From Professor Nick Martin:

Some of you have been helping our studies at QIMR for over 20 years now and I wanted to let you know just how important the contributions are that you have made. Twins and their families are important to medical research because they allow us to estimate the relative importance of hereditary, genetic factors compared to those from the environment in which we live. Specifically, identical (one-egg) twins share all their genes in common, while non-identical twins share on average one half of their genes in common; so comparing the similarity of these two types of twin enables us to put a number of the percentage of genetic versus environmental influence on a trait. Over the last 20 years, using your data, we have applied this method to hundreds of traits we have measured on you and have shown, for example, that the number of moles on the skin (an important indicator of risk for melanoma) is quite strongly genetic (around 70%), whereas whether you are left-handed is only weakly genetic (around 20%).

This newsletter is just a brief selection of the many studies we have done and that are actively underway making use of the data that you have so generously provided. The scientific output from the studies you have taken part in is enormous, with over 160 papers published so far, and comprising up to 5% of the total world output in this area – not bad for little old Brisbane! All our scientific papers are listed on our website http://genepi.qimr.edu.au and are downloadable by anyone, so help yourself! If any of you have particular interest in any of them, I would be glad to answer your questions. In particular, we are keen to encourage graduate students to come and work with us on this wonderful twin resource you have contributed to, so if you are interested, please contact me. Many thanks again for your continued cooperation.

GWAS — Genome-Wide Association Scan

The molecular genetics revolution that has overtaken science this last decade has enabled us now to go much further than ever before. Most of you have generously donated blood and/or saliva samples and from these we have been able to extract a sample of your DNA. Using ‘SNP chips’ that were first developed in 2005, we have typed your DNA for up to a million genetic variants called single nucleotide polymorphisms, or SNPs [pronounced ‘snips’]. We have then tested every one of these SNPs to see if it is associated with our measurement of interest; this technique is called a genome-wide association scan, or GWAS for short. Because we are performing so many tests there is a danger that some associations might seem large just by chance, so we have to use very stringent criteria to decide whether an association is formally significant or not. Nevertheless, in our work with your DNA we have found many associations that meet these exacting criteria and shed fascinating light on the causes of many medically related traits.

Look out for these DNA Discoveries throughout the newsletter.

Please keep in touch!
If you’re moving, let us know!

Phone: 1800 257179 (Free Call)
Email: QIMRTwinfamstudies@qimrberghofer.edu.au
Web: www.genepi.qimr.edu.au

DNA Discovery

Most of you first took part in our studies on factors that increase the risk of melanoma. In particular, we counted your moles and measured your skin, hair and eye colour. Together with our colleagues at the UK Twin Registry in London, we were the first to identify a major gene called MTAP on chromosome 9 which affects mole count and melanoma risk.

Dr Dale Nyholt, Neurogenetics Group Leader at QIMR Berghofer Medical Research Institute

Migraine

Playing a key role in the International Headache Genetics Consortium (IHGC), we studied 23,000 migraine cases and 95,000 controls to identify 12 chromosomal regions (loci) significantly associated with migraine. We have identified some candidate pathways, with 8 of the 12 loci harbouring genes with known function in nerve cell regulation, and 2 loci with genes that are well documented in vascular diseases, supporting the view that both neuronal and vascular pathways are involved in the functional changes that accompany migraine. We continue to extend our studies to discover new risk loci and will soon begin experiments to identify the specific causative gene alterations which will provide clues to the further elucidation of the complex molecular pathways of migraine and, finally, will help in the development of diagnostic tests and rational treatment strategies.
**Anorexia Nervosa Genetics Initiative (ANGI)**

ANGI is a research study just started at QIMR Berghofer. It is part of a global effort to identify genes that contribute to eating disorders. The goal of the study is to transform our knowledge about the causes of eating disorders and to work toward greater understanding and ultimately a cure. Researchers in the United States, Sweden, Australia, and Denmark will collect clinical information and blood samples from over 8,000 individuals with and without an eating disorder.

Sample size has been shown to be the critical ingredient for genomic discovery for complex diseases — the larger the sample size, the stronger the genetic ‘signal’ and the more likely the genes associated with anorexia nervosa will be identified. QIMR Berghofer will contribute data from over 2,000 participants to the initiative.

Participants will be asked to complete an online screening questionnaire and, if eligible, will be asked to provide a blood sample for DNA analysis. The project was launched on national TV and print in May 2013 and received a very positive response, with over 600 people completing the survey in the first week. To date over 1,300 people have completed the online screening questionnaire, and over 75% of these participants are eligible for the DNA collection phase, where we send out a blood sample collection kit to participants.

