University of Otago
Te Whare Wananga o Otago

Centre for Gene Research
NEWSLETTER

Volume 2 Number 2 June 1995

Guest Editorial Dr Ron Heath is Assistant Vice-Chancellor for the Division of Science

The knowledge uncovered by gene research represents one of the major accomplishments of modern science - as a (ex) physical oceanographer I am, of course, unqualified to comment on the details! The importance of gene research is recognised by the University in setting up the Centre for Gene Research to provide a research focus in the University and the wider scientific community. This focus is facilitated via research workshops newsletters and the Centre acting as a host for specialised equipment such as the DNA sequencer.

Centres, such as the Gene Research Centre, can have a very short life as initial enthusiasm wanes. Clearly this is not the case for the Centre for Gene Research, having been established in 1990, the Centre is clearly now well established and highly successful. The success undoubtedly depends not only on the significance of the research, the co-operative attitude of the scientists involved but must to a large extent be due to those who continually promote the Centre and maintain its infrastructure, the Centre's Director, Associate Professor Murray Grigor, the Editor of the Newsletter, Craig Marshall. Congratulations to all those involved with the Centre, I wish you continued success for the future.

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New Faces:

Herman Pel, Post Doctoral Fellow, Department of Biochemistry outlines his journey to Dunedin:

Amsterdam -> Orsay -> Dunedin

My trip towards New Zealand started in 1989 when I worked as a PhD student under the supervision of Prof. Les Grivell in the department of Molecular Cell Biology of the University of Amsterdam. At that time I incidentally cloned a gene that turned out to code for a mitochondrial peptide chain release factor in the yeast Saccharomyces cerevisiae. Even though I was supposed to work on mitochondrial self-splicing introns, I was quite happy to analyze two release factor mutants as well. After my PhD I went to the laboratory of Dr. Monique Bolotin-Fukuhara (Institute for Genetics and Microbiology of the University of South-Paris) and exploited the powerful yeast genetics for the isolation of mutations in the mitochondrial small ribosomal RNA that suppress a release factor mutation. The aim of my current stay in Warren Tate's laboratory is a biochemical characterization of wild-type and mutant mitochondrial release factors. If you would like to contact me: don't hesitate and try room 138 or herman@sanger.otago.ac.nz.

Another new face in the Tate group,

Elisabeth Grundner-Culemann, describes her journey to New Zealand

Hanover (Germany) ----> Dunedin

Perhaps I should mention beforehand I studied Biology and Theology/Philosophy and I am interested in evolution theory for longer time. In 1992 I was working as a microbiologist in the Gene Laboratory of the Department of Haematology and Oncology in Hanover University Medical School (Prof. Poliwoda). From there it was only a five minutes walk to the Max Planck Institute of Endocrinology to attend Prof. Warren Tate's lecture on how termination codon directs selenocysteine insertion and the interesting evolutionary aspects of this mechanism.

After finishing my PhD in February on the identification and characterization of a human serum protein, I came to NZ 1st March 95, and I am glad to continue Martin Oertel's work on selenoproteins in Warren Tate's laboratory.

contact address: room 138 ph. 479-7859 or grucu@sanger.otago.ac.nz.

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Dr David Grattan, Department of Anatomy and Structural Biology

Dave has recently been appointed as a Lecturer in the department of Anatomy and Structural Biology, following completion of a three year postdoctoral research fellowship in the Centre for Studies in Reproduction at the University of Maryland at Baltimore (UMAB), U.S.A. He is interested in the neuroendocrine regulation

