



2010 Annual General Meeting

The 2010 Annual General Meeting of the NSERC EmbryoGENE Strategic Research Network was held June 14-16 in Edmonton, Alberta. The meeting was attended by 51 delegates including 5 industry representatives, 12 graduate students, and 34 researchers involved with the Network.

The meeting opened with an overview of Network activities to date presented by Co-Directors, Marc-André Sirard and George Foxcroft. This was followed by an update on the developmental progress of the transcriptomics platform given by Philippe Rigault and Claude Robert. Jason Grant and Philippe Rigault then gave an overview of the bioinformatics progress of the

Network, with explanations of ELMA and Flex-Array. The epigenomics platform was highlighted by Claude Robert and Beatrice de Montera. To end the day, EmbryoGENE graduate students gave summary presentations of their projects in a session chaired by Michael Dyck.

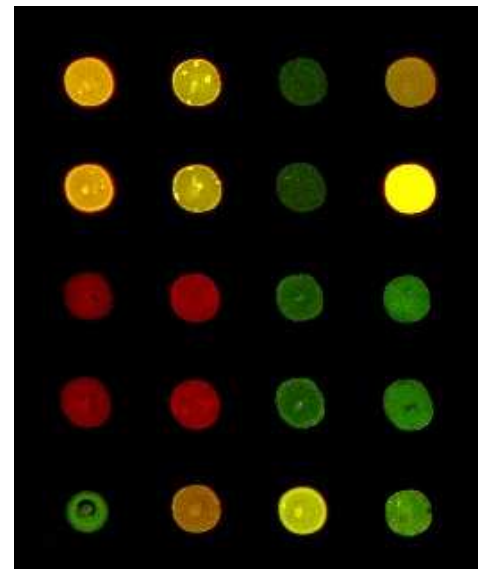
The second day was devoted to guest speakers. Kevin Sinclair, a member of EmbryoGENE's International Scientific Advisory Committee and Associate Professor at the University of Nottingham, presented on "The Developmental Origins of Health and Disease: B-vitamins and DNA methylation programming in the oocyte and early embryo". Invited guest, Jorge Piedrahita, Professor of Genomics

at North Carolina State University, presented on "Understanding porcine placental function through gene expression profiling". Lyne Letourneau, a member of EmbryoGENE and Professor of Biotechnology and Society at Laval University, presented on the "Diffusion of innovation in biotechnology: is 'copy-paste' an appropriate answer?". The scientific meeting ended with a student poster session followed by closing remarks by George Foxcroft.

The final day was devoted to meetings of the International Scientific Advisory Committee and Board of Directors. Summaries of these meetings will be featured in the next newsletter.

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Platform Update

We are pleased to announce that EmbryoGENE's Bovine Transcriptomics Platform is now available for use. After processing more than 1 million bovine reads to extract targets for bovine genes, embryo specific genes, 3' UTR variants, and indel splice variants, the EmbryoGENE Bovine EST and Splice Transcriptome (BEST) microarray was designed by Gydlle inc. In addition, they produced an augmented version of the bovine genome which includes information retrieved from sequencing results. As mentioned in the previous Newsletter, Agilent was chosen for the manufacturing of the slides and a series of benchmarking experiments were undertaken to test the microar-

ray. We were very satisfied with the results and are now ready to distribute the microarray to EmbryoGENE collaborators (please contact your team leader for more info).

The transcriptomics platform also includes all the bioinformatics tools necessary for the analysis of microarray data, including ELMA (EmbryoGENE LIMS and microarray analysis), a QC module, and microarray analysis software.

ELMA (<http://elma.embryogene.ca>) was developed by Jason Grant at the University of Alberta. Its first goal is to store microarray data in a MI-AME compliant fashion. Upon completion of a microarray experi-

ment, users are asked to provide all the information about their experiment through ELMA and to upload their microarray intensity files. This step is essential for future meta-analyses and will greatly facilitate microarray data analysis. Protocols and Standard Operating Procedures (SOPs) are already available in ELMA and should be used for all microarray-related experiments. ELMA also produces output files to be used by the analysis software. Over time, analysis components will be added to ELMA.