So far, approximately 670 participants have provided a blood sample, and plans to deliver the remaining participant kits currently in operation.

This project is currently looking for volunteers — if you have ever suffered from anorexia nervosa at any point in your life, please go to [https://angi.qimr.edu.au/](https://angi.qimr.edu.au/) and complete a brief 20-minute screening questionnaire. If eligible, we will contact you.

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**Actigraphy: Investigating the Sleep-Wake Cycle**

Obtaining adequate sleep is important. When sleep is restricted or disturbed, or the patterns of your normal 24-hour body clock are disrupted, this can have negative effects on your health, including change in weight, increased risk of cardiovascular disease and a greater risk of diabetes type2. It can also affect behavioural factors such as mood, cognitive performance and accidents.

We are collaborating with Professor Ian Hickie and his colleagues at the Brain and Mind Research Institute at the University of Sydney to examine sleep architecture and patterns of sleep behaviour, including the timing, duration and quality of sleep.

All 12-year-old twins who participate in the Twin Mole Study are invited to take part in the project at the time of their clinic visit at QIMR Berghofer. Studies of twins who are brought up together and therefore share the same family and social environment provide an opportunity to examine the contribution of genetic and environmental factors in normal sleep. Participation involves wearing an actiwatch (a wrist activity monitor) for a two-week period and completing a sleep diary.

This study commenced in May 2010 and to date over 660 twins have taken part in the project. Analysis of the data collected so far demonstrates an overall stronger association between the sleep habits of identical twins compared to non-identical twin pairs, which shows genes play a stronger role in sleep patterns than the environment.

To enable us to discover more about the effects of genes and the environment on sleep, we have recently started asking 14-year-old twins to wear the activewatches too, and we will soon be inviting 16-year-old twins and also young adult twins to join our study … so wake up and get ready to sleep!

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**19UP — Cannabis Connection**

Over 2,700 twins and their siblings have completed the 19UP project so far. Research analysts have recently started looking at these data and discovered, in the first instance, some pretty interesting things about cannabis use. First off, there has been a longstanding argument as to whether the symptoms of cannabis abuse (e.g., legal problems, using drugs in a hazardous situation, while doing something important, use causes problems with family, missing school), cannabis dependence (e.g., loss of control, using way more cannabis than planned, cannabis use interferes with work, needing larger doses), and withdrawal (e.g., feeling sick when stopping and cutting down) represent separate and distinct consequences of cannabis use, or indicate a single general tendency to develop a cannabis use disorder. Using twin data from Virginia, USA and Brisbane we have shown that all of these symptoms tend to measure a broad, general risk of developing Cannabis Use Disorder (CUD). Very recently, we have also shown that increased consumption of cannabis and other drugs such as methamphetamine and ecstasy is significantly associated with a decrease in right-side amygdala brain volume. The amygdala is part of the limbic system, which plays an important role in the processing of memory and emotional reactions. We still don’t know if it is drug use that causes shrinking or if people with lower right amygdala volume are more likely to use more drugs. Studies that we are currently working on using the Brisbane twin data will help us work out if increased drug use and smaller brain volumes have the same genetic and environmental risk factors. With more longitudinal data we hope to be able to determine the direction of causation. So watch this space!

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**DNA Discovery**

We also found another moliness gene, IRF4, on chromosome 6. Interestingly, at first we did not see the same association in the UK sample but then, in a brilliant piece of detective work by our QIMR Berghofer colleague Dr David Duffy, he realised that this gene increased mole count in teenagers but decreased it in adults. When he allowed for this the effect was apparent in the UK sample. This gene also appears to affect melanoma risk.
The Older Australian Twins Study (OATS) is the most comprehensive ageing study involving twins ever undertaken in Australia. It aims to uncover what promotes good intellectual and mental health, and what predicts decline in memory and thinking abilities later in life. Specifically, the study looks at the genetic and environmental influences, and their interaction, that may affect memory and brain health as we get older. We hope that results from our study will lead to approaches that could slow the ageing process and prevent age-related decline in function and age-related diseases such as Alzheimer’s disease.

OATS is a collaborative project with researchers in New South Wales, Queensland and Victoria. Since the OATS study started ten years ago, we have followed up our twin volunteers every two years to check on their psychological and physical health. We finished our two-year assessments in 2013 and started our four-year follow-ups. Since 2006, we have performed 1,460 memory and thinking assessments, collected 1,300 blood samples, and scanned 934 brains!

