Society for Oncology Conference (July 2013)</li> <li>5th Next Generation Sequencing Conference, (Aug 2013)</li> <li>Queenstown Research Week, (Aug 2013), including Genomic Medicine Satellite</li> </ul>



## MĀORI AND PACIFIKA

Investment Case anticipated benefit to Māori and Pacifica communities. Specifically:

*“In the biomedical field, it will be possible to study health problems unique to New Zealanders, such as those which disproportionately affect Māori and Pacific Islanders”*

**[Source: NZGL Investment Case, p7]**

*“The research infrastructure will also enable all of New Zealand’s population, including Māori and Pacifica, to benefit from medical advances enabled by genomics”*

**[Source: NZGL Investment Case, p12]**

*“The governance and management structures are designed to ensure that the company has:*

*...appropriate relationship and consultation with Māori”*

**[Source: NZGL Investment Case, p19]**

NZGL has engaged in a series of initiatives, including workshops, and commissioned Phillip Wilcox (Scion) to produce a report on how to engage with Māori and Pacifica.

A framework of engagement is needed to ensure that researchers are culturally informed and provided with appropriate resources to engage effectively and respectfully. It is anticipated that the HRC Te Mata Ira project, involving Maui Hudson (Waikato), will assist with refining this framework during 2014.

Table 10 provides a summary of projects with significance to Māori and/or Pacifica communities.

**Table 10: Summary highlighting project contributions to Māori and Pacifica**

Institution or Company	Principle Investigator	Platform	Project Title	Description	Contracted End Date
University of Otago	Neil Gemmell	Illumina HiSeq	Tuatara genome sequencing	8 lanes Illumina HiSeq	Delivered during 2012
Victoria University	Kristina Ramstead	Illumina HiSeq	Little spotted kiwi and the rowi; genetic differences impacting on breeding numbers	4 lanes Illumina HiSeq	Delivered during 2012
University of Otago	Neil Gemmell	Illumina HiSeq	Genomic sequencing of the green mussel	4 lanes Illumina HiSeq	Delivered during 2012
University of Auckland	Agnès Le Port	Roche 454 GS Junior & Bioinformatics analysis	Microsatellite sequencing from stingray	1 GS Junior run and 30 hours bioinformatics analysis.	Delivered during 2012
University of Otago	Tony Merriman	Illumina HiSeq	Gout in the NZ population including Māori and Pacifica	13 lanes Illumina HiSeq	Delivered during 2012
University of Otago	Michael Knapp	Illumina HiSeq	Experimental sequencing of ancient DNA from New Zealand Haast’s Eagle	2 lanes Illumina HiSeq	Ongoing
Landcare Research	Thomas Buckley	Illumina HiSeq	Whole genome sequencing of Weta	8 lanes Illumina HiSeq	Ongoing

Institution or Company	Principle Investigator	Platform	Project Title	Description	Contracted End Date
University of Auckland	Daniel Baker	Illumina HiSeq & Bioinformatics analysis	Developing larval transcriptome profiles as a tool for assessing ocean acidification impacts on sea urchin recruitment.	1 lane Illumina HiSeq	Delivered during 2013
Massey University	Jennifer Tate	Illumina MiSeq	Development of microsatellite and SNP markers for 4 native New Zealand plants; Korthalsella, Myosotis, Manuka, and Nematoceras	1 MiSeq run	To be delivered during 2013
University of Otago	Miriam Sharpe	Bioinformatics analysis	De novo assembly of the New Zealand glow-worm, titiwai, or Arachnocampa to help to identify proteins involved in bioluminescence.	2 MiSeq runs	To be delivered during 2013
Landcare Research	Dagmar Goeke	Illumina HiSeq Illumina HiSeq	Cordyline australis transcriptomics	1 lane Illumina HiSeq	To be delivered during 2013
Massey University	Alastair Robertson	GS Junior	Mating systems of native kowhai and tree fuschia and the potential for declines in bird pollination	1 GS Junior run	Delivered during 2012



## APPENDIX I – ADDITIONAL CASE STUDIES



### REBECCA LAURIE

Manager, University of Otago Genomics Facility

*“The presence of a New Zealand-focused sequencing facility means we are able to prioritise projects of national importance. Professor Poulter required rapid turnaround of library preparation and sequencing to meet critical timeframes and requirements. We were able to prioritise his projects and deliver high quality data from sub-optimal available samples.”*

**Associate Professor Russell Poulter and Dr Margi Butler.**

### REVEALING THE SOURCE OF NEW ZEALAND’S KIWIFRUIT PSA OUTBREAK

Thanks to NZGL technology, Otago biochemists were able to accurately discover the source of New Zealand’s *Pseudomonas syringae* pv. *Actinidiae* (Psa) outbreak in kiwifruit.