The screenshot shows the ELMA web application interface. The top navigation bar includes a search field, the ELMA logo, and the user name 'jason (Log out) Admin User'. A left sidebar contains a navigation menu with categories like 'EmbryoGENE', 'EXPERIMENTS', 'PROTOCOLS', 'PLATFORMS', 'SAMPLES', 'ARRAYS', 'About', 'HOME', 'HELP', 'CONTACTS', 'LINKS', 'Admin', 'USERS', 'NEWS', 'TRAIT TYPES', and 'TRAIT GROUPS'. The main content area displays a 'New Sample' page with a table of samples. A 'Context Help' button is in the top right, and an 'Options' menu is shown in the bottom right corner.

Menu Bar

Search

Navigation Bar

Current Selection

Admin Users

Context Help

Main View

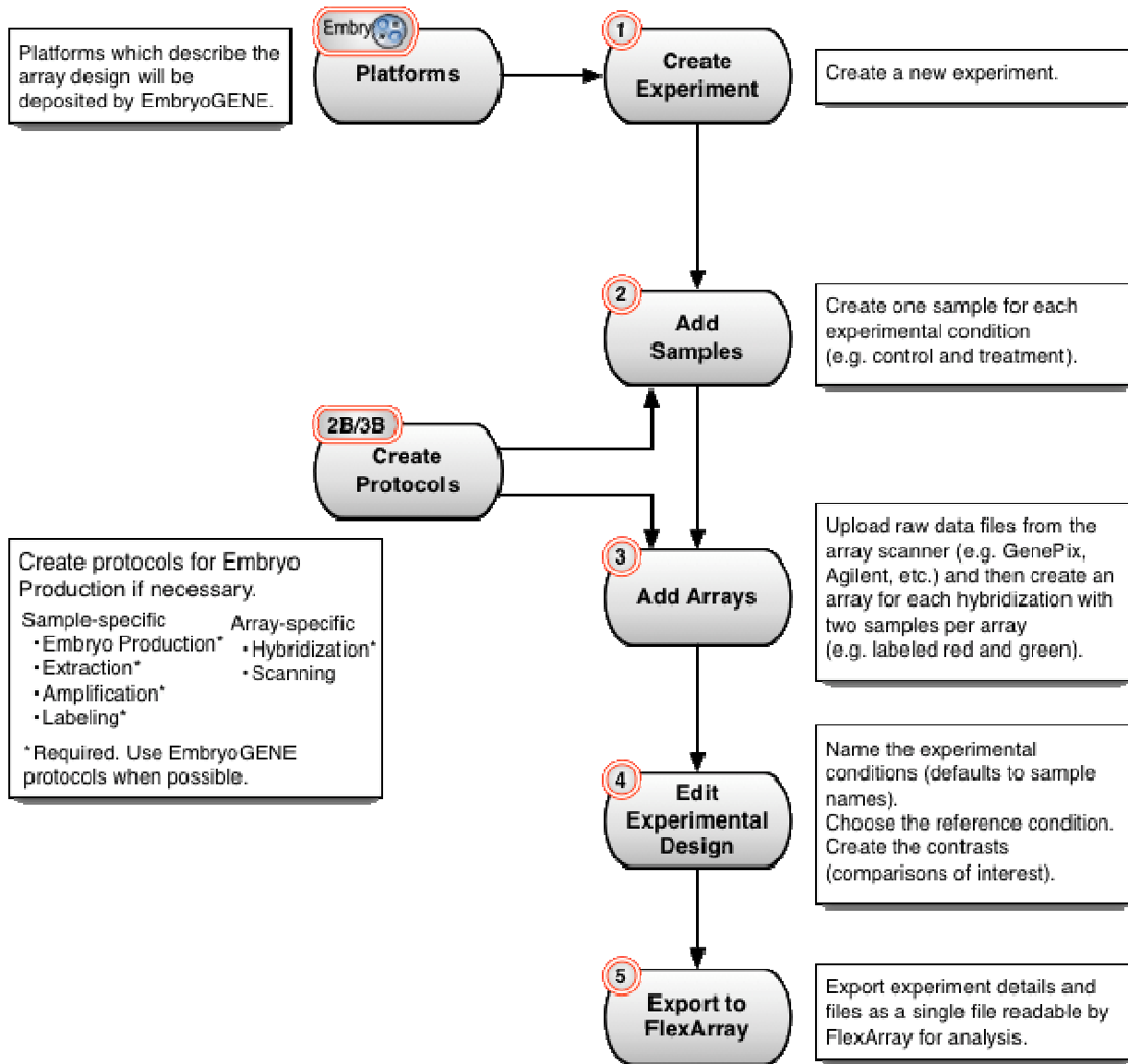
Options

- Copy Record
- Edit Record
- Delete Record

Name	Organism	Replicates	Access	Characteristics	Comments	Options
embryo_treated	pig	2	Private	Sample Type: in_vivo		[Icons]
wildtype	cow	4	Private	Sample Type: in_vivo		[Icons]
treatment	cow	2	Private	Compound added: Glucose Sample Type: in_vivo		[Icons]
swirl	cow	4	Private	Sample Type: in_vivo		[Icons]
embryo_control	cow	4	Private	Time of Embryo Collection: 1 hpf (hours post-in-vitro fertilization) Developmental Stage: early_blastocyst Embryo Quality Score (IETS codes): 6-1 show all		[Icons]