The OATS team greatly values your time and enthusiasm, and your continued support. In order for us to stay in touch with you at the various research intervals, please inform us of any changes to your contact details or availability, including your email address, as soon as possible by calling Natalie on (07) 3845 3572.

How do you find genes?
By producing genotyping data from purified DNA we look for genetic linkages between a condition/disease and one or more regions of a chromosome. When a genetic link is found, the next step is finding the exact gene responsible. This is done by using a range of molecular biology techniques, including looking directly at the composition of the DNA. This process is time consuming, highly skilled, and very expensive — but we could do nothing at all without your DNA. Incidentally, identical twins are vital to the earlier stages of our research but when it comes to actually finding the genes, it is non-identical twins and their brothers and sisters who are crucial to our success.

DNA Discovery
Everyone knows that sunburn damages skin, but by measuring the patterning on the skin on the back of your hands (remember that gooey green stuff!) we were able to quantify the sun damage and surprisingly showed that the extent of damage is affected by your genes, particularly if you are carrying red hair genes.

Along the way we have detected several new genes for hair colour and eye colour. Besides affecting melanoma risk, these also have interesting forensic applications in enabling predictions of hair and eye and skin colour from a DNA sample left at a crime, for example. We also found a major gene for hair curliness and since then I have been besieged with emails wanting us to make a straight hair pill! Unfortunately, there is no prospect of this anytime soon.

Project staff Twin Studies
L-R front row: Anthony Conciatore, Kerrie McAloney, Coral Pink, Marlene Grace, Roberta Blake, Lorelle Nunn

Genetics and computational biology
L-R: Dr Scott Gordon, Dr Gu Zhu and Dr David Duffy.

Twinning in Families
Why do some families have many twins in their family tree? Female relatives of mothers with non-identical twins are more likely to have non-identical twins themselves. We have previously shown that rare genetic variants in a gene called GDF9 expressed in developing eggs contributes to increased twinning in a small number of families. In 2010, we published a study including over 500 of our families that revealed several chromosomal locations that may contain more genes for twinning. It is now clear that many genes are likely to be responsible for increased non-identical twinning, and the search for their identity continues. We are currently conducting a new GWAS study to find these genes and hope to share new discoveries in the future.
The Asthma Genetics Study

The investigation into the genes that contribute to the risk of developing asthma has been a priority of the genetic epidemiology unit since the late 1990s. Early analysis suggested an asthma gene is located at the end of chromosome 20, a finding we reported in 2005 (American Journal of Human Genetics 77: 1075–1085). Since then, the technology used to analyse genetic data has improved dramatically. It is now possible to conduct genetic studies with much greater resolution and with many thousands of participants. In 2010, Dr Manuel Ferreira established a collaboration between our group and investigators in Melbourne, Perth and Sydney to perform such a study. The Australian Asthma Genetics Consortium constitutes the largest study of asthma genetics to date in Australia.

The goal of this project is to compare the genetic makeup (or DNA) of people with and without asthma and find genes that are different between the two groups. Identifying genes that do not work as they should in people with asthma is important because these genes may turn out to be good targets for new asthma drugs. Since the start of the project, more than 800 participants from across Australia completed the Asthma Genetics Study survey online. Over 650 were eligible to participate and asked to donate a DNA sample. As part of this project, we carried out a large international study on the genetics of allergies (asthma is often triggered by allergies) and found ten genes that increase the risk of developing allergies. Eight of these genes had been found in previous genetic studies, so our results confirm that these are indeed important in determining allergies.

On the other hand, the other two genes — called MYC and BCL6 — were particularly interesting because no one had previously suspected that they could be important for allergies. More research is now needed to understand what these genes do and whether drugs that target these genes may prove useful to treat allergies. This research was published in the prestigious scientific journal Nature Genetics in 2013. Through this project, in the next few years, we expect to find many more genes that increase the risk of asthma.

Other progress

• In 2011 we found that the interleukin-6 receptor gene (IL6R) has a more active and a less active version. The more active version is often found in asthmatics and contributes to inflammation. We have now completed a study that shows that a drug that blocks the IL6R gene — called tocilizumab — can help prevent asthma symptoms in mice. This is an important step towards being able to test if it may be useful to treat asthma in humans.

• Following on from this, we are conducting a clinical trial to test whether tocilizumab may be useful to treat asthma. This drug is currently approved for the treatment of rheumatoid arthritis but not asthma.