Associate Professor Russell Poulter, Professor Iain Lamont and Dr Margi Butler worked with the kiwifruit industry to determine the source of the 2010 outbreak.

Initially, the technology was not available within New Zealand to carry out sequencing the whole genetic code of the New Zealand Psa strain. But, the establishment of NZGL allowed the Otago biochemists to proceed, and to do so quickly.

Through a process of elimination, Chinese pollen was confirmed as the source of New Zealand’s outbreak.

Associate Professor Poulter says NZGL’s services were critical. “New Zealand is a major agricultural and horticultural producer. It’s what we are. It’s how we earn a living. If something goes wrong, are we going to put a sample on the courier and send it to another country for sequencing? No. We need to be able to respond, prioritise and act quickly. If NZGL wasn’t here, we would never have been able to sequence the bacterium and answer the industry’s questions. The speed with which NZGL was able to process the samples, demonstrates exactly why it’s so critical to have this advanced technology available within New Zealand.”

**Client:** Associate Professor Russell Poulter, University of Otago

**Services:** Two HiSeq lanes, multiple library preparations







### MAURO TRUGLIO

Bioinformatics technician, Massey University Genome Service

*“A de novo assembly was performed on the reads using Velvet software with a variety of assembly k-mers.*

*The final assembly was obtained with the optimal k-mer size of 69. The obtained contigs were further scaffolded taking advantage of original reads’ information. The assembly was checked for 8s, 18s and 28s mRNA presence, using the software RNAmmer. Once extracted and saved, the obtained sequences were mapped against the NCBI database using BLAST search tools, producing high-scoring alignments to close family members.”*

**Researchers are using genomics technology to understand camellia petal blight.**

## SEQUENCING THE CAUSAL AGENT OF CAMELLIA PETAL BLIGHT

Camellia petal blight is caused by the fungal pathogen, *Ciborinia camelliae* (Sclerotiniaceae). This microbe infects the floral tissue of Camellia shrubs, causing an annual cycle of unsightly flower necrosis and premature bloom death. The pathogen’s spread throughout New Zealand during the 1990s devastated the domestic camellia industry and severely dented the enthusiasm of thousands of devoted New Zealand camellia growers.

NZGL’s MiSeq sequencing and bioinformatics service was used to sequence and assemble the genome of *C. camelliae*.

Massey University researcher Matthew Denton-Giles wanted to use the draft genome of *C. camelliae* to complement plant-pathogen transcriptome data previously sequenced by NZGL. A draft genome would also expand the limited sequencing resource available for this pathogen.

“Prior to obtaining the genome of *C. camelliae*, we had been unable to efficiently sort our plant-pathogen transcriptome into plant and fungal expressed sequence tags. Using the *C. camelliae* genome as the query reference, we identified about 13,000 putative fungal expressed sequence tags. Furthermore, we were able to rank the putative fungal tags based on their abundance. These data will be used to characterize the infection-associated transcriptome of *C. camelliae*.”

Denton-Giles also took the opportunity to understand the reproductive biology of *C. camelliae*, which has implications for pathogen epidemiology and will improve researchers’ ability to culture *C. camelliae* in the lab.

He says the draft sequence of *C. camelliae* has been of enormous benefit to the overall research. “It will serve as a useful resource for future endeavours to study molecular characteristics of *Ciborinia camelliae* and how they compare with other related plant pathogens.”

**Client:** Matthew Denton-Giles, Massey University

**Services:** 1 MiSeq flow cell of data, delivered March 2013



## THE DISCOVERY OF NEW HUMAN AND ANIMAL PATHOGENS

In 2009, ESR established a Pathogen Discovery Research group that uses next-generation sequencing to discover new, rare or unexpected viruses that are implicated in both human and animal disease.

The group has identified at least 24 new or interesting viruses. Some of these studies have now been published, including the report of a new enterovirus in New Zealand. Three other papers are under review and another nine publications are planned for the coming 18 months.