of reproduction, focusing on the mechanisms by which pituitary and gonadal hormones feedback on the central nervous system to regulate activity of specific hypothalamic neuronal systems. While his experience is primarily in the use of neurochemical assays to study neuronal activity, he has recently begun to use molecular approaches to quantify changes in levels of expression of mRNA in the brain in various reproductive states. His specific interest has been in examining the effects of gonadal steroids on level of expression of mRNA for glutamic acid decarboxylase (GAD), the rate limiting enzyme responsible for GABA synthesis. A modified RNase protection assay has been used to quantify GAD mRNA in microdissected brain nuclei (100-200 µg issue). This "microlysate" RNase protection assay involves homogenizing the microdissected tissue in a solution of guanidine isothiocyanate (GuSCN), hybridizing with riboprobe in the GuSCN solution and then exposing the entire homogenate to RNase digestion. Thus, the assay does not require prior extraction of RNA, avoiding potential extraction problems dealing with such small tissue samples. Together with Drs. Mike Selmanoff and Peg McCarthy at UMAB, Dave has demonstrated that mRNA levels for both forms of GAD (GAD65 and GAD67) are significantly reduced in the rostral preoptic region of the rat hypothalamus during the estrogen-induced surge of luteinizing hormone (LH) secretion. GABAergic neurons are known to exert a tonic inhibitory action over LH-releasing hormone neurones in the hypothalamus. The observed decrease in GAD mRNA concentrations in this region, thought to be indicative of a decrease in GABAergic neuronal activity, may be a critical factor allowing the generation of the LH surge.

Dave is currently in the middle of writing numerous grant applications, in order to establish his research program here in Dunedin. As well as continuing to use neurochemical assays for measurement of GABA and catecholamines in the brain, future plans include the use of the microlysate RNase protection assay for quantification of mRNA for GAD and tyrosine hydroxylase in microdissected brain regions, and PCR for detection and quantification of mRNA for prolactin receptors in specific nuclei of the hypothalamus.

David can be contacted by phone, extn 7442, Fax, extn 7254 or email david.grattan@stonebow.otago.ac.nz

Ralf Meisel, Postdoctoral fellow, Department of Biochemistry

Ralf came to New Zealand on a grant from Germany's DAAD to join Mike Murphy's group working on mitochondrial stress in human diseases.
Ralf studies biochemistry at the University of Tubingen, Germany. During his PhD work at Prof. Ulrich Weser's lab he developed a non-immunogenic low molecular weight active centre analogue of Cu_2Zn_2 superoxide dismutase (SOD), which is now used in the treatment of oxidative stress-related diseases. Ralf specialized on oxidative stress-dependent signal transduction pathways and spent the last 4 years at Prof. Avrion Mitchison's German Rheumatology Research Centre, Berlin, working on the aethiopathogeneisi of inflammatory and autoimmune diseases. During his stay in Dunedin, Ralf will concentrate on the influence of cytokines on mitochondria and their effects on nitrogen- and oxygen-radical-dependent signalling processes.

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Meeting Report: Liz Poole writes:
In May, Warren Tate, Herman Pel, Jules Horsfield and myself flew summerwards to attend the **"Frontiers in Translation - an International Conference on the Structure and Function of the Ribosome"** held in Victoria, BC. Canada. This meeting is THE one for ribosomologists and aficionados of translation. Held every three years somewhere in the rich parts of the northern hemisphere, it is a forum of the latest ideas on how the multifaceted ribosome, transfer RNA's and helper protein factors interact to produce polypeptides.

Mostly this was a meeting where structure and function dominated. Harry Noller gave the opening lecture on "New approaches to understanding the structure and function of ribosomal RNA". For those not familiar with his work, he is one of the "heavyweights" of structural ribosomology. His group has been one of those at the forefront using new methods such as localised hydroxyl radical probing from Fe(II) tethered to specific positions of individual ribosomal proteins to study three-dimensional folding of 16S rRNA. Also they have recently used a damage-selection approach which combines chemical modification of bases with selection of active, modified 30S subunits using

3' biotin-linked tRNA and found, for example, that modification of any of a small number of bases in 16S rRNA abolishes tRNA binding to the P site on 30S rRNA. These nifty technical advances set the scene for what followed, with groups using all kinds of sophisticated tags such as phenanthroline (which can be tethered to thio-'anything', then in the presence of Cu^{++} and reducing conditions cleavage occurs of anything near it) as well as more conventional approaches using cross-linking and footprinting, to specifically probe the ribosome, ribosome-tRNA and ribosome-protein interactions. One particularly novel approach was to use designed oligo analogues of the decoding region of 16S rRNA to study function.

