Twenty Seventh Annual

Biotechnology Training Retreat

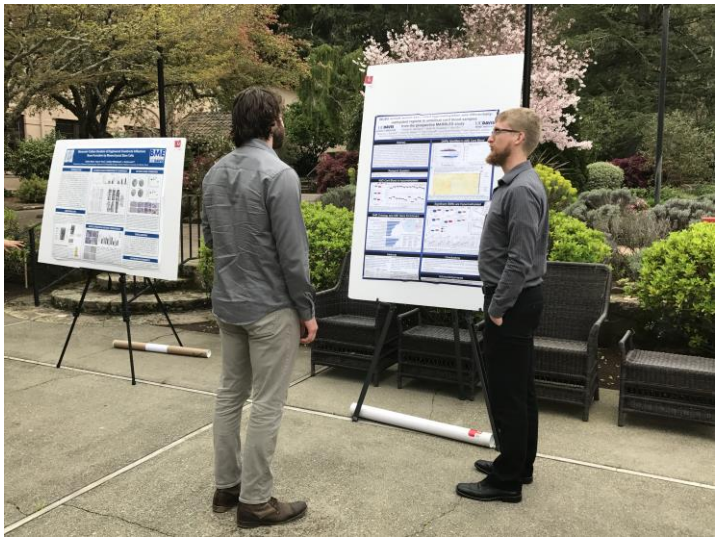
Saturday,
April 14, 2018

UC Davis Genome Center

Twenty Seventh Annual Biotechnology Training Retreat

UC Davis Designated Emphasis in Biotechnology Graduate Program (DEB)

UC Davis Biotechnology Program



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2018 Welcome

On behalf of the UC Davis Biotechnology Program, the directors and executive committee of the NIH T32 Training Program in Biomolecular Technology, and the executive committee of the Designated Emphasis in Biotechnology (DEB), we thank you for helping us celebrate our 27th anniversary of the Biotechnology Training Retreat. I have attended 22 of these wonderful events. This annual event honors our **2017-18 Biotech Fellows and their preceptors**, as well as **our industry affiliates**. In addition, our other DEB students are showcasing their research in the poster session. The DEB graduate program continues to be a model program for the 21st century and keeps growing. We currently have ~230 students from 29 graduate programs and over 250 graduates. More information can be found at http://deb.ucdavis.edu.

Many thanks go out to our Biotechnology Program team. The logistics of this retreat have been expertly overseen by **Jacki Balderama** (Event Manager)**, Marianne Hunter** (Assistant Director of Administration), **Lorella Gino (**Program Assistant), and our Associate Director, **Dr. Denneal Jamison-McClung, who will present the bioethics question.** Our BTP director, Kent Leach and associate directors, **Joanna Chiu** and **Luis Carvajal Carmona,** will be welcoming everyone chairing the morning and afternoon sessions today**.**

It is a pleasure to introduce our current Biotechnology Fellows. They include: **Linda Su Feher** Biochemistry, Molecular, Cellular & Developmental Biology (preceptor is Alex Nord); **Cody Yothers,** Chemistry (preceptor is Annaliese Franz); and **Amanda Dang,** Materials Science (preceptor is Tonya Kuhl).

As many of you know, we submitted a 5-year competitive renewal of the NIH T32 BTP earlier this year. We feel confident that we can be successful in our efforts to regain NIH's support. In the meantime, we are holding our annual retreat at the Genome Center this year with the support of bridge funding from campus to support that enabled us to offer a second year of funding for three of our fellows. We are hopeful that we will be able to host the retreat in Napa next year.

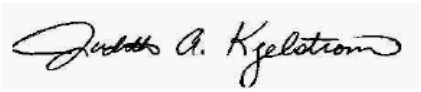
In regard to DEB internships, we placed **35** students in 2016/2017. Included are: **Amyris Biotechnologies**, Emeryville, CA – Amelia Manlove; **AstRoNa**, Berkeley, CA – Marc Pollack; **BASF**, Tarrytown, NY – Scott Strobel; **Bayer HealthCare**, Berkeley, CA – Douglas Gettel; **NIH Cancer Research**, Bethesda, MD – Pui Yan Ho; **Chr. Hansen**, Hoersholm, Denmark – Xiaochen (Ellie) Yin; **Desktop Genetics**, London, UK – Keith Dunaway; **Genentech**, San Francisco, CA – Douglas Banda, Samantha Feng, Simon Lopez, Angela Monterrubio, Juan

Reyes, Kim Truong, Tiffany Tu; **Gilead**, Oceanside, CA – Nicole Nunez; **GlaxoSmithKline**, PA – Nicole Nozzi; **HM Clause**, Woodland, CA – Nicholas Thomas; **IBM Almaden Research Center**, San Jose, CA – Luiz Carlos Irber Jr., Samuel Westreich; **Intrexon Corp**, Davis, CA – Betsy Alford, Mark Lemos, Cintia Helena Duarte Sagawa, Yuxuan (Eric) Zheng; **Lawrence Livermore National Laboratory**, Livermore, CA – Maher Elsheikh; **Monsanto**, Woodland, CA – Jenna Gallegos; **NASA Johnson Space Center**, Houston, TX – Forrest Ryan Dowdy; **Notable Labs**, San Fr4ancisco, CA – Jordan Mancuso; **OncoMed Pharmaceuticals**, Sacramento CA – Malgorzata Liro; **PinPoint Testing**, Little Rock, AK – Karan Agrawal; **REG Life Sciences**, San Francisco – Shuchi Desai; **Roche Molecular Diagnostics**, Pleasanton, CA – Krishna Choudhary; **Sac City College**, Sacramento, CA – Andrew Burch; **Starkey**, Berkeley, CA – Britt Yazel; **UC Davis Environmental Health & Safety** – Brittany Anderson. We could not run our Training Grant and DEB graduate program without our partners! Thanks so much.

Twenty-one DEB students graduated in the 2016-2017 academic year with their PhDs in one of 29 disciplines along with a Designated Emphasis in Biotechnology. Our **250 plus** graduates have found positions in both academia and industry. Please see our **2017 Biotech Times** (link is on our Biotech Program home page) for more information on our students and activities. We hope our graduates stay connected and even present a Biotech Seminar in the future! We had a number of our graduates return this past year (or will speak this spring) to present a DEB/ECH 294 seminar: **Garrick Yuen** (BluePrint Research Group); **Michael Howland** (Genentech); **Allison Hoch** (Boehringer Ingelheim); **Kevin Holden** (Synthego Corp.); **Kristen Beck** (IBM - Almaden); **Mike Plesha** (Bayer); and **Jeni Lee** (Novo Ventures). Our alumni continue to pay it forward.

Thank you for coming to our biotechnology retreat. We value all of you…..You are all part of our Biotech Family. Enjoy the day and make new friends.

With warmest wishes,



Judith "Judy" Kjelstrom, PhD
Director, UC Davis Biotechnology Program

Designated Emphasis in Biotechnology (DEB) Graduate Program

www.deb.ucdavis.edu

Executive Committee

Abhaya Dandekar (Co-Chair)
Karen McDonald (Co-Chair)
David Rocke
Shota Atsumi
Donald Gibson, Student Member

Judith A. Kjelstrom
Program Coordinator

UC Davis Biotechnology Program
www.biotech.ucdavis.edu

Judith A. Kjelstrom, Ph.D.
Director

Denneal Jamison-McClung, Ph.D.
Associate Director

Marianne Hunter; Assistant Director, Administration
Jacki Balderama; Event Manager
Lorella Gino; Program Associate
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UC Davis Twenty Seventh Annual Biotechnology Training Retreat
April 14, 2018
UC Davis Genome Center Auditorium