Confidentiality constraints prevent the full disclosure of all virus discovery projects, but examples include:

- Candidate zoonotic viruses in indigenous fauna; in collaboration with Landcare Research (Dr Dan Tompkins), New Zealand Centre for Conservation Medicine at Auckland Zoo and the Department of Conservation.
- The first reported aerosol detection of human infective agents and veterinary pathogens in an occupational setting; in collaboration with the Centre for Public Health Research at Massey University (Dr David McLean). This work was published in PLOS ONE.
- The characterisation of emerging human enteroviruses; in collaboration with ESR Clinical Virology Laboratory (Dr Sue Huang). This work was largely done in collaboration with Dr Jo-Ann Stanton, using the GS Junior sequencer at the Otago Anatomy Department. We also have a second paper in press with PLOS ONE.
- Refinement of methods for virus enrichment in metagenomic studies. Publication has been accepted in the Journal of Virological Methods.

ESR scientist Dr Richard Hall says a core technique for the projects has been the use of NZGL next-generation sequencing platforms, including the Illumina HiSeq and Illumina MiSeq instruments.

“In principle, we compare the unbiased sequence data produced from a sample to the public sequence databases. Matches between our data and the databases may indicate the presence of a new or unexpected virus (or other pathogenic micro-organism).

“Next-generation sequencing is the cornerstone of our projects and we are reliant on the provision of this from NZGL. Many of our samples cannot be sent overseas due to ethical reasons or requirements pertaining to indigenous fauna.”