Some of you might be bored silly with all these fancy ways of revealing interactions, I make no apologies. What did not fail to really excite all participants was the presentations from those designing ribosomal models. Richard Brimacombe's group had used a high-resolution three-dimensional EM model and a computer to intelligently place known structural components within the model, taking into account all known interactions. The result was an impressive colourful model that rivalled those of the crystallographers presentations later. Of these, Joachim Frank presented a video of his particularly beautiful ribosome model based on cryo-EM reconstruction. It was intriguing that in this model there is two possible exit sites for the polypeptide - why this might be so is anyone's guess at the moment.

For those of you with a microbiological bent, several presentations dealt with the specific sites of action of antibiotics that inhibit ribosomal function. Of particular interest to us was one describing the structural basis of paromomycin binding in the decoding site of *E. coli* 16S rRNA. These workers had made an oligonucleotide to the decoding site and looked for bases protected from chemical probes by binding of A site tRNA or aminoglycoside antibiotics. Other studies had been done using mutants.

The meeting wasn't entirely structural or functional. The 'Translation' session contained Warren's presentation on translational termination efficiency in bacteria and mammals being regulated by the base following the stop codon (very well received[no parochial bias of course!]), a description of the newly described eukaryotic release factor, as well as presentations concerning various factors involved in translation. At the end of the meeting the session on 'Fidelity' discussed alternative events during translation such as frameshifting, suppression etc.

This brief review can't hope to do justice to the breadth of the Meeting. It was attended by nearly 300 participants (a very congenial size) and there were well over 50 speakers and 238 posters. In general, it was the leaders of groups that gave oral presentations with the rest of the 'troops' 'person-ing' the posters. The venue was a very up-market Conference Centre in the centre of Victoria which is situated around a most beautiful harbour. Of course, we were all avidly listening to every presentation, but when we did get out into the mid-20oC bright sunny days (at lunchtimes) we were able to enjoy the street cafe's, buskers, flowers, Hermann's beer and other little hedonistic delights!
Unfortunately, Warren had booked our tickets and we had to whisk ourselves back immediately afterwards to regenerate the home group. So, we will have to explore the very beautiful (honestly) Vancouver Island another time. In any event, it was a superb meeting and if any of you would like to examine the proceedings in more detail then feel free to come and borrow the books from one of us.

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Sequencer news

The last month has not been a happy one for the sequencing service. Because of an intermittent fault in the printer we have been unable to print a hardcopy of anyones results. Despite sending the printer to the agents in Auckland and the computer being thoroughly tested by experts from Computer Services the problem remains so ABI is replacing the printer. The new printer should arrive early next week and we shall be able to send out the hard copy of your results. Please be patient while we try and print out all the results required. If the printing on the new printer takes as long per page as the old one it will probably take about three days to get all the printing done.

Perhaps the only good thing that has come from this month is that a number of groups have been forced to use the SeqEd software to look at their sequencing data and are realising how useful it is. If you haven't tried looking at your sequence with this software we suggest that you give it a try. A copy of the application

plus a reference tutorial is in a folder labelled "SeqEd" on the DNA Sequencer Mac. Just use the AppleShare command under chooser to select the Biochemistry Zone and then DD's Mac (we must change the name some time!). Register as a guest and then open the biochemistry folder. You can copy the contents of the Seqed folder into your own Mac. If you are not a Mac user - tough, this programme only works with Macs. Also you really need a colour monitor to make best use of it.

Our thanks to Betty Lumsden who has filled Vicky Morrison's place until a permanent replacement can be found.