8:00 – 8:30 am	**Registration/Continental Breakfast**
8:30 – 8:45 am	**Welcome** **Kent Leach, PhD** Director, NIH Training Grant in Biomolecular Technology
8:45 – 12:00 pm	**Session Chair** **Joanna Chiu, PhD** Assoc. Director; NIH Training Grant in Biomolecular Technology
8:45 – 10:15 am	**Presentations** 8:45 am Amanda Dang ..... *Mentor: Tonya Kuhl* 9:10 am **Alberto Iandolino, PhD** ..... ***Monsanto*** 9:30 am Linda Su-Feher ..... *Mentor: Alex Nord* 9:55 am Denneal Jamison-McClung, PhD ..... *Bioethics Question (Handout)*
10:15 – 10:40 am	**Break / Poster Viewing** **Photo Taking for Biotech Trainees and their PIs**
10:40 – 12:05 pm	**Presentations** 10:40am Denneal Jamison-McClung, PhD ..... *Bioethics Question (Discussion)* 11:00 am **Brad Niles, PhD**..... ***ARIZ Precision Medicine*** 11:20 am Cody Watson Yothers..... *Mentor: Annaliese Franz* 11:45 am **Pankaj Pathak, PhD** ..... ***Marrone Bio***
12:05 pm	**Closing Remarks** Kent Leach, PhD Director, NIH Training Grant in Biomolecular Technology
12:15 – 1:15 pm	**Lunch / Poster Viewing**

For social media, use #BiotechRetreat

2018 Poster Titles

A. **"Aerosol Particle Emission During Human Speech"**
Sima Asadi*, Anthony S. Wexler, Christopher D. Cappa, Nicole M. Bouvier, Santiago Barreda, and William D. Ristenpart
Department of Chemical Engineering, University of California, Davis

B. **"Analysis of Eukaryotic Translation Initiation Factor (Eif) Phosphorylation By Mass Spectrometry"**
Katherine Beglinger*, Armann Andaya, Julie Leary, Christopher Fraser
Department of Molecular and Cellular Biology, University of California, Davis

C. **"Developing A Genome-Wide RNAiKnock Down Screen In *Entamoeba Histolytica*"**
Akhila Bettadapur* and Katherine S. Ralston
Department of Microbiology and Molecular Genetics, University of California, Davis

D. **"Nanoporous Gold as a Multifunctional Neural Electrode Coating"**
Noah Goshi*, Zidong Li, Jovana Veselinovic, Christopher Chapman, Ozge Polat, Pallavi Daggumati, Josh Garrison, Hao Chen, Marianna Stamou, Ling Wang, Juergen Biener, Monika Biener, Manyalibo Matthews, Pamela Lein and Erkin Seker
Department of Biomedical Engineering, University of California, Davis

E. **"Osteophytes And Fracture Calluses Share Developmental Milestone And Are Diminished By Unloading"**
Allison W. Hsia*, Armaun J. Emami, Franklin D Tarke, Hailey C. Cunningham, Priscilla M. Tjandra, Alice Wong, Blaine A. Christiansen, Nicole M. Collette
Department of Orthopaedic Surgery, University of California, Davis Medical Center, Sacramento, CA
Biosciences and Biotechnology Division, Lawrence Livermore National Laboratory, Livermore, CA

F. **"Design and Expression of PTH-FC Fusion Protein In Lettuce Plant For Microgravity Induced Bone Loss"**
Kalimuthu Karuppanan, Pauline Marie Famy, Matthew McNulty, Jesse Delzio, Somen Nandi and Karen A. McDonald
Department of Chemical Engineering, University of California, Davis

G. **"Identification of Loci Associated With Foot Warts And Sole Ulcers In Holstein Cattle"**
E. Lai*[1], A.I. Danner[1], J.M. Belanger[1], T.R. Famula[1], J.M. Heguy[2], A. Oberbauer[1]
[1]Department of Animal Science, University of California, Davis
[2]University of California Cooperative Extension, 3800 Cornucopia Way, Suite A, Modesto, California

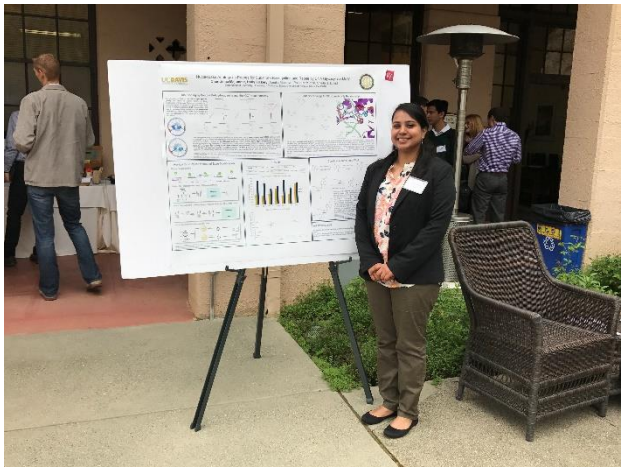
H. **"Influence Of Dissolved Oxygen On Recombinant Butyrylcholinerase Production In Transgenic Rice Cell Suspension Cultures"**
Kantharakorn Macharoen*, Somen Nandi and Karen McDonald
Department of Chemical Engineering, University of California, Davis

I. **"Understanding OG: A Lesion Recognition And Repair By The Base Excision Glycosylase MUTY Through Structure-Activity Relationships"**
Chandrima Majumdar*, Amelia H. Manlove*, Paige L. McKibbin, Michelle L. Hamm, Sheila S. David
Department of Chemistry, University of California, Davis

J. **"Genotype And Sex Influences On Serum Cytokine Levels in Mice Developmentally Exposed To A Mixture Of Polychlorinated Biphenyls (PCBs)"**
Lauren Matelski*[1], Sunjay Sethi[2], Kimberly P. Keil[2], Hans-Joachim Lehmler[3], Judy Van de Water[1], Isaac N. Pessah[2], Pamela J. Lein[2]
[1]Department of Internal Medicine, University of California, Davis
[2]Department of Molecular Biosciences, University of California, Davis
[3]Department of Occupational & Environmental Health, University of Iowa, Iowa City, IA

K. **"Techno-Economic And Alternative Scenario Analysis Of A Plant-Based Platform For Manufacturing Food Safety Antimicrobials"**
Matt McNulty*[1], Yuri Gleba[2], Daniel Tuse[3], Somen Nandi[1,4], and Karen A. McDonald[1,4]
[1]Department of Chemical Engineering, University of California, Davis
[2]Nomad Bioscience GmbH, Halle, Germany
[3]DT/Consulting Group, Sacramento, California
[4]Global HealthShare® Inititiative, University of California, Davis

L. **"Orthogonal Site-Directed RNA Editing System Utilizing Structure-Guided Engineering Of A Protein-RNA Interface"**
Leanna Monteleone*, Melissa Matthews, Cody Palumbo, Justin Thomas, Yuxuan Zheng, Yao Chiang, Andrew Fisher, and Peter Beal
Department of Chemistry, University of California, Davis



M. **"Methylomic And Transcriptomic Perturbations Associated With Autism At Birth In Umbilical Cord Blood Samples From The Prospective Marbles Study"**

Charles E. Mardaunt[*1-4], Keith W. Dunaway[1-4], Yihui Zhu[1-4], Rebecca J. Schmidt[3-5], Cheryl K. Walker[3,4,6], Sally Ozonoff[3-7], Irva Hertz-Picciotto[3-5], and Janine M. LaSalle[1-4]

[1]Department of Medical Microbiology and Immunology, University of California, Davis

[2]Genome Center, University of California, Davis

[3]MIND Institute, UC Davis Health System, Sacramento, University of California, Davis

[4]Center for Children's Environmental Health, UC Davis Health System, University of California, Davis

[5]Public Health Sciences, School of Medicine, University of California, Davis

[6]Obstetrics and Gynecology, UC Davis Health System, Sacramento, University of California, Davis

[7]Psychiatry and Behavioral Sciences, UC Davis Health System, Sacramento, University of California, Davis

N. **"Discovery of Dolabralexins, Previously Unrecognized Terpenoid Defense Compounds in Maize"**

Katherine M Murphy[*1], Sibongile Mafu[2], Yezhang Ding[3], Eric Schmelz[e], and Philipp Zerbe[1]

[1]Department of Plant Biology, University of California, Davis

[2]University of Massachusetts, Amherst, Amherst, Massachusetts

[3]Department of Cell and Developmental Biology, University of California, San Diego