• Between September 2012 and October 2013 we clinically tested 150 participants at the QIMR Berghofer Medical Research Institute. This included performing lung function and allergy tests, as well as collecting a blood sample for analysis. These participants may be contacted and invited to participate in our clinical trial.

• We have started studying a specific asthma risk gene called ZBTB10 to help us understand what this gene does and whether it may represent a promising new drug target for asthma.

If you would like to participate in the Asthma Genetics study, please visit www.asthma.qimr.edu.au.

Brain Changes in People at Risk of Alzheimer’s Disease

Dementia affects over 321,600 Australians, causing problems with memory, attention, language and problem solving. Late onset Alzheimer’s is the most common form of dementia, which develops in people aged over 60 and is a complex disease that is caused by a combination of our environment and our genes. There are 20 genes that have been identified to have an effect on a person’s risk of developing Alzheimer’s. We have teamed up with Alzheimer’s disease researchers to investigate whether genetic risk factors that cause deterioration in the brains of people with Alzheimer’s also make a difference in healthy people, before any disease symptoms. We are using Magnetic Resonance Imaging (MRI) data to look at the volumes of parts of the brain most affected in Alzheimer’s disease to see if people with a high genetic risk for Alzheimer’s have smaller volumes. We are investigating both older and young people. Included in this study are the brain scans of people who have volunteered the Older Australian Twin Study (OATS), 105 of which are from here in Queensland. We hope to identify a way of detecting which people are more likely to get Alzheimer’s later in their lives, and to try and understand how and when the disease starts to develop.

DNA Discovery

From your blood samples we also measured a large number of things of medical interest, like your cholesterol level, iron levels and numbers of various kinds of blood cells. In all of these cases, and many more, we have found new genes which may eventually have application in disease prevention.
Between 1996 and 2012, in the Memory, Attention and Problem Solving (MAPS) study led by Dr Margie Wright, we collected a wide range of cognitive measures to help us understand the factors underlying intellectual ability. Twins (and their siblings) were asked to participate once they had turned 16 years of age, and data were collected from over 2,700 individuals. One of the cognitive traits assessed was relational complexity (RC) — collected in over 1,000 participants. RC reflects the number of related pieces of information that must be considered in order to solve a problem. Complex problems require us to remember more relationships. Some examples of RC tasks are Sentence Comprehension tasks, the N-term task, and the Latin Square task. In the Sentence Comprehension task, participants were given a sentence and needed to remember who did what. In the N-term task, participants needed to order a set of letters based on information given in paired sets (i.e. premises) that show greater than (>) and less than (<) relationships (see example). The Latin Square task follows the same rules as a Sudoku puzzle, with each symbol occurring only once in each row and in each column (see example). Participants were asked to solve for a particular square.

Even though these tasks appear to be quite different, performance on one task is a good indicator of performance on the other tasks. This is because each task taps the same skill — the ability to remember paired relationships. We found that this ability also predicted overall cognitive ability. Therefore, although cognitive function is a complex behaviour, this finding tells us that much of what makes us more or less intelligent than another individual is due to this basic skill. The RC metric was pioneered by Prof Graeme Halford (Griffith University) and we are fortunate to be able to collaborate with him on this project, along with his long-time collaborators, Drs Glenda Andrews and David Shum.

**Binocular Rivalry**

The Necker cube (pictured below) is a static 2-dimensional image, yet when viewed, our perception changes between two different 3-dimensional interpretations: one cube appears to sit on its base with the front face towards the left, while the other cube has its front face towards the right. Rubin’s vase (also pictured) is another well-known ambiguous figure. Like the Necker cube, it’s a static image, yet when viewed our perception spontaneously alternates between seeing the faces as being dominant or in the ‘foreground’, while the vase is in the ‘background’, and vice versa for as long as the image is viewed.

At QIMR Berghofer, we have been using a very similar visual task called binocular rivalry (depicted below). Like the Necker cube and Rubin’s vase, binocular rivalry involves viewing static stimuli. However, instead of viewing one stimulus with both eyes, each eye is presented with a different stimulus; for example, vertical gratings to the left eye and horizontal gratings to the right eye. During normal vision, our eyes view slightly different images that enable the perception of depth; however, during binocular rivalry, with very different images such as vertical and horizontal lines, to make sense of this ambiguity our perception spontaneously switches between the two alternatives. Thus, we see the vertical image for a few seconds, followed by the horizontal image for a few seconds, then back to the vertical lines and so on, for as long as the stimuli are viewed. Previous studies have shown that this rate of switching between the two images (i.e., binocular rivalry rate) is different in individuals with bipolar disorder, a highly heritable psychiatric condition. This finding has significant implications for improving clinical diagnosis and treatments to help people with mental illness.