We are also very grateful to Craig Marshall for allowing us to down-load all the gel information from the last month on to his optical disc drive. Without this we would have been unable to keep the service operating.
What is the best way to make DNA templates ??????? the perennial question we get asked. Below are two methods we suggest but if your current method is working well we suggest you be conservative and stick with it. If you are having problems however the following two methods have proved very successful.

Jo Penty from the AgResearch MBU recently trialed the Promega product, Wizard 373 DNA preparation kit, which according to the manufacturer was designed especially for the DNA sequencer. Jo used the kit to prepare plasmid DNA and got very high quality sequence from the sequencer and is now planning to use the kit routinely.

Martyn Kennedy from the Zoology Department has been get getting consistently very good sequence for his PCR products and so we have asked him to share his method with everyone. Martyn writes very modestly:

"Apparently my sequence results are reasonably consistently good. I manage this through good fortune, persistence and a relatively easy system with which to work. Part of my study is on the phylogeny of the Pelecaniforms (tropic birds, frigate birds, pelicans, gannets, boobies, darters and shags) and to construct this I'm sequencing about 400bp of mtDNA. Once the DNA is extracted (from muscle/liver tissue mainly but occasionally feathers) it's then PCR'd using universal human 12S primers with optimised annealing temperature (57°C) and $MgCl_2$ ([1mM]).

Once I have PCR product I gel purify it using GELase (Intermed Scientific) to digest the low melt agarose. The DNA can then be ethanol precipitated. This method has worked consistently well for me (to date anyway) From there I simply resuspend it (checking the purified product on a gel) and take it to be sequenced. For the sequencing I use internal forward and reverse primers which generally work well with the exception of a couple of species. The internal primers were designed from seabird sequence that had previously been generated in Graham Wallis' lab."

Once again please be patient until we can get the new printer installed

Allan Crawford and Tracee Lawrence

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Other travels: David Jones has recently returned from study leave spent partly in the US, Europe and South Africa.
He was able to attend three major meetings relating to the genetics and physiology of anaerobic industrial microorganisms. These included a specialist meeting, CLOSTRIDIUM III, held at Northwestern University, Ill, International meetings on the Genetics of Industrial Microorganisms the congress of the International Union of Microbiological Societies in Prague. Time was spent in Washington at the US Patent Office perusing some 60 patents relating to the acetone butanol fermentation process. The second part of his leave he spent in South Africa mainly at the University of Cape Town. David notes the recent changes in South Africa:
"The period following the April elections proved an extremely interesting time to pay a return visit to South Africa. One was aware of a noticeable change in atmosphere and many positive developments were evident. Unfortunately these were balanced by many negative aspects including the very high level of crime, violence, inflation, unemployment , social problems and a general trend to lawlessness. Whilst in Cape Town I received invitations to visit and deliver seminars at the University of Stellenbosch and the University of the Western Cape, extending the opportunity of experiencing first-hand the changes which are taking place within the South African university system. As a result I find it difficult to remain optimistic about the top universities being able to maintain international standards."

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Group Profiles
Deer Research Group - University of Otago

Deer: A New Animal Model for the Study of Tuberculosis

In 1983 Dr Frank Griffin began to study the impact of stress on intensively managed deer as an example of a newly domesticated species. A diagnostic laboratory was subsequently set up in response to a threat posed by the spread of tuberculosis Mycobacterium bovis) within the rapidly expanding deer farming industry. While the development of better diagnostic assays was the initial research objective, it soon became evident that farmed deer represented a new animal model for tuberculosis (Tb) research which had many advantages over laboratory animal models. In 1986 the Deer Research Laboratory (DRL) was formally established to investigate the immunology, epidemiology, pathology and diagnosis of Tb in this natural host. The findings in deer have been extended to include other ruminants e.g. cattle, and exotic wildlife such as oryx, gazelles and camelids. Major collaborative studies are currently underway to identify in vitro markers of immunity to Tb and thereby develop more effective vaccines against it.