embryo_glucose	cow	4	Private	Time of Embryo Collection: 1 hpf (hours post-in-vitro fertilization) Developmental Stage: early_blastocyst Embryo Quality Score (IETS codes): 6-1 show all		[Icons]
embryo_lab_A	cow	4	Private	Time of Embryo Collection: 5 hpf (hours post-in-vitro fertilization) Developmental Stage: early_blastocyst Embryo Quality Score (IETS codes): 6-1 show all		[Icons]
embryo_lab_B	cow	4	Private	Time of Embryo Collection: 5 hpf (hours post-in-vitro fertilization) Developmental Stage: early_blastocyst Embryo Quality Score (IETS codes): 6-1 show all		[Icons]

Elma Screen Shot

Platform Update—continued



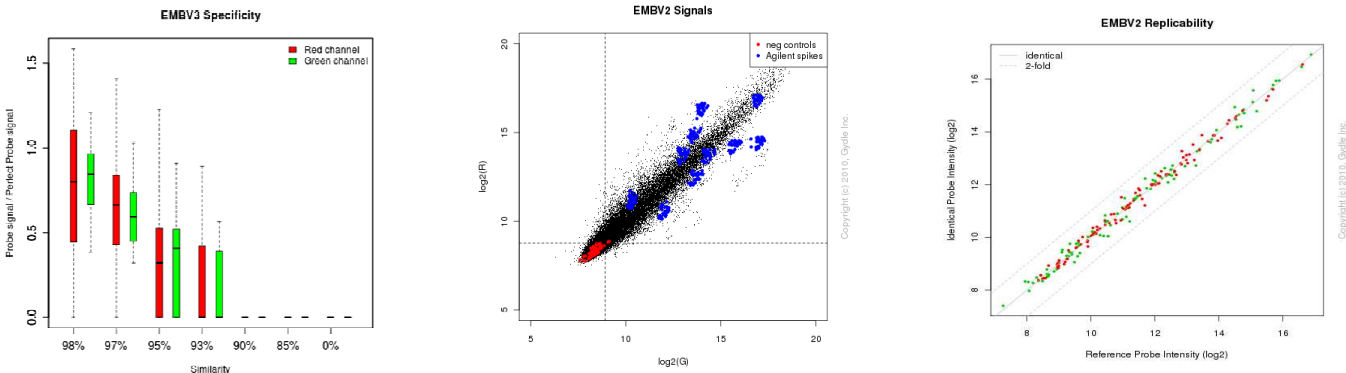
The QC module (<https://www.gydle.com/embryogene/qc/user/> optimized for [Google Chrome](#)) developed by Gydle inc. analyzes ELMA files to determine whether they can be used for further analyses. Distribution of signals for both channels is analyzed, as well

as negative and spiked-in controls to determine hybridization quality. To assess repeatability and specificity, the distribution across channels of repeated probes and of control probes is analyzed. For a group of microarrays within an experiment, a correlation matrix is used to identi-

fy discrepancies. Results are presented in the form of 4 easily interpretable graphs and datasets that do not meet minimum quality levels are flagged.