O. **"Covalent Trapping of Human Adar Catalytic Domain Using Thiol Modified dsRNA"**

SeHee Park*, Cody Palumbo, and Peter Beal

Department of Chemistry, University of California, Davis

P. **"*Escherichia Coli* Response To Biocide Exposure"**

Beatriz Merchel P. Pereira*, Xiaokang Wang, Ilias Tagkopoulos

Genome and Biomedical Sciences Facility, University of California Davis

Q. **"Parallel Enhancer Analysis In Mouse Brain To Characterize Regulatory Variants"**

Linda Su-Feher*[1], Jessica L. Haigh[1], Iva Zdilar[1], Kenneth J. Lim[1], Diana M. Quintero[1], Vasco Morais[1], Tyler W. Stradleigh[1], Leah C. Byrne[2], Alex S. Nord[1]

[1]Department of Neurobiology, Physiology, and Behavior, University of California, Davis

[2]Department of Opthalmology, University of Pittsburgh, California

R. **"Transient Recombinant Protein Production In Glycoengineered Plant Cell Suspension Cultures"**

Sara C. Sukenik*[1], Kalimuthu Karuppanan[1], Qiongyu Li[2], Carlito B. Lebrilla[2], Somen Nandi[1,3] and Karen A. McDonald[1,3]

[1]Department of Chemical Engineering, University of California, Davis

[2]Department of Chemistry, University of California, Davis

[3]Global HealthShare Initiative, University of California, Davis

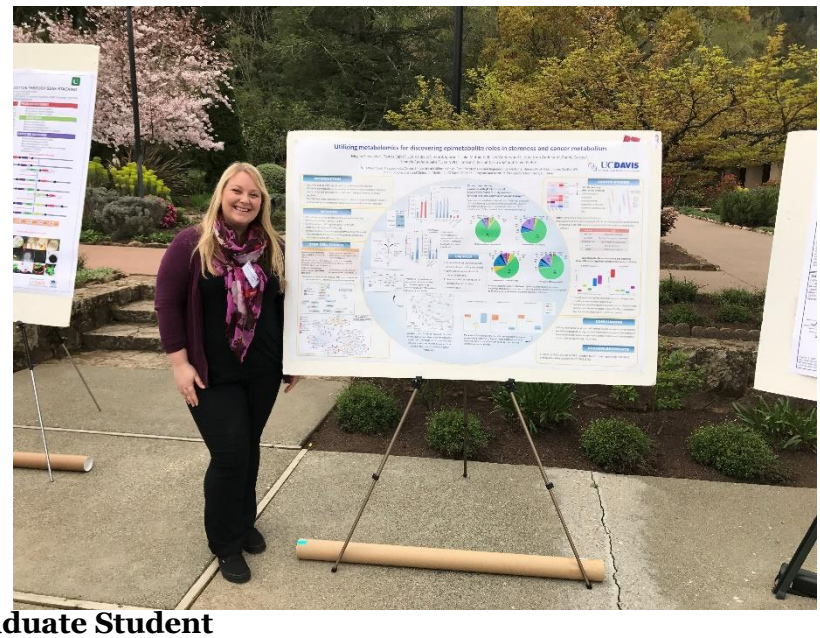
S. **"Molecular Dynamics Simulation Of Toll-Like Receptor 4 (TLR4) Ectodomain"**
Alireza Tafazzol* and Yong Duan
Department of Biomedical Engineering and Genome Center, University of California, Davis

T. **"Purification, Functional Study and N-glycosylation Modification Of A Plant-Made Anthrax Decoy Protein (CMG2-Fc)"**
Yongao Xiong*, Somen Nandi and Karen McDonald
Department of Chemical Engineering, University of California, Davis

U. **"$GABA_A$ Receptor Subtype Selectivity Of Chemical Threat Agents Picrotoxin And TETS In Larval Zebrafish"**
Bianca Yaghoobi*, Suren B. Bandara, Galen W. Miller, and Pamela J. Lein
Department of Molecular Biosciences, School of Veterinary Medicine, University of California, Davis

V. **"Utilizing Crispr/Cas9 Technology To Knockout Juno In The Pig Genome"**
Kelly Zacanti*, Pablo Ross and Trish Berger
Department of Animal Science, University of California, Davis

W. **"Investigating Placental DNA Methylation at Autism Spectrum Disorder in the MARBLES Prospective Autism Study"**
Yihui Zhu, Charles Mordaunt, Keith Dunaway, Ria Marathe, Theresa Totah, Cheryl Walker, Sally Ozonoff, Paul Krakowiak, Irva Hertz-Picciotto, Rebecca Schmidt and Janine LaSalle
Department of Medical Microbiology and Immunology, University of California, Davis



***DEB Graduate Student**

2018 Presentation Titles

1. **"Probing Nanolipoprotein Particle Interactions With Supported Lipid Bilayers"**
   Amanda Dang*, Matthew A. Coleman and Tonya Kuhl
   Department of Chemical Engineering, University of California, Davis

2. **"Monsanto's RNA-Based Solutions For Integrated And Sustainable Farming"**
   Alberto Iandolino, PhD
   Agriculture Productivity Innovations, Monsanto, Woodland, CA

3. **"Transcriptional Programming Of Interneuron Specification In Developing Mouse Brain"**
   Linda Su-Feher*[1], Anna N. Rubin[2], Shanni Silberberg[2], Kenneth Lim[1], John L. Rubenstein[2], and Alex S. Nord[1]
   [1]Department of Neurobiology, Physiology, and Behavior, University of California, Davis
   [2]Nina Ireland Laboratory of Developmental neurobiology, Department of Psychiatry, University of California San Francisco

4. **"I'm Too Smart To Take A DTC Test For IQ Alleles!"**
   Ethics Discussion
   Denneal Jamison-McClung, PhD

5. **"Developing Revolutionary Drugs Targeting Cancer At The Root Cause"**
   Brad Niles, PhD and Lonnie Bookbinder, MBA, PhD
   ARIZ Precision Medicine, UCD-HM Claus Life Sciences Innovation Center, Davis, California

6. **"Production And Measure Of Therapeutic Lipid Derivatives In Microalgae"**
   Cody Watson Yothers*[1], Ameer Taha[2] and Annaliese K. Franz[1]
   [1]Department of Chemistry, University of California, Davis
   [2]Department of Food Science and Technology, University of California, Davis

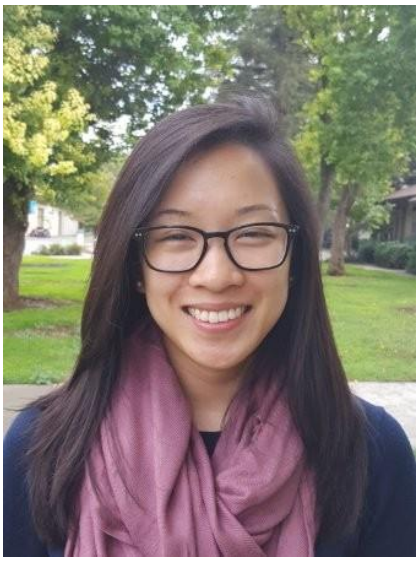
7. **"Development Of Biological Product For Pest Management"**
   Pankaj Pathak, PhD, MBA candidate (Haas School of Business, UC Berkeley)
   Group Leader, Formulations, Marrone Bio Innovations, Davis, California

***DEB Graduate Student**

Oral Presentation Abstracts

1. BIOTECH FELLOW: Amanda Dang

PROBING NANOLIPOPROTEIN PARTICLE INTERACTIONS WITH SUPPORTED LIPID BILAYERS



Presenter: Amanda T. Dang*

Authors: **Amanda T. Dang***, Tonya

Affiliations: Department of Chemical Engineering

Preceptor: Tonya Kuhl

A nanolipoprotein particle (NLP) is a lipid bilayer disc that is stabilized by two amphipathic "scaffold" apolipoproteins. The scaffold proteins insulate the hydrophobic core of the membrane and maintain the disc structure with sizes of about 20-30 nm. In recent years, the NLP has garnered considerable attention for its capability to solubilize membrane-associated proteins by forming stable membrane protein-NLP (MP-NLP) complexes. Importantly, membrane proteins incorporated into MP-NLP complexes have been shown to retain their functionality. MP-NLPs can be straightforwardly produced by in vitro cell free expression methods with high yields and minimal purification. This work evaluates the potential for NLPs to be applied as vehicles for the targeted delivery of membrane protein cargo into supported lipid bilayer (SLB) platforms. Incorporation of membrane proteins into SLBs, particularly if the native structure of the protein is preserved upon transfer, enables new opportunities for two-dimensional protein crystallization and studies on protein-protein interactions. In preliminary experiments, we analyzed the interactions between NLPs and SLBs at the nanoscale using atomic force microscopy (AFM). When combined with results from fluorescence microscopy experiments, results from AFM experiments point to a complex mechanism of interaction through which NLPs readily deposit lipids into SLBs. This information informs optimization of SLBs for NLP-mediated delivery of membrane proteins in ongoing work for this project.