Diagnosis of Tuberculosis: The development of an improved in vitro diagnostic test for tuberculosis was an early research goal of the DRL. A highly specific (98%) and sensitivity (>95%) test called the blood test for tuberculosis (BTB) was developed and is now widely used within New Zealand and North America. This is the first composite diagnostic test which monitors the changes in the relative contributions of cellular and hum;oral immune mechanisms at various stages of infection by tubercle bacilli.

Infection: As the DRL receives blood samples from throughout New Zealand and North America it is well placed to identify herds of "interest". Longitudinal studies of such herds have allowed us to gain valuable epidemiological information concerning factors that predispose to Tb, the spread of Tb under various environment conditions and the pathology of natural infection. The quantitative nature of the BTB has applications in identifying the severity of disease and gives some insight as to whether immunity to Tb may have developed.

Though collaborative with Colin Mackintosh (AgResearch) we have access to a quarantine farm to establish experimental infection under strictly controlled conditions. The pathology of experimentally induced disease has been compared with naturally acquired disease. The route and dose of M.bovis have been manipulated to give the normal spectrum of pathology while leaving a proportion of the animals disease free (immune?). An intratonsilar challenge route produces Tb which is indistinguishable from natural infection. This model also provides the opportunity to test vaccine efficacy under controlled conditions by introducing animals given various candidate vaccines.

Vaccine Development: Initial studies centred on establishing the kinetics and type of response obtained after vaccination and boosting with the prototype human BCG vaccine. Results indicated that the use of killed BCG in an oil adjuvant induced an immune response that mimicked the response found in naturally diseased animals. If live BCG alone was used then the immune response induced was similar to that found in naturally infected animals without disease. Subsequent trials have looked at the effect of prior exposure to nonpathogenic, environmental mycobacteria on vaccine responses. Initial studies show the vaccination with live BCG produces significant protection against experimental infection with M.bovis

Current trials are designed to measure the efficacy of different strains of BCG as vaccines, the influence of vaccine dosage and route of vaccination. The discovery that killed BCG in oil adjuvant induces a disease-like response in deer is a valuable spinoff from the vaccine trials. A noninfectious disease model, allow us to test immunological hypotheses before confirming them in the virulent challenge model. As the vast majority of published evidence suggests that BCG in immunogenic in immunologically competent individuals our research has begun to focus on vaccinating the compromised host. New recombinant forms of BCG are also being developed in an attempt to improve the efficacy of BCG in such individuals, by immunopotentiating their response to the vaccine.

Predisposing Factors: As with humans most healthy deer are resistant to Tb. Susceptibility may be determined by genotype or factors such as climate, nutrition, age and stress. In collaboration with Allan Crawford; Molecular Biology Unit (Ag Research), the Class II MHC genes of deer are being cloned and sequenced to identify the various DR alleles and whether these may be associated with resistance or susceptibility. Genes (NRAMP) known to be involved in innate resistance are also being studied in stags which are susceptible or resistant to Tb. Collaborative studies are also being carried out between our laboratory and Joe Templeton's group at Texas A & M University who have a bovine model for Tb resistance. The predisposing effect of stress on disease susceptibility is well documented. Experiments are underway using dexamethasone to immunocompromise animals and simulate a 'stressed state' before exposing them to experimental challenge with M.bovis.

Characterisation of the Cervine Immune Response: A battery of monoclonal antibodies specific for lymphocyte subpopulations have been identified. The genes for IL-2, IL-4, IL-10 and γ-IFN have been cloned and bioassays to detect cervine cytokines have been developed. A Fluorescent In situ

Hybridisation technique based on the production of fluorescent copies of cytokine mRNA by "in cell" PCR is being developed to allow Type 1 and Type 2 T-cells to be identified and quantitated. By adapting up-to-date technology and using cross-reactive reagents developed in other species we have been able to rapidly expand our knowledge of the cervine immune response, its components and how they interact. To date, we have shown that there is considerable cross reactively between monoclonal antibodies against lymphocyte surface markers, cytokines and gene probes in the ruminants. There is little cross reactivity between the components of the ruminant and human, or murine, immune system. In addition, the cervine immune system appears to be like other ruminant systems as seen by the relatively large number of circulating γδ-T-cells.