At QIMR Berghofer, we conducted a large 10-year twin study of binocular rivalry (Miller et al. *Proc Natl Acad Sci USA* 2010; 107:2664–68) that is ongoing. It was the first in the world to show that binocular rivalry rate is heritable. This finding supports further studies we are currently engaged in, which aim to identify genes associated with binocular rivalry rate that overlap with genes known to be involved in bipolar disorder. Thus, with the help of our Brisbane twin volunteers, along with their parents and siblings, we are working towards making important and meaningful contributions to psychiatric research that will benefit individuals with mental illness and the broader community.
The Twin Mole Study

The Twin Mole Study is one of the longest running studies of the Genetic Epidemiology laboratory. It was launched in 1992 and its aim is to assess the contributions of genetic and environmental factors to the development of moles in adolescent twins. The number of moles on the body is the strongest known predictor of melanoma risk, yet relatively little is known about the causes and natural history of these common skin lesions.

When they turn 12, twins and their siblings who have registered with the Queensland Twin Registry are invited to come to QIMR Berghofer and have their moles counted and other melanoma risk factors assessed. We then ask them to return when they are 14 to be retested. Since its inception, we have seen over 5,700 twins and 890 of their siblings as part of our study. Of these participants, over 2,700 returned to take part in another adolescent twin study, the MAPS study (see related article), when they were 16 years old.

At each of the visits the twins make to QIMR Berghofer, along with counting moles and taking a DNA sample, we also collect other measures in an attempt to identify further genetic variables that may affect melanoma. With the assistance of all this extra data we have made many ‘DNA Discoveries’ some of which you can find scattered around in this newsletter. The twins also complete components of other studies when they visit us. These include the binocular rivalry task and actigraphy study. Further information on both of these interesting studies is also included in this newsletter.

Through their willingness to be involved in a longitudinal study, our Brisbane twin volunteers (and their parents and siblings) are helping us make fundamental breakthroughs in melanoma research and assisting the discovery of many new genes.

Brain Imaging Study

The Queensland Twin Imaging (QTIM) study, which began in 2007 (led by Dr Margie Wright), has MRI scanned the brains of over 1,200 adolescents and young adults, and has led to some remarkable discoveries. For example, we now have a much better understanding of the degree to which our genes and the environment influence the volumes and shapes of various brain structures and the way they connect and ‘talk’ to each other. With our colleagues in the United States (Prof Paul Thompson and his team) and the University of Queensland (Drs Greig de Zubicaray and Katie McMahon), we have also pioneered new ways to analyse the information obtained from brain scans. More recently, we persuaded other groups from around the world to pool resources in order to find genes associated with the brain. Many researchers are needed for such a study to put together the large samples that are required. Because the way our brain works is still very much an enigma, we named the consortium ENIGMA — ‘Enhancing Neuro Imaging Genetics through Meta-Analysis’ (http://ENIGMA.ini.usc.edu). ENIGMA currently comprises 125 institutions with brain images from ~21,000 people. It includes data from the elderly and the young, and both healthy people and patients (e.g., with diseases such as Alzheimer’s). In our first ENIGMA project, published in the journal Nature Genetics and led by Dr Sarah Medland from our group, we identified a genetic variant influencing overall brain size, and another influencing the size of the hippocampus. The hippocampus is a key brain structure for learning and memory. It has reduced volume in people with schizophrenia and major depression, and it is a biomarker for Alzheimer’s disease. The work is currently being extended to reveal new biological mechanisms and advance our understanding of the genetic components of brain development and brain disease.
We have measured the eyes of over 1,000 sets of twins from the Brisbane Adolescent Twin Study and the Twin Eye Study in Tasmania. Most participants were teenagers or young adults and had healthy eyes. We looked at a large number of different eye measurements in the twins, linking each trait to DNA markers across the genome. Our goal was to understand how genetic differences between individuals led to changes in the healthy eye. Although understanding the genes involved in natural variation in eye traits is interesting in and of itself, our findings have also proved very useful in understanding eye disease.