***DEB Graduate Student**

2. COMPANY AFFILIATE: Monsanto, Calgene Campus

MONSANTO'S RNA-BASED SOLUTIONS FOR INTEGRATED AND SUSTAINABLE FARMING

Presenter: Alberto Iandolino, PhD

Authors: **Alberto Iandolino**

Affiliations: Agricultural Productivity Innovations, Monsanto, Woodland, CA

Monsanto's product and services innovation pipeline is addressing challenges imposed by farmer needs to meet an ever-growing food and feed demand in an environmentally-sustainable and more productive way. Our pipeline of seed production, genetic trait integration, pest control and yield protection/enhancement through chemical and biologically derived products, and data science enables the delivery of integrated solutions that can help produce more food using fewer resources. This talk will provide an overview of Monsanto's integrated solutions R&D pipeline with emphasis on RNA-based technologies: transgenic RNA interference (RNAi) and BioDirectTM Technology, one of our core Ag Biological product platforms.

***DEB Alum**

3. BIOTECH FELLOW: Linda Su-Feher

TRANSCRIPTIONAL PROGRAMMING OF INTERNEURON SPECIFICATION IN DEVELOPING MOUSE BRAIN

Presenter:	Linda Su-Feher*
Authors:	**Linda Su-Feher*[1]**, Anna N. Rubin[2], Shanni Silberberg[2], Kenneth Lim[1], John L. Rubenstein[2], and Alex S. Nord[1]
Affiliations	[1]Department of Neurobiology, Physiology, and Behavior, University of California, Davis [2]Nina Ireland Laboratory of Developmental Neurobiology, Department of Psychiatry, University of California San Francisco, California
Preceptor:	Alex S. Nord

The basal ganglia (BG), an anatomical region in the embryonic brain, contains progenitor zones that give rise to inhibitory interneurons that populate the adult brain. Interneurons are vital components of brain circuitry; perturbation to interneuron specification has been linked to neurodevelopmental disorders such as autism and schizophrenia. Early lineage specification of inhibitory interneurons is regulated by complex, region-specific transcriptional factor pathways within the BG. However, the transcriptional networks regulating early cell fate decisions are not entirely known. We aim to understand how transcription factor networks selectively regulate gene expression and genomic programming to control cell identity in the BG. We performed single-cell RNA-sequencing on dissociated BG from embryonic day 11.5 mice, incorporating a novel genetic labeling strategy to mark transient cell populations. Profiled cells labeled with our novel reporters represent distinct transient developmental states of interneuron progenitors. Using both guided and unguided approaches to identify key transcriptional markers of transient cell states, we identified major progenitor populations and cell types within the BG and demonstrate our genetic reporters mark subpopulations within identified cell types. By identifying transcriptional networks regulating early lineage specification of inhibitory interneurons via our genetic labeling strategy, we hope to examine functional changes in interneuron specification in pathogenic brain development and to develop new cellular markers for future studies.

***DEB Graduate Student**

Bioethics Discussion

ETHICS QUESTION

"I'M TOO SMART TO TAKE A DTC TEST FOR IQ ALLELES!"

Written and Presented by

Denneal Jamison-McClung, PhD
Associate Director of the Biotechnology Program

4. ASSOCIATE DIRECTOR: Denneal Jamison-McClung, PhD

I'M TOO SMART TO TAKE A DTC TEST FOR IQ ALLELES!

An April 2, 2018 article by Antonio Regalado for MIT's Technology Review, "DNA tests for IQ are coming, but it might not be smart to take one," dives into the state of the art for personal genomics applied to the complex, polygenic trait of "intelligence". Discussion of intelligence quotient (IQ) measures has has been fraught with ethical debate for decades, as IQ testing was historically used to discriminate against specific demographic groups and to justify eugenics-based forced sterilization of people in state-run facilities. The predictive value of IQ tests in determining how individuals will perform or succeed in social, academic, professional or other settings remains controversial

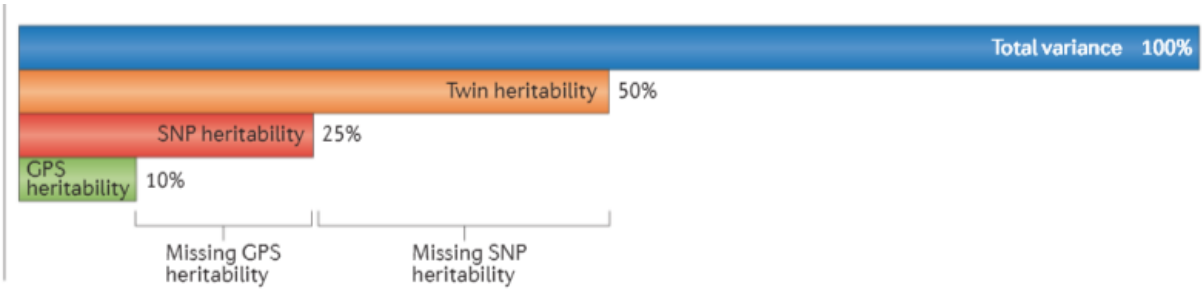
.

A recently published Nature Review of genome-wide association studies (GWAS) and genome-wide polygenic studies (GPS) highlighted the cumulative role of hundreds to thousands of genetic variants, each with a small effect, in determining the ~50% heritable component of intelligence. Review authors, Robert Plomin (King's College London) and Sophie von Stumm (London School of Economics and Political Science) state in the abstract:

> *"Recent genome-wide association studies have successfully identified inherited genome sequence differences that account for 20% of the 50% heritability of intelligence. These findings open new avenues for research into the causes and consequences of intelligence using genome-wide polygenic scores that aggregate the effects of thousands of genetic variants."*

The authors go on to present their work in twin studies that underscore a large body of work on the relatively high heritability of intelligence.

> *"Heritability is the proportion of observed (phenotypic) differences among individuals that can be attributed to genetic differences in a particular population… Twin heritability compares the resemblance of identical and fraternal twins to estimate genetic and environmental components of variance. For intelligence, twin estimates of broad heritability are 50% on average. Adoption studies of first-degree relatives yield similar estimates of narrow heritability of intelligence, suggesting that most genetic influence on intelligence is additive." (Plomin & von Stumm, 2018 - Box 4)*



Using GPS to aggregate the small effects of thousands of SNPs currently explains about 10% of the heritability of intelligence. Critics of the utility of GPS in estimating IQ point out that giving a person a standard IQ test is currently more informative. However, researchers in this area are optimistic that GPS will ultimately be useful in identifying all of the key genetic variants responsible for the high heritability of human intelligence. If so, scenarios, such as prenatal testing and selection for "smart babies" may not be farfetched.

Discussion Questions

1. Should there be federal guidelines or regulatory policies guiding the use of direct-to-consumer genetic tests for the assessment of IQ? Why or why not?

2. At least one psychologist mentioned in the MIT article indicated that school children should be GPS screened for variants related to intelligence. When might individual genetic screening for IQ be useful to society at large? When might it be damaging or divisive?

3. Would you be comfortable submitting your DNA for SNP profiling if the results were to be used to generate an assessment of your IQ?

References

Plomin, R and von Stumm, S (March 2018), "The new genetics of intelligence", Nature Reviews, v19, pp 148-159.