The Future

The facilities now available at Otago University are unique. The DRL and its associated experimental farm (AgResearch) plus the network of collaborative projects that have been established will, for the first time, allow well controlled field experiments to be carried out on a naturally susceptible host. The data generated will greatly advance our knowledge of tuberculosis and immunity to it. The model system developed at Otago offers other workers the opportunity to test potential candidate vaccines in the field under conditions of natural infection. Research efforts aimed in defining strategies to identify "protective immunity" rather than immune responsiveness per se , will hasten the generation of data from vaccine studies, of direct relevance field situation.

Acknowledgments: Work carried out in the DRL is funded by the New Zealand Animal Health Board (AHB), the Game & Industry Board (GIB), the Foundation for Research, Science & Technology (FRST) and the Deer Farmers Association (NZDFA). Most of the research has been carried out in collaboration with AgResearch.

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Group profile: Mammalian gene expression - Murray Grigor writes:

This title is about the best I can do for a group that covers studies on lactation in the possum, membrane transport systems and molecular genetics of hypertension.

Our possum work arises from a long standing interest in gene expression in the mammary gland. This is the perfect organ for studying regulation of gene expression. Each cycle of lactation is accompanied by growth of the gland during pregnancy, differentiation around parturition, secretion of large amounts of a biologically unique fluid during lactation and then regression and apoptosis following weaning. Each of these changes is controlled by hormones on which the effect of various nutritional regulations can be superimposed. We began to study the possum several years ago because of the unusual lactation strategy that marsupials have adopted. Two years ago we obtained FRST funding which has enabled us to step up our work here with the goal of understanding the regulation of possum mammary gene expression. Lactation in marsupials is characterised two distinct phases. In the early phase (< 110 days in the possum) the pouch young remains firmly attached to the nipple. Growth is slow and the milk has a low protein/high carbohydrate content. Around 100 to 120 days the milk switches to become much more like that of other mammals. The pouch young can leave the pouch and growth is now much more rapid. **Christine Piotte** (post-doctoral fellow) has been working for the last 18 months on a systematic identification of the whey proteins and their changes during lactation. She also has produced a couple of mammary cDNA libraries corresponding to the early and late lactation phases. Screening these has helped us identify novel milk proteins that are expressed in a stage-specific fashion during lactation. **Melanie Ginger** (PhD student funded by MAF Policy) is doing similar things with the casein fraction and **Airlie Hunter** (BSc Hons) is examining the possum β-lactoglobulin. Shortly the team will be joined by **Jerome Demmer** and **Ian Ross** with funding from a new FRST grant. Their task will be to examine the promoters and transcription factors involved in the regulation of selected milk protein genes, particularly those expressed in only one phase of lactation. This will allow Jerome to continue the work on the regulation of milk protein synthesis he was doing on his post-doc in Edinburgh.

Other work examines the molecular genetics of hypertension and is funded by the HRC. High blood pressure has been shown to have a strong genetic component with multiple genes likely to be involved. Studies with inbred rats are facilitating the identification of these genes. We are fortunate in having access to the New Zealand Genetically Hypertensive (GH) rat, inbred here at Otago some 35 years ago. This strain has not previously been subjected to modern genetic analysis. **Jean Harris**, **Bill Porteous** and **Tumi Toro** (MSc student) are currently examining a F2 cross between the GH and normotensive Brown Norway (BN) rats looking for genes that co-segregate with blood pressure or cardiac hypertrophy. Results to date have been most exciting showing the presence of new genes and new associations not detected previously in the analysis of other rat crosses. This work has recently expanded with collaborations with groups in Boston and Melbourne. The Boston group has recently published the gene map of the rat and we are working together on the characterisation of QTLs in the GH rat detectable using the markers developed for the rat gene map. The Melbourne group has another rat cross and DNA is being shared across the Tasman and we plan to develop a new rat cross in Melbourne which will be

analysed in all three centres.