Platform Update—continued

Datasets that meet all quality criterion can be uploaded into the FlexArray microarray analysis platform (<http://genomequebec.mcgill.ca/FlexArray/>). The two colour component of FlexArray was developed for EmbryoGENE by Michal Blazejczyk at Genome Québec with the help of Jason Grant at University of Alberta and Éric Fournier at Laval University. FlexArray is a Bioconductor R-based software for the analysis of microarray data in a user-friendly environment



The screenshot shows the FlexArray 1.5 software interface with the following components:

- Analysis Pipeline:** A flowchart showing the analysis steps: Raw data → bgccorr-simple → MA norm-within (loess) → norm-between → limma (simple) → Bonferroni → FDR → Smaller than Threshold / Larger than Threshold.
- Experimental Design:** A table listing sample IDs, comments, and groups (Co-culture, In_vitro).
- Gene List:** A table showing the results of the limma (simple) analysis for Co-culture_B2-BRL - In_vitro. The table includes columns for Probe ID, log2(Fold change), T statistic, P-value, Mean, and Degree of freedom.
- Volcano Plot:** A plot of -log10(p-values) vs log2(Fold change) for Co-culture_B2-BRL - In_vitro. The plot shows a distribution of points with a red shaded area indicating significant changes. A legend on the right allows for filtering by FC and P-value.

We believe you will find that these tools will greatly facilitate your gene expression analyses within the EmbryoGENE Network. A workshop is planned in upcoming months in Quebec City for students wishing to familiarize themselves with the platform (see other article in this Newsletter for more info). You should contact your team leader for more information and for assistance planning your microarray experiments.

Profiles and Introductions

Isabelle Hue—ISAC



Isabelle Hue works in the BDR research unit which is part of the INRA Institute at Jouy en Josas, France. Her research aims to elucidate the molecular and cellular basis of blastocyst growth and differentiation in ruminants as an alternative model to rodents, due to the striking elongation process encountered in these embryos. She has gathered experience in molecular and cellular biology and developed

collaborations with embryologists to compare gastrulating embryos among species, as well as with statisticians to analyze gene expression profiles. Whereas her previous topic mainly aimed at deciphering the impact of somatic nuclear transfer on this late pre-implantation phase, her new interest is to understand pre-implanting development in relation to uterine receptivity and maternal metabolism

Patrick Blondin—Board of Directors

Dr. Patrick Blondin obtained a Master's degree in Physiology-Endocrinology (1993) and a Doctorate degree in Animal Science (1997) at Laval University and then went on to complete a 2-year postdoctoral internship at North Carolina State University (1999). He then joined L'Alliance Bovine as an Industrial Research Fellow to assist in the development of novel assisted reproductive technologies. Dr. Blondin transferred to Procrea BioScience as Director of Clinical Research and then McGill University as a business developer in the Office of Technology Transfer. Finally, Dr Blondin returned with L'Alliance Boviteq in 2003 as Director of Research & Development.

L'Alliance Boviteq (LAB) is The Semex Alliance's research subsidiary and includes an embryology laboratory that focuses on the development of various biotech-

nologies such as *in vitro* fertilization, embryo freezing and genomics, and a semen laboratory that focuses on semen quality, semen sexing, and various biotechnologies relating to sperm fertility and cryopreservation. LAB collaborates with many scientists from academic, private, and government laboratories. LAB also offers producers from Canada and the USA various assisted reproductive technologies to accelerate the genetic gain of their herds or treat infertility problems for elite cows. LAB encompasses 46 employees including 7 PhD, 6 MSc and 7 BSc or specialized DEC trained in Canadian universities.

Dr. Blondin is part of the Scientific Program Committee for the next International Congress on Animal Reproduction meeting in Vancouver (2012). He is also a nominee for the next International



Embryo Transfer Society (IETS) Board of Governors. He is a member of the Scientific Committee of the Quebec Research Network on Reproduction (RQR). Dr. Blondin is an Associate Professor with Université Laval, Université de Montreal and University of Guelph.

Alan Mileham—Board of Directors



Alan was educated at the Universities of Leeds (BSc in Genetics, 1977) and Edinburgh (PhD in Molecular Biology, 1980) and worked at the University of California, San Diego and the University of Leicester, before joining PIC's former parent company, Dalgety in 1987. Alan worked on numerous PIC pro-

jects, including semen sexing, developing DNA markers in pigs, and a rapid test for the presence of the PRRS virus in semen, before joining PIC as Group Reproduction Research Manager in 1996. In 1998, Alan led the relocation of PIC's molecular biology group to the Department of Pathology at the University of Cambridge. The Cambridge Laboratory also specialized in gene expression work based on microarray technology. He was also instrumental in the development and management of PIC's PhD programme in the UK. In July 2000, Alan relocated to Berkeley California where he managed PIC's new research laboratory. The Berkeley Laboratory carried out research in molecular biology and embryo technology. In 2001, PIC International was renamed Sygen