MIT article citation: https://www.technologyreview.com/s/610339/dna-tests-for-iq-are-coming-but-it-might-not-be-smart-to-take-one/?utm_campaign=add_this&utm_source=linkedin&utm_medium=post

Image citation/credit: Janet Gonzalez Emoji Stickers https://www.redbubble.com/people/janetgonzalez/works/12481383-smart-emoji?p=sticker

5. COMPANY AFFILIATE: ARIZ Precision Medicine

DEVELOPING REVOLUTIONARY DRUGS TARGETING CANCER AT THE ROOT CAUSE

Presenter:	Brad Niles, PhD
Authors:	**Brad Niles, PhD***, Lonnie Bookbinder, MBA, PhD
Affiliations:	ARIZ Precision Medicine, UCD-HM Claus Life Sciences Innovation Center, Davis, CA

ARIZ Precision Medicine is developing potentially curative drugs that selectively deliver fatal genetic messages to cancer cells at the right time, the right place and the right dose– all while avoiding damage to healthy cells.

Our technology: Getting the right drug to the right place at the right time to kill cancer cells, while avoiding normal cells is the Holy Grail of cancer therapy. ARIZ fights against cancer by using Nobel Prize winning methods, and specialized drug delivery systems to find, enter and concentrate the right dose of biological agents within cancer cells. Our primary goals are Safety and increased Survival rates of patients with a high Quality of Life. We have data that shows our technology is able to destroy cancer-driving proteins while restoring good proteins. This is a major advancement in cancer therapy and predicts success in future animal and human trials.

Our business plan: The ARIZ business strategy is to de-risk products by partnering early with pharmaceutical companies (pharma). As cancer drugs are

very expensive to develop, we aim to provide pharma with drug candidates that are ready for clinical trials, thus increasing assurance of safety and efficacy at a lower cost. This makes ARIZ products attractive to pharma buyers, allows ARIZ to monetize products quickly, reducing risk and increasing the opportunity for a fast ROI to shareholders within 18-24 months.

Our team: ARIZ leadership consists of former executives from pharma and biotech, including Genentech, Immunomedics, Lederle (Pfizer) and Ribi (GSK). Our team has extensive and successful experience in cancer drug development, fund-raising, legal and patents, as well as licensing to pharma companies. We also have a Advisory board with experts in different cancer types and drug delivery.

Our collaborators: ARIZ Precision Medicine is based in Davis, CA and closely affiliated with UC Davis (UCD), has agreements with Auburn University (in process) as well as with Keystone Nano for drug delivery systems. Our lab, located at the UC Davis-HM Clause Life Science Innovation Center, is equipped for proof of principle studies and we are working with UCD to complete animal studies.

***DEB Alum**

6. BIOTECH FELLOW: Cody Watson Yothers

PRODUCTION AND MEASURE OF THERAPEUTIC LIPID DERIVATIVES IN MICROALGAE

Presenter:	Cody Watson Yothers*
Authors:	**Cody Watson Yothers*[1]**, Ameer Taha[2] and Annaliese Franz[1]
Affiliations	[1]Department of Chemistry, University of California, Davis [2]Department of Food Science and Technology, University of California, Davis
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The co-production of value added chemicals from microalgae-based biofuel production systems is crucial to their commercial adaptation of sustainable fuels. We have investigated the production of one class of valuable co-product, oxidized lipids (oxylipins), that regulate diverse biological functions and are important to human health. My presentation will describe the development of methods to produce and measure lipids and oxylipins in microalgae, and includes the first report of algae growth conditions that induce the production of a valuable class of oxylipins. Treating an oleaginous marine diatom, *Phaeodactylum tricornutum*, with hydrogen peroxide while under nitrogen deprivation increased the accumulation of oxylipins by up to 400%. The predominant oxylipin species accumulated in this system is an epoxy-derivative of the omega-3 eicosapentaenoic acid (EPA), which is of therapeutic interest due to its anti-inflammatory properties. The synergistic approach of utilizing nutrient stress and a chemical trigger to enrich the oxylipin content in microalgae uses methods congruent with industrial cultivation practices. This system provides a foundation for studying the mechanisms of formation for oxylipins in microalgae and the development of a novel biological production route for specific classes of oxylipin compounds.

***DEB Graduate Student**

7. COMPANY AFFILIATE: Marrone Bio Innovations

DEVELOPING OF BIOLOGICAL PRODUCT FOR PEST MANAGEMENT

Presenter:	Pankaj Pathak, PhD
Authors:	**Pankaj Pathak, PhD***, MBA Candidate (Haas School of Business, UC Berkeley)
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Marrone Bio Innovations (MBI), based in Davis California, is an industry leader in developing natural biostimulants and biopesticide products. For the past 10 years, the company has developed and commercialized a broad portfolio of products that includes Fungicides, Insecticides, Nematicides and Plant health products in addition to a Molluscide for water based invasive muscles. These bio- and plant- based products are approved for virtually every cultivated crop, from fruits and vegetables to cereal grains and nuts, from turfgrass and flowers to alfalfa and cotton. These products are organic-compliant and when incorporated into an IPM (Integrated Pest Management) program, they can be an effective solution to pest control problems in conventional, transitional or certified organic production systems. For the last couple of years, technology (fermentation/formulation/chemistry) team at MBI has guided the development of atleast four bio based products from proof of concept to scale up and commercialization. The effort not only involved foliar and soil application but also seed treatment for protection against pests as well providing plant growth and yield enhancement. This presentation will discuss the complex multidisciplinary approach involving microbiology, chemistry, fermentation, formulation and plant sciences to screen bioactive ingredients and develop them into products through scale up and manufacturing.

Poster Abstracts

A. AEROSOL PARTICLE EMISSION DURING HUMAN SPEECH

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The traditional emphasis for airborne disease transmission has been on coughing and sneezing, which are dramatic expiratory events that yield easily visible droplets. Nonetheless, it has long been known that normal speech also yields expiratory aerosol particles. Recent research indicates that, compared to coughing, speech can actually release even larger quantities of such particles that are too small to see by eye, but are large enough to carry a variety of communicable respiratory pathogens. Here we show that the rate of aerosol particle emission during normal human speech is strongly correlated with the loudness (amplitude) of vocalization, ranging from approximately 1 particle per second for soft speech to over 50 particles per second at high amplitudes, regardless of the language spoken (English, Spanish, Mandarin, or Arabic). Furthermore, a small fraction of individuals behave as "superemitters," consistently releasing an order of magnitude more aerosol particles than their peers. The results suggest that individual speech patterns could affect the probability of airborne respiratory disease transmission, and also help explain the existence of "superspreaders" who are disproportionately responsible for outbreaks of airborne infectious disease.

***DEB Graduate Student**

B. ANALYSIS OF EUKARYOTIC TRANSLATION INITIATION FACTOR (eIF) PHOSPHORYLATION BY MASS SPECTROMETRY

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Translation initiation is the rate-limiting step of protein synthesis and is regulated by eukaryotic initiation factors (eIFs), which work together to recruit a mRNA to the ribosome and locate the initiation codon. An additional layer of regulation of this pathway is likely influenced by post-translational modifications of initiation factors, specifically phosphorylation. While several global studies have identified extensive numbers of phosphorylation sites, it is still unclear which sites are important in regulating translation. The objective of this study to to identify which phosphorylation sites are key in regulating translation initiation and to determine how phosphorylation regulates the function and structure of translation initiation factors.

We have started to determine which phosphorylation sites on the cap binding complex, eIF4F, are important in regulating translation. To build on our previous work, we are recombinantly expressing and purifying this complex from HeLa cells that have been treated with various kinase inhibitors. We are quantifying sites-specific phosphorylation stoichiometries using a novel cerium oxide dephosphorylation and tandem mass tagging (TMT) method followed by nanoLC-MS/MS. Identified phosphorylation sites that change in response to kinase inhibitors will be characterized using functional and structural assays.

The translation initiation factor eIF4B has been shown to have an important role in translation initiation by stimulation the unwinding of mRNA in preparation of recruitment to the ribosome. Prior studies have identified a phosphorylation site at Serine 422 of eIF4B. This site is known to be important in stimulating translation initiation as well as increasing its affinity to eIF3, however the mechanism in which this site works is poorly understood. To study the role of this phosphorylation site, we expressed and purified recombinant phosphomimetic (Ser422Glu) and null phosphorylation (Ser422Ala) mutants from SF9 cells. We are employing ion mobility mass spectrometry to study the structural changes that occur when eIF4B is phosphorylated. In addition, we are using a reconstituted translation initiation system to understand the effect of eIF4B phosphorylation on eIF4A-dependent helicase activity and mRNA recruitment.