We are also examining the transport of various substrates into cultured vascular smooth muscle cells from normotensive and hypertensive rats and its regulation by various vasoactive hormones. **Boon Low** began this work four years ago looking at the regulation of glucose uptake into these cells and he has recently submitted his PhD thesis describing the regulation of amino acid uptake. He has characterised several transport systems and examined the regulation of System L (carries leucine, phenylalanine etc) in response to changes in the glucose concentrations of the media and of System y+ (lysine and arginine) in response to agents such as angiotensin II. A smooth muscle form of the gene responsible for this, CAT-1, has been cloned. Boon is currently working in the department as an Assistant Lecturer before leaving us later this year to take up a post-doc in Singapore at the Institute of Molecular and Cellular Biology of the Singapore National University. His current interests and those of **Denzil Gill** (BSc Hons) are in the interaction of the arginine transport and nitric oxide production in muscle cells in response to different cytokines and vasoactive agents. In parallel with this work we have been studying the same transport systems in the mammary gland with support from AgResearch at Ruakura. **Brydon Bennett** lead the way here examining glucose transport and its regulation in rodent and ruminant mammary tissue. His work included the cloning of a Glut-3 gene from the sheep. He is now on post-doc in Michigan (with Tony Manning who gained his PhD at Otago some years back). **Mahmoud Kiaei** is continuing the mammary aspect of the work looking at the System y+ transport system for his PhD work.

Recent publications:

Low, B.C., Ross, I.K. and Grigor, M.R. (1992) Angiotensin II stimulates glucose transport activity in cultured vascular smooth muscle cells. J. Biol. Chem. 267, 20740-20745.

Low, B.C., Ross, I.K. and Grigor, M.R. (1993) Characterization of system L and system y+ amino acid transport activity in cultured vascular smooth muscle cells. J. Cell Physiol. 156, 626-634.

McCracken, J.Y., Molenaar, A.J., Wilkins, R.J. and Grigor, M.R. (1994) Transferrin gene expression in the rat mammary gland: spatial and temporal expression. J. Dairy Sci. 77, 1828-1834.

Burdon T.G. , Demmer J., Clark A.J. and Watson C.J. (1994) The mammary factor MPBF is a prolactin-induced transcriptional regulator which binds STAT factor recognition sites. *FEBS letters* **350**:117-182

Watson C.J. and Demmer J. (1994) Procedures for cDNA cloning. in *DNA cloning-core techniques: A practical approach.* (Ed D.M. Glover) IRL Press (Oxford U.K.) p85-119

Demmer J., Burdon T.G., Dijane J., Watson C.J. and Clark A.J. (1994) The proximal MPBF (MGF) binding site mediates the prolactin responsiveness of the sheep BLG promoter in CHO cells. *Molecular and Cellular Endocrinology* (accepted)

Low. B.C., Ross, I.K. and Grigor, M.R. (1994) Glucose deprivation and acute cycloheximide treatment stimulate system L amino acid transport in cultured vascular smooth muscle cells. J. Biol. Chem. 269, 32098-32103.

Bennett, B.L., Grigor, M.R. and Prosser, C.G. (1994) Isolation of cDNA subclones encoding ovine glucose transporter proteins. Proc. N.Z. Soc. Animal Prod. 54, 99-100.

Harris, E.L., Phelan, E.L., Millar, J.A. and Grigor, M.R. (1995) Heart mass and blood pressure have independent genetic determinants in the New Zealand Genetically Hypertensive (GH) rat. J. Hypertension 13, 397-404.