**Client:** Dr Richard Hall, ESR

**Services:** A total of 56 Miseq flow cells and 2 Hiseq lanes of data were delivered progressively during 2012 and 2013

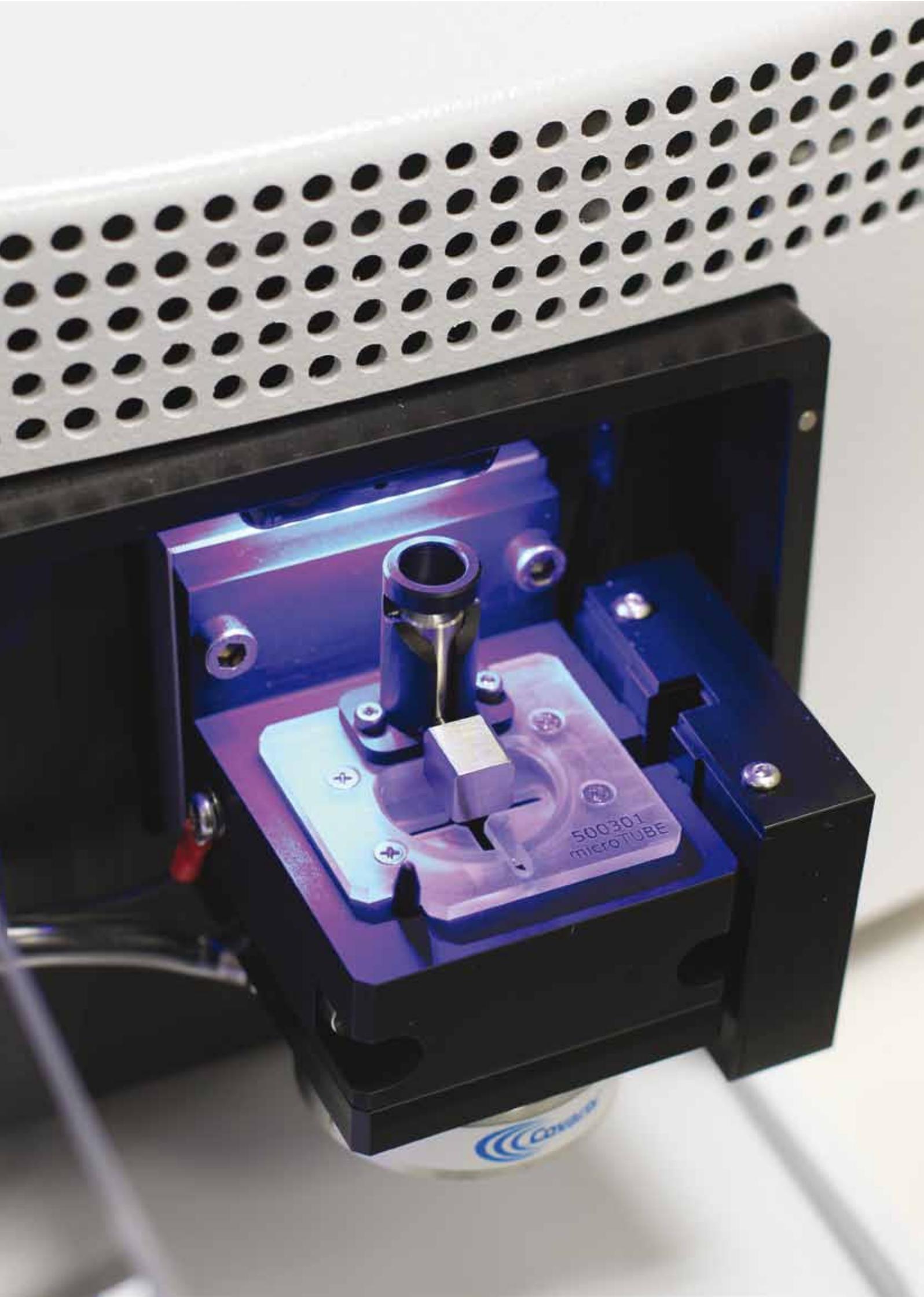


### LORRAINE BERRY

Facility Manager, Massey University Genome Service

*“The Massey University Genome Service has carried out a significant volume of work with Dr Hall, including additional sample purification work, with the removal of RNA and protein from the samples. We continue to work closely with the client and keep him abreast of new developments with regards to library preparation and Illumina MiSeq instrument developments.”*

**ESR uses NZGL Next-generation sequencing as a core technique to investigate viruses that affect human and animal health.**



## MICROBIAL RESPONSES TO ENVIRONMENTAL CHANGE

One of the most unexpected features of Antarctic lakes, is the spectacular photosynthetic microbial mat communities that develop on the lake beds, under many meters of perennial ice.

Canterbury University's Dr Ian Hawes was one of two successful NZGL-Illumina MiSeq competition winners and has received financial support to progress his work.

Dr Hawes says that, in the virtual absence of disturbance by wave action, microbial mats take on complex 3-D macroscopic morphologies. "Our research has focused on ecosystem processes associated with these complex mats. To date there has been little attention paid to microbial diversity and this proposal hopes to kick-start research towards a more thorough molecular understanding of microbial diversity in polar lakes."

Dr Hawes is using samples from Lake Fryxell, one of the perennially ice-covered lakes in the McMurdo Dry Valleys. The lake supports thick, laminated, complex photosynthetic microbial mats that cover the floor of the lake to 11.5m depth.

"Our first goal is to understand how community composition is linked to environment and macroscopic form. However, the environment in Lake Fryxell, and other Antarctic lakes, has been changing in recent decades as local climate amelioration results in lake level rise and thinning of ice cover. We need to take that into account.

"Our second goal then is to determine whether microbial community analysis provides an indicator of change. We are particularly interested in determining whether annual growth bands seen in microbial mats form a chronosequence that can be used to document such change."

The NZGL-Illumina MiSeq support will generate key baseline data and create a molecular SSU rRNA gene sequence database for bacteria to facilitate future monitoring and management of Antarctica's pristine freshwater environments.