***DEB Graduate Student**

C. DEVELOPING A GENOME-WIDE RNAi KNOCK DOWN SCREEN IN *ENTAMOEBA HISTOLYTICA*

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Entamoeba histolytica is a microbial eukaryote and causative agent of the disease amoebiasis, responsible for approximately 50 million cases of disease and 100,000 deaths annually. This disease is predominantly in developing nations, and transmission is caused through contaminated water sources and poor sanitation practices. Pathogenesis is associated with a spectrum of symptoms, ranging from asymptomatic transmission, diarrheal symptoms, ulceration of the intestinal wall due to invasion, to soft tissue dissemination and abscess formation in the liver. This profound damage to human tissues is likely caused by *E. histolytica* cells ("amoebae") attacking and killing human cells through the novel cell-nibbling process named trogocytosis (*trogo-:* nibble). Drugs are required to combat amoebae that cause the latter manifestations of amoebiasis, and treatment options are limited. In addition, the emergence of drug resistant amoebae threatens current drug regimens. I aim to construct a genome-wide RNA interference (RNAi) knock down library, which is an effective method for the identification of genes involved in many different processes, in an unbiased manner. This plasmid-based library will utilize the endogenous RNAi pathway in *E. histolytica*, and has many potential future applications. This includes, but is not limited to, understanding the potential avenues of drug resistance, the mode of action or uptake of drug candidates, as well as the molecular mechanism of trogocytosis. This work will improve understanding of amoebiasis pathogenesis as a whole, and provide new opportunities for future drug regimen techniques.

***DEB Graduate Student**

D. NANOPOROUS GOLD AS A MULTIFUNCTIONAL NEURAL ELECTRODE COATING

Noah Goshi*, Zidong li, Jovana Veselinovic, Christopher Chapman, Ozge Polat, Pallavi Daggumati, Josh Garrison, Hao Chen, Marianna Stamou, ling Wang, Juergen Biener, Monika Biener, Manyalibo Matthews, Pamela Lein and Erkin Seker
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Implantable neural electrodes constitute an important tool for monitoring and modulating the electrophysiological activity of the nervous system. A major obstacle in the long-term reliability of these devices is the undesired aggregation of glial cells on the surface of the electrode and the subsequent death and/or detachment of neurons from the electrode surface. Among different strategies to enhance the neuron-electrode interface, multifunctional electrode coatings have shown promise. Nanoporous gold (np-Au), produced by a nano-scale self-assembly process, is a relatively new material, and has mostly attracted attention for catalytic applications due to its high effective surface area, electrical conductivity, and ease of surface functionalization. Here we demonstrate our group's efforts into realizing the biomedical potential of this material, including elucidating the nano-/micor-scale properties of np-Au and the application of micropatterning techniques for fabricating high-fidelity multiple electrode arrays for neural electrophysiology studies. Specifically, we illustrate how tunable properties of np-Au (e.g. surface topography and chemistry) are utilized to enhance the recording fidelity in organotypic brain slices and cortical cell cultures. To that end, we focus on (i) np-Au's in situ drug delivery performance (dictated by molecule-surface interactions and mass transport in nanofluidic pore network); (ii) np-Au's performance in selectively reducing astrogliosis while maintaining high neuronal coverage (driven largely by topographical cues); and (iii) np-Au's biofouling-resilience in preventing the permeation of large biomolecules while allowing ionic transport to sustain electrochemical activity and electrophysiological recordings. These features taken together identifies np-Au as a promising material for multifunctional neural electrode coatings.

***DEB Graduate Student**

E. OSTEOPHYTES AND FRACTURE CALLUSES SHARE DEVELOPMENTAL MILESTONES AND ARE DIMINISHED BY UNLOADING

Allison W. Hsia*, Armaun J. Emami, Franklin D. Tarke, Hailey C. Cunningham, Priscilla M. Tjandra, Alice Wong, Blaine A. Christiansen, Nicole M. Collette
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Osteophytes are a typical radiographic finding during osteoarthritis (OA), but the mechanisms leading to their formation are not well known. Comparatively, fracture calluses have been studied extensively; therefore, drawing comparisons between osteophytes and fracture calluses may lead to a deeper understanding of osteophyte formation. In this study, we compared the time courses of osteophyte and fracture callus formation, and investigated mechanisms contributing to development of these structure. Additionally, we investigated the effect of mechanical unloading on the formation of both fracture calluses and osteophytes. Mice underwent either transverse femoral fracture or non-invasive anterior cruciate ligament rupture. Fracture callus and osteophyte size and ossification were evaluated after 3, 5, 7, 14, 21, or 28 days. Additional mice were subjected to hindlimb unloading after injury for 3, 7, or 14 days. Protease activity and gene expression profiles after injury were evaluated after 3 or 7 days of normal ambulation or hindlimb unloading using in vivo fluorescence reflectance imaging (FRI) and quantitative PCR. We found that fracture callus and osteophyte growth achieved similar developmental milestones, but fracture calluses formed and ossified at earlier time points. Hindlimb unloading ultimately led to a threefold decrease in chondro/osteophyte area, and a twofold decrease in fracture callus area. Unloading was also associated with decreased inflammation and protease activity in injured limbs detected with FRI, particularly following ACL rupture. qPCR analysis revealed disparate cellular responses in fractured femurs and injured joints, suggesting that fracture calluses and osteophytes may form via different inflammatory, anabolic, and catabolic pathways.

***DEB Graduate Student**

F. DESIGN AND EXPRESSION OF PTCH-FC FUSION PROTEIN IN LETTUCE PLANT FOR MICROGRAVITY INDUCED BONE LOSS

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Planetary missions on Mars will require in situ production systems for pharmaceuticals to prevent anticipated health problems. We have designed and expressed parathyroid hormone (PTH) fusion protein in lettuce plants to address issues related to bone health with the goal of edible delivery of the compound. For this research study, lettuce codon optimized N-terminal fragment (1-34) of human PTH fused with aglycosylated Fc domain of human IgG1 was designed. To retain the PTH-Fc fusion protein in the endoplasmic reticulum, a SEKDEL sequence was included on the C-terminus and the 2S2 signal peptide was inserted on the N-terminus. Also, an omega leader sequence was included to enhance the translation of PTH-Fc mRNA. Transient expression of the PTH-Fc fusion protein in lettuce plants was achieved using CaMV double 35S promoter. We have optimized growth of six different lettuce varieties (Grand Rapids, Great Lakes, Bibb, Iceberg, Romaine, Simpson) in the greenhouse and confirmed that two-week old lettuce is the optimal size for the transient protein expression. Vacuum agroinfiltration of lettuce and *Nicotiana benthamiana* plants was performed using two recombinant agrobacterial strains, one carrying the PTH-Fc gene and other carrying a viral gene silencing suppressor. After the co-infiltration, plants were incubated in the controlled environmental chamber for six days, leaf biomass was extracted using phosphate buffer (pH=7.0) and filtered through a 0.22µm filter. Immunoblots in a dot-blot format were performed on the 0.22µm filtered crude extracts, using an antibody specific to the Fc region of IgG. The dot-blot indicates that the fusion protein was produced in lettuce varieties including model plant *Nicotiana benthamiana* plants. Among the six different varieties, Great Lakes showed the highest dot density, which was similar to the model plant *Nicotiana benthamiana*. The PTH-Fc fusion protein was purified from extracts from Great Lakes and *Nicotiana benthamiana* using Protein A chromatography and a band of the expected size of PTH-Fc monomer, 30KDa, was observed on the Western Blot. PTH-Fc fusion protein titer in the Great Lakes lettuce variety was estimated to be 0.8 mg/g dry weight lettuce.

***DEB Graduate Student**

G. DESIGN OF LOCI ASSOCIATED WITH FOOT WARTS AND SOLE ULCERS IN HOLSTEIN CATTLE

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Rationale: Lameness affects 36% of dairy cows in the US[1] and is associated with reduced milk production and premature culling, raising welfare and economic concerns. Lameness is often caused by claw lesions that manifest as open wounds in the soft tissue behind the hoof, commonly foot warts (FW) and sole ulcers (SU). To enable genomic selection against these conditions, the genomic regions that govern susceptibility to FW and SU must first be identified.