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A Bit of Gossip - A couple of weeks ago the Guardian Weekly had a section headed: **Biochemist Arrested in Oklahoma Bombing**. Chris Jenkinson, former Otago PhD student now post-doc at UCLA in an email message notes: "The second major suspect in the Oklahoma bombing is a guy called Steve Colbern who used to work as a student helper in the lab directly across the corridor from mine. That was a couple of years before I arrived here I'm currently probing some zooblots that he made and have been consulting his notebooks. I'm not too impressed with his biochemical lab skills but maybe he was better with explosives."

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Grants received: Since the last Newsletter this year's successful FRST applications have been announced. They include:

Glenn Buchan (year 1 of 3)	$180,000
Murray Grigor (year 1 or 3)	$182,000
Diana Hill (year 3 of 3)	$101,000
Clive Ronson	$120,000
Par Sullivan (year 2 of 3)	$88,000

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Computer Corner: Craig Marshall is overseas at present so this C.C. is just to remind you that the Centre's Bulletin Board is now up and going and we are wating for people to use it to its fullest advantage. Recently we emailed all those people who had given us their email addresses for our database last year with the message of how to join up. If you did not get this message and wish to join up, all you have to do is type a message to majordomo@stonebow.otago.ac.nz saying: subscribe cgr-list your_email_address.

You can unsubscribe at anytime by typing the same message using unsubscribe in place of subscribe. To post messages on the board, mail them to:
cgr-list@stonebow.otago.ac.nz. (Once you are one the mailing list, all you need to do is use the reply command on you mailer to any message from cgr-list.)
We are presently preparing a WWW (World Wide Web) frontpage for the Centre that will be part of the University's WWW information. The Centre's page will give access to our Newsletter electronically, information about any lectures and meetings coming up and information about our sequencer service. Watch out for this.

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Upcoming Meetings

GCG Computer Course: This course is fully subscribed and by the time you receive this newsletter, it will either be about to start or under way. Depending on its success, we will look to running another course next year.

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One-day Meeting on Yeast Technology: This is being planned for October 7, a Saturday. Yeast systems provide powerful approaches to modern molecular biology and this meeting will take advantage of the expertise developed in a number of laboratories round Dunedin. The keynote talk will be given by Dr Yoshi Nakamura, Tokyo, Japan on the application of some of this technology to study selenoproteins. Look for more information in our next newsletter, but in the meantime mark that date in you diary. We have chosen a Saturday so that we can have ready access to lecture theatres and wont have various teaching activities disrupting our programme. There is no charge for this meeting. Contact Brian Monk (extn 7099 or email eobatp@otago.ac.nz) for more information. People outside Dunedin who would like accommodation booked should also let Brian know by the end of September.

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Queenstown and FAOB (Sydney) meetings: Readers are reminded that the closing dates for abstracts for these meetings are 16 and 30 June respectively. The Queenstown meeting now has its own WWW frontpage which can be accessed at:
http://www.auckland.ac.nz/mmm/Queenstown95.html

NZ Microbiology Society Meeting, Dunedin 27-30 August. The Centre has agreed to sponsor the visit of Dr Julian Rood of Monash University to this meeting. Dr Rood's interests are in the genetics of pathogenic clostridia and, as well as giving two talks at the meeting, it is expected that he will give a lecture to the Centre whilst he is in Dunedin on the molecular genetic and functional analysis of Tn4451 from *C perfrinens*. Look out for information about this.

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HRC Meeting on "Whose Genes are they anyway?": This meeting is scheduled for July 25-27. The committee considered that someone from the Centre should be represented at this meeting and accordingly we are sending Warren Tate to it. Look forward to a report in due course.

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New Zealand Genetical Society and Australasian Gene Mapping Workshop: A combined meeting will be held in Dunedin November.28 - 30 followed by a one day workshop at Invermay on Mammalian Interspecies Hybrids. Many overseas speakers are expected and this should be a very exciting meeting. We should have a listing of the major speakers in a later newsletter. Contact Grant Montgomery (ext 7660 or email: montgomeryg@agresearch.cri.nz) for more information.

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