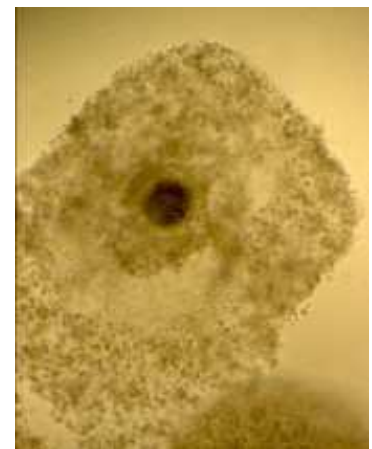
International and as the focus of the company was now all livestock species, Alan's molecular biology group began working on DNA markers in shrimp, poultry, and cattle. In 2004, Sygen's head office relocated from Berkeley to the UK and the Sygen Laboratories moved to PIC's US headquarters in Franklin Kentucky. In December 2005 Sygen was bought by Genus plc, the world's leading cattle breeding business. Together, Genus' cattle breeding business, better known as ABS, and PIC, form the world's largest livestock breeding company. In the summer of 2006 Alan again led the relocation of the laboratory, this time to the ABS Headquarters in DeForest, Wisconsin. He is currently Head of Genomics for Genus plc.

Carl Lessard—New EmbryoGENE Member

Carl Lessard received his B.Sc in Biochemistry from University of Sherbrooke in 1994. He completed a master degree in Experimental Medicine at University Laval in 1998. After receiving his PhD in Physiology and Endocrinology (University Laval) in 2003, he completed a postdoctoral fellowship in the field of genetics of reproduction at The Jackson Laboratory (Maine, USA). In 2006, he joined Agriculture and Agri-Food Canada (AAFC) to start a new program to preserve the Canadian Animal Genetic Resources (CAGR). This program is a joint initiative between AAFC and University of Saskatchewan and the mission of

this program is to ensure the genetic diversity of Canadian livestock and poultry, support environmentally friendly livestock and poultry production, and maintain food security, by acquiring, evaluating, and cryopreserving tissue and germplasm. His lab facilities are currently located at the Western College of Veterinary Medicine. Dr Lessard is also an Adjunct Professor at the department of Veterinary Biomedical Sciences. His interests are related to spermatogenesis, fertilization processes, embryology, and genetics. He is currently working to improve the *in vitro* production of pig embryos. Also, he is developing new methods to improve sperm banking and identify

essential genes important in the bovine fertilization processes.



Alex Pasternak—New EmbryoGENE Student



Alex Pasternak completed his B.Sc. in Agriculture, with a Major in Animal Science, at the University of Alberta. After working with both the Poultry Reproduction Group and Swine Reproduction and Development Program throughout his undergraduate degree, Alex began an MSc. program with Dr. Michael Dyck in 2007 and subsequently transferred to a Ph.D. program in 2009. His graduate work focuses on characterizing the macromolecules such as hyaluronic acid and proteins present in the “normal” porcine oviductal and uterine environment. This work is being carried out in carefully timed samples collected in tandem with

the *in vivo* embryos used to generate the pig cDNA library used for EmbryoGENE’s deep sequencing efforts. The information gleaned from the *in vivo* environment will be utilized to develop new *in vitro* embryo development media for swine under the porcine assisted reproductive technologies theme. The transcriptomic effects of successful media formulations will be assessed using the EmbryoGENE porcine array and compared with the transcriptome of *in vivo* produced embryos in an effort to identify media components which are key to the development of healthy embryos *in vitro*.

Microarray Workshop

A workshop is planned this spring to cover EmbryoGENE’s microarray analysis platform. The goal of this workshop is to give participants the required knowledge to perform microarray analysis on their own and generate statistically significant gene lists, as well as ensure the efficient storage of data in EmbryoGENE’s database. The workshop will cover the three

analysis tools included in the analysis platform:

- ELMA (EmbryoGENE’s LIMS and Microarray Analysis – Database and repository for microarray experiments data)
- QC module (Quality Control of microarray experiments)

FlexArray (microarray analysis software)

A small introduction to pathway analysis will also be included. The workshop will be held in Quebec City mid-March (stay tuned for more information) and will include in-class tutorials and computer exercises with actual microarray data. EmbryoGENE members will receive an official invitation and details for registration early next year.

In Closing



Visit us at:
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This issue was prepared by Tracy Gartner. Should you have any questions or concerns, please don't hesitate to contact Tracy at:

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