Methods: DNA from healthy and affected cows was used in a genome wide association (GWA) analysis for identification of chromosomal regions linked to case/control status. We used hoof scoring phenotypes and genotypes from the high-density single nucleotide polymorphism (SNP) panel (800K SNPs) using FW $n = 40$, SU $n = 11$, controls $n = 97$. The GWA was performed using stratified case-control allelic association.

Results: For FW, after correcting for population stratification and multiple testing, no SNPs were genome-wide significant, suggesting that many loci, each with a small effect size, contributed to the susceptibility to FW. For SU, an insufficient number of cows were cases for SU ($n = 11$) to sufficiently power the GWA for susceptibility to SU and draw meaningful conclusions.

Conclusions: The power of both GWASs must be increased to find and narrow down regions of association. Thus, future research will consist of adding animals to the dataset from the same dairies and repeating the stated procedure, or using targeted sequencing at candidate genes involved in the immune response to FW and SU.

References

1 USDA. Dairy 2014, Dairy Cattle Management Practices in the United States. (USDA–APHIS–VS–CEAH–NAHMS, Fort Collins, CO, 2016).

***DEB Graduate Student**

H. INFLUENCE OF DISSOLVED OXYGEN ON RECOMBINANT BUTYRYLCHOLINERASE PRODUCTION IN TRANSGENIC RICE CELL SUSPENSION CULTERS

Kantharakorn Macharoen*, Somen Nandi and Karen McDonald
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Butyrylcholinesterase (BChE), a complex tetrameric hydrolase enzyme composed of four identical monomers, binds tightly to organophosphorus (OP) nerve agents and pesticides, making it a potent bio-scavenger against these compounds. Recombinant butyrylcholinesterase (rBChE) has been expressed in various host systems aiming to compete with human BChE (hBChE) purified from outdated blood plasma which is very expensive. Among several systems, metabolically regulated transgenic rice cell suspension culture is a potentially cost-effective platform. Even though rice recombinant butyrylcholinesterase (rrBChE) has been successfully produced in a bioreactor, process optimization is necessary to improve rrBChE yield. Dissolved oxygen (DO) concentration is one of the bioreactor variables that may affect the production level of rrBChE. In this study, DO was controlled at 10%, 20%, 30% and 40% DO air saturation during the production phase in bioreactors to investigate the influence of oxygen on rrBChE productivity. The maximum cell-associated rrBChE levels were reached at day 4 after induction in all experiments: 49.8 ± 0.3, 53.3 ± 0.5, 47.6 ± 0.6 and 53.2 ± 2.2 μg rrBChE/g fresh weight at 10% DO, 20% DO, 30% DO and 40% DO, respectively. The results show that the maximum cell-associated rrBChE level from each experiment is comparable. Therefore, we may conclude that the production level of cell-associated rrBChE does not depend significantly on dissolved oxygen over the 10-40% DO range investigated.

***DEB Graduate Student**

I. UNDERSTANDING OG: A LESION RECOGNITION AND REPAIR BY THE BASE EXCISION GLYCOSYLASE MUTY THROUGH STRUCTURE-ACTIVITY RELATIONSHIPS

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8-oxo-7,8-dihydroguanine (OG) arises in the genome when guanine is oxidized by reactive oxygen species (ROS) originating from endogenous or exogeneous sources. This lesion is insidious due to its ability to aberrantly code like a thymine, leading to the conversion of G:C base pairs to OG:A mis-pairs and then to T:A base pairs. The accumulation of G:C to T:A mutations is prevented by the 'GO' repair pathway, in which the glycosylase Fpg excises OG lesions base paired opposite C. The OG:A mispairs that arise if DNA replication precedes Fpg's activity are repaired by a second glycosylase called MutY. Although these OG:A mispairs are structurally almost identical to undamaged T:A base pairs, MutY is proficient at locating these lesions within the genome and catalyzing their repair. In this work, we study the structural basis by which MutY identifies the OG:A lesion and distinguishes it from a normal, undamaged T:A. We employ DNA duplexes containing OG and A substrate analogs that have modified steric, electronic and base pairing properties, and evaluate their effects on *in vitro* parameters such as enzyme-substrate binding and kinetics of base cleavage, as well as on overall repair in a bacterial cell assay. The results thus obtained allow us to explore a structure activity relationship (SAR) that provides insight into the structural basis for lesion identification and excision by MutY and can reveal the regions and residues of MutY that are responsible for OG:A recognition. By mutating these residues and utilizing the aforementioned *in vitro* and cellular assays, we hope to characterize their role in the enzymes search and damage recognition process. Taken together, these studies will help us understand the mechanism by which MutY identifies its OG:A target base pair and discriminates it from undamaged DNA.

***DEB Graduate Student**

J. GENOTYPE AND SEX INFLUENCES ON SERUM CYTOKINE LEVELS IN MICE DEVELOPMENTALLY EXPOSED TO A MIXTURE OF POLYCHLORINATED BIPHENYLS (PCBs)

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Autism spectrum disorder (ASD) is considered to be one of the most heritable of the complex neurodevelopmental disorders (NDD). However, the sharp increase in rates of ASD in recent decades has prompted the search for gene X environment interactions that influence individual risk for ASD. PCBs, a class of persistent organic pollutants, have been implicated as environmental risk factors for NDDs, and immune system abnormalities are a frequently observed comorbidity in ASD. Therefore, the goal of this study was to examine how genotype and sex influence serum cytokine responses to PCBs. Mice were developmentally exposed to a mixture of PCB congeners (MARBLES mix) present in the serum of women who are at high risk for having a child with ASD at 4 dose groups (0, 0.1, 1, and 6 mg/kg/day in the maternal diet throughout gestation and lactation). Four genotypes were studied: knock in mice expressing a human ryanodine receptor (RyR) gain-of-function mutation (T4826I-RyR1), the X-linked *FMR1* CGG repeat expansion (PreCGG with 170 repeats) or both mutations (double mutation, DM), and congenic wildtype (WT) mice. At postnatal day 28, serum was collected and analyzed for 23 cytokines and chemokines using a Luminex multiplex assay. Genotype affects the serum cytokine responses to PCBs, with WT males exhibiting a non-monotonic dose response for most of the cytokines tested that was not observed for the other genotypes. Sex differences were also observed in serum cytokine profiles, with data analysis to date indicating that circulating serum cytokines in males are more responsive to PCB dose than females. This sex difference is most pronounced in WT and PreCGG animals. These data suggest that male immune responses may be more susceptible to modulation by environmental factors implicated in ASD pathogenesis.

***DEB Graduate Student**

K. TECHNO-ECONOMIC AND ALTERNATIVE SCENARIO ANALYSIS OF A PLANT-BASED PLATFORM FOR MANUFACTURING FOOD SAFETY ANTIMICROBIALS

Matt McNulty*[1], Yuri Gleba[2], Daniel Tuse[3], Somen Nandi[1,4], and Karen A. McDonald[1,4]

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Continuous reports of foodborne illnesses worldwide and the prevalence of antibiotic-resistant bacteria mandate novel interventions to assure the safety of our food. We performed a comprehensive techno-economic evaluation of a plant-based platform for manufacturing a novel and highly promising class of antibacterial proteins for use in food. Our analysis focused on bacteriophage endolysins (lysins), which are natural hydrolytic enzymes produced by bacteriophages to cleave the host's cell wall during the final stage of the lytic cycle. Lysins can be produced recombinantly and applied to various foods to prevent or minimize the growth of pathogenic bacteria. Humans are exposed to bacteriophages and lysins naturally in their diet. Recombinant lysins can meet key performance criteria, and by being nature-identical they are predicted to be safe when used in foods at low yet effective levels.