One trait we have made great progress with is the thickness of the cornea, the transparent front part of the eye. Following our early successes in finding genes influencing corneal thickness using primarily twin volunteers in 2010, we led an international effort, resulting in the publication in 2013 of a set of 27 genes involved in this trait. Although this list of 27 genes was derived from healthy individuals, we were successful in linking six of these genes to greatly increased risk in a set of keratoconus patients. Keratoconus is a degenerative eye disorder where the cornea bulges out, and is one of the leading causes of corneal transplants in Australia.

Our early twin studies helped show that myopia (short-sightedness) and related traits such as the length of the eye (axial length) are highly heritable. However, our initial studies in the Australian twins alone were unable to clearly identify any specific genes influencing myopia. We speculated that this was because each individual gene only had a small effect on myopia. We were able to confirm this was the case by joining forces with collaborators worldwide in the Consortium for Refractive Error And Myopia (CREAM). In 2013, CREAM published a set of 26 genes conferring myopia risk. Although each gene only subtly increases myopia risk, in aggregate their effect is substantial, with those carrying the highest number of susceptibility variants incurring a tenfold increase in risk. We subsequently identified further loci influencing the length of the eye.

Australian twins also helped advance our understanding of intraocular pressure, a key risk factor in open angle glaucoma. Glaucoma is the leading cause of irreversible blindness among Australians. We found two genes that influence intraocular pressure in healthy individuals, with the same genes also conferring risk of disease in cohorts of glaucoma cases and controls.

The twin eye research at QIMR Berghofer is conducted by the Statistical Genetics and Genetic Epidemiology labs, in collaboration with Professor David Mackey and colleagues at the Lions Eye Institute, Western Australia.
Height: hunting high and low
The genetics of height has been studied for over a century, because it shows a strong resemblance between relatives and has a typical bell-shaped distribution in the population. Height has also been associated with a number of diseases. We have shown in a number of studies that use twins and their siblings that the heritability of height is very high, about 80 to 90%. This means that of all variation between people in height, most is due to the genetic difference between these people. We found that self-reported height is almost as accurate as clinically measured height, which is reassuring and evidence that participating twin families take care when filling in questionnaires or answering questions on the phone. Thank you!

Most people shrink a bit when they get older but forget about this when self-reporting height. Quite understandable — presumably everyone remembers their height from measurements when they were young, or simply report the measure as given in their driver’s licence.

We are now conducting research in finding genes that can explain some of the variation in height between people. Our studies at the DNA level have shown clear evidence that very many genes are involved. We have teamed up with overseas colleagues, using data on DNA and height from hundreds of thousands of people, in an endeavour to detect more genes that influence height.

Effects of Early Experiences and Alcohol Use
This study has been collecting information from twins and their family members over the past three years to better understand the effects of childhood experiences on later life. The research originated from previous QIMR studies that have shown trauma survivors to have increased rates of alcohol and drug dependence, but did not identify the actual causal role of trauma, controlled for other environmental stressors and genetic factors. To this end, this study combines alcohol, cigarette and drug use data from prior studies, as well as previously collected DNA, with new information on childhood events and relationships to better examine the role childhood trauma has in the development of alcohol and drug use. The project commenced in 2010 and finished in August 2013. During this period, we invited 3,600 twins, siblings and their spouses to participate in the study. Overall, 1,880 completed a telephone interview and online questionnaire. Data is now being cleaned for analysis.

Are you a twin? Do you know other twins?
Would you like to help medical research?

QTWIN NEEDS YOU!
QTwin is a population-based registry of identical and non-identical twins (including boy-girl twins) of all ages. All adult and child twins, born in or currently living in Queensland, are eligible to register. Triplets and other multiples are also encouraged to join. Twins under 18 need a parent’s signature on the registration form.

Registering with QTwin does not mean you are obliged to participate in any particular study. We will contact you about each new study that is proposed and invite you to consider participating. Membership is free, and you may be eligible to receive monetary reimbursements (from $25–$100) for your participation.

Register online now to be involved in current research projects looking in to:
Twinning in families; the genetics of brain ageing; substance misuse and mental health; eating disorders; human behaviour and health outcomes; the genetics of decision making; and many more!

To register online, visit our website
www.qtwin.org.au

Queensland Twin Registry (QTwin), Genetic Epidemiology Unit
QIMR Berghofer Medical Research Institute, Brisbane, Queensland, 4006
Phone: 1800 257 179 (free call) Fax: (07) 3362 0101
Email: info@qtwin.org.au Website: www.qtwin.org.au

Q Twin observes the National Privacy Principles (Privacy Act 1988) and the code of conduct set out in the National Statement of Ethical Conduct in Human Research.