2015/2016 Summer Studentship Project Application Form

Send to: Research Office, University of Otago Christchurch, PO Box 4345, Christchurch, by 5pm on **3 July 2015**

Supervisor Information (First named supervisor will be the contact):	
Supervisor's Name and Title(s): **Dr Andrew Laurie and Prof Peter George**	
Department: **Molecular Pathology, Canterbury Health Labs**	Institution: **CDHB**
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Mailing Address**: PO Box 151, Christchurch**	

Research Category (Choose one category only – to be used for judging the students' presentations):		
Clinical	**Laboratory**	**Community**

Project Title (20 words MAXIMUM):

Investigation of the role of founder effect in familial hypercholesterolaemia patients with LDLR gene mutations

Project Description:

Introduction: Familial hypercholesterolaemia (FH) is caused by mutations in the LDL receptor gene (LDLR). Over the past 12 years, testing of >1300 hyperlipidaemia patients at Canterbury Health Labs has identified almost 200 index patients with an LDLR mutation. Some mutations have been detected in multiple index cases, for example, D461N has been identified in 12 different families, and c.313+1G>A in 7 families. Due to New Zealand's small and isolated population, this is likely explained by a founder effect, and the different occurrences of the same mutation represent identity-by-descent.

Aim: To investigate whether multiple instances of the same LDLR mutation observed in apparently unrelated families represents identity-by-descent (i.e. founder effect).

Method: The project will involve using short tandem repeat markers (STRs) that flank the LDLR locus to construct haplotypes for the various LDLR mutation alleles represented in the cohort. This will enable identification of instances of identity-by-descent to be identified, and allow the contribution of founder effect to be quantified in the Canterbury FH patient cohort.
Specific steps in the project will involve:

1. Analysis of the CHL database of LDLR mutation patients to select mutations identified in two or more index patients.
2. Identify which samples have stored DNA available for analysis (including appropriate relatives of the index patient if available).
3. Develop a panel of STR markers linked to LDLR which can be amplified as a multiplex.
4. Analyse all samples using STR panel
5. Perform phasing analysis to construct haplotypes of the LDLR mutation allele for each family
6. Identify instances of identity-by-descent.
7. Write up findings for publication as a short report.

Student Prerequisites (eg. Medical Student) if applicable:

Laboratory experience, especially molecular (PCR etc) preferred.