**Client:** Dr Ian Hawes, University of Canterbury

**Services:** 1 MiSeq flowcell and 10 hours of bioinformatics consultancy

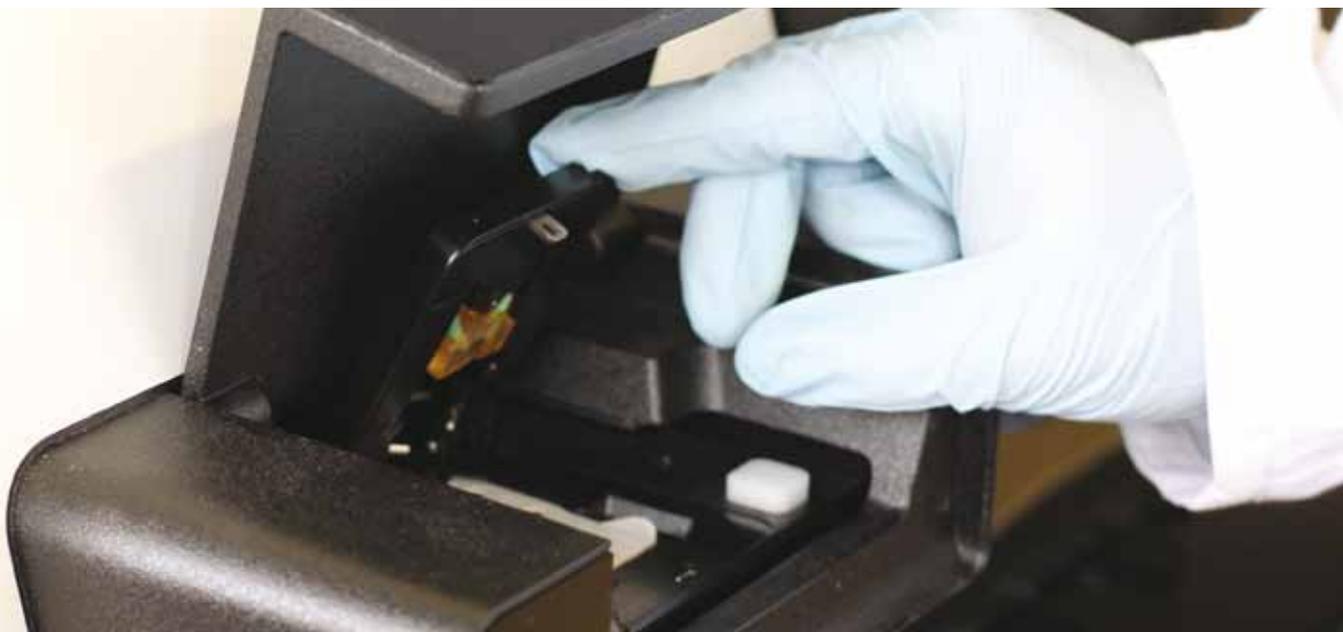


### PATRICK BIGGS

Massey University  
Genome Service

*"The Massey Genome Service has developed a protocol for 16S amplicon sequencing on the Illumina MiSeq platform and this was used for this project. The bioinformatics analysis included quality assessments of the combined reads, so that multiple outputs were generated at a couple of different quality cut-offs. In addition, tools within the QIIME software package were used for chimera analysis of the resulting FLASH software combined reads."*

**MiSeq competition winner Dr Ian Hawes uses NZGL to research microbial communities in Antarctic Lakes.**





**PETER TSAI**

Bioinformatician, The University of Auckland Bioinformatics Institute

*“For this project, we developed a highly customised bioinformatics analysis protocol with input from Dr Blenkiron and her colleagues. The protocol iteratively identified the origin of the sequenced small RNA, by searching through several publicly-available databases to accurately identify and quantify the RNAome within the wound healing maggot. This project gave us an opportunity to broaden the biological knowledge of how the clinical-grade maggot assists with wound healing.”*

**The University of Auckland’s Applied Surgical and Metabolism Laboratory is researching the role of maggots’ small RNA in the wound healing process.**

**A NEW LOOK AT MAGGOTS**

There is more to the much-maligned maggot than meets the eye.

Biotherapy that uses maggots to help heal wounds has been used around the world since antiquity.

University of Auckland researcher Dr Cherie Blenkiron is investigating “medicinal maggots” – the larval phase of the *Lucilia sericata* blowfly, bred in captivity and specifically prepared for laboratory use. She is interested in the specific small RNA molecules produced by these maggots and the possible role the molecules play in the wound healing process.

Dr Blenkiron, who is part of Dr Anthony Phillips’ Applied Surgical and Metabolism Laboratory, used NZGL to sequence the RNA molecules, then bioinformatics analysis of the RNA to determine its source. Small RNA sequencing is a powerful tool, as it can be used even where an organism’s genome is not yet fully mapped, as in the case of *L. sericata*.

Dr Blenkiron’s work confirmed that small RNA molecules are present in the maggots’ bioactive secretions. The next step is to determine if those molecules are an active contributor to the healing process.

Dr Blenkiron has already begun a series of follow-up projects with NZGL to progress the research to the next stage.

**Client:** Dr Cherie Blenkiron, The University of Auckland

**Services:** 2 MiSeq flow cells of data and six hours of bioinformatics analysis delivered during 2012