The most significant barrier to the adoption of lysins as a food safety intervention by the food industry is the high production cost using current fermentation-based approaches. To capitalize on potential economic advantages and scalability, we evaluated a highly efficient transgenic plant-based production process developed by Nomad Bioscience GmbH, which can express a range of lysins at levels up to 5 g/kg fresh weight with demonstrated activity against multiple serovars of *Listeria monocytogenes* and *Clostridium perfringens* in turkey and beef food matrices. A detailed process simulation model was developed to de-risk the business and commercial application of the technology as well as to help identify economic "hot spots," process operating parameters, unit operations, consumables, and/or raw materials that have the most significant impact on production costs and/or capital expenditures.

The process simulation base case scenario (production volume = 500 kg lysin/year; expression level = 1 g lysin/kg fresh weight biomass; overall recovery efficiency = 75%) was developed using SuperPro Designer® (Intelligen Inc, Scotch Plains, New Jersey, USA), a software tool for process simulation and flowsheet development that performs mass and energy balances, equipment sizing, batch scheduling/debottlenecking, capital investment and operating cost analysis, and profitability analysis. The results of our analysis are presented. Future work in our project will include a robust cost-guided process optimization. Upon completion, the full technoeconomic model will be made available for others to consult or adapt to alternative designs.

***DEB Graduate Student**

L. ORTHOGONAL SITE-DIRECTED RNA EDITING SYSTEM UTILIZING STRUCTURE-GUIDED ENGINEERING OF A PROTEIN-RNA INTERFACE

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It has been of great interest to design new, precise systems that allow for directing specific changes in nucleic acid sequences. This has great potential for therapeutic applications and acts as a biotechnology tool. However, for the systems thus far developed there has been undesired side reactions at off-target sites. To develop an orthogonal site-directed RNA editing system, the protein RNA interface from a high-resolution crystal structure of human ADAR2 (adenosine deaminase acting on RNA 2) bound to double stranded RNA was utilized. From the crystal structure, a key intercalating residue at position 488 interacts with the orphan base, the base across from the editing site. If the 488 residue is mutated to a bulky aromatic residue it is suggested that a steric clash would occur with the orphan base therefore reducing editing activity. However, to restore editing activity with the bulky ADAR mutants the nucleobase of the orphan base can be replaced by a hydrogen (a reduced abasic site) resulting in removal of the clash. Using the bulky ADAR mutants in combination with a reduced abasic guide RNA we have demonstrated efficient site-directed RNA editing in vitro and in human cells with reduced off-target editing. A crystal structure of the E488Y mutant bound to double stranded RNA containing the reduced abasic site demonstrated the incorporation of the tyrosine side chain in the duplex RNA. This approach for site-directed RNA editing has great promise for correcting deleterious mutations with minimal reactions at off-target sites.

***DEB Graduate Student**

M. UMBILICAL CORD BLOOD SAMPLES FROM THE PROSPECTIVE MARBLES STUDY

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Autism spectrum disorders (ASD) have complex etiologies, likely involving multiple genetic and environmental insults in perinatal life. Biomarkers for ASD at birth are largely unknown and would facilitate earlier diagnosis and more effective treatment. We performed this study to identify DNA methylation biomarkers predictive of ASD diagnosis by age three. The MARBLES prospective study is an enriched risk cohort that enrolls couples who have already had a child with ASD and follows their subsequent pregnancy. We investigated human umbilical cord blood samples from the MARBLES study by whole-genome bisulfite sequencing (WGBS) and expression microarray. ASD cord blood samples showed significantly lower global percent CpG methylation compared to typically-developing (TD) controls. Smaller differentially-methylated regions (DMRs) were also identified in ASD cord blood. Methylation in DMRs was associated with measured behavioral outcomes and could distinguish ASD from TD subjects. Additionally, differential gene expression was associated with DMR methylation. Global hypomethylation in ASD cord blood suggests a methylation deficiency in ASD during perinatal life, which could be a cumulative effect of genetic variants, environmental exposures, and/or shortage in methyl donors. Identified DMRs and differentially expressed genes are relevant to ASD and have potential as a diagnostic tool. In future studies, methylation will be examined in relation to demographic, genetic, environmental, and nutritional information collected in the MARBLES study. These results are expected to improve understanding of perinatal factors in ASD etiology and aid in future preventative and therapeutic treatments.

***DEB Student**

N. DISCOVERY OF DOLABRALEXINS, PREVIOUSLY UNRECOGNIZED TERPENOID DEFENSE COMPOUNDS IN MAIZE

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Specialized terpenoids are major components of complex maize (*Zea mays*) chemical defenses that mediate responses to herbivores, pathogens and other environmental challenges. Here we describe the discovery, biosynthesis and elicited production of a new class of maize diterpenoids, named dolabralexins. Metabolite profiling of common maize cultivars under field conditions supports the widespread biosynthesis of dolabralexins as predominant metabolites in roots. Oxidative stress and elicitation with fungal *Fusarium* pathogens elicit the accumulation of dolabralexins and the transcript expression of corresponding biosynthetic genes. Consistent with fungal-elicited defenses, select pathway intermediates significantly inhibit fungal growth in vitro. Together, these findings support defense-related roles for dolabralexins in maize stress interactions and expand the known chemical space of diterpenoid defenses as genetic targets for understanding and ultimately improving maize resilience.

***DEB Graduate Student**

O. COVALENT TRAPPING OF HUMAN ADAR CATALYTIC DOMAIN USING THIOL MODIFIED dsRNA

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Adenosine Deaminases Acting on RNA (ADARs) are a family of enzymes that catalyze the hydrolytic deamination of Adenosine (A) to Inosine (I). Since Inosine is recognized as Guanosine during translation, A-to-I editing can change the meaning of codons and the protein function. Many studies have shown that aberrant activities of ADARs are highly associated with various human disease including cancers. In 2016, our lab in collaboration with Dr. Andrew Fisher's lab at UC Davis, solved a crystal structure of human ADAR2 catalytic domain (hADAR2d) bound to double stranded RNA (dsRNA) using an adenosine analog, 8-azanebularine to stabilize the complex. This crystal structure provided insights into substrate recognition by hADAR2d as well as possible explanations for its specificity. However, 8-azanebularine trapping is only useful for a ADAR-dsRNA complex bearing a tetrahedral intermediate mimic because 8-azanebularine is hydrated by ADAR and trapped as tetrahedral intermediate mimic in the active site. Therefore, we attempted to stabilize a protein-RNA complex using a covalent trapping method called disulfide crosslinking, which utilizes a disulfide bond between a cysteine residue of mutant protein and thiol modified dsRNA as a strategy to obtain stabilized ADAR-dsRNA complexes. Disulfide crosslinking results of catalytic domain of hADARs show that it is a promising trapping strategy which allow us to use it for solving an x-ray crystal structure of various ADAR-dsRNA complexes.

***DEB Graduate Student**

P. *ESCHERICHIA COLI* RESPONSE TO BIOCIDE EXPOSURE

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The development of resistance to antimicrobials by bacteria is a matter of increasing concern for modern society. Cross-resistance occurs when bacteria exposed to one antimicrobial product develops tolerance to another. Recently, the possibility of cross-resistance between biocides (antiseptics and disinfectants) and antibiotics has called the attention of the FDA, which asked for further data on the subject. Our long-term goals are to identify the mechanisms involved in cross-resistance and the genetic basis of acquired resistance to biocides. As a first step towards these goals, we used RNAseq to evaluate the transcriptomic response of the bacteria *Escherichia coli* to sub-inhibitory concentrations of biocides commonly utilized in households, hospitals, dentistry and/or food industry: chlorhexidine, chlorophene, glutaraldehyde, ethanol, isopropanol, peracetic acid, povidone-iodine, sodium hypochlorite, hydrogen peroxide and benzalkonium chloride. The data was comprehensive analyzed for gene ontology terms (biological processes) and the differentially expressed genes were organized in networks using Cytoscape-STRING. We observed a considerable difference between short-term (30 min) and long-term (8-12h) response to exposure to the biocides. In general, *E. coli* overexpressed chaperones and chaperonines as an early response to biocide stress, which was later replaced by downregulation of genes related to motility and chemotaxis, and upregulation of biofim-related genes. Additionally, *E. coli* rewired the respiration pathway: the late response resulted in downregulation of enzymes from the TCA cycle and upregulation of genes correlated to anaerobiosis. As a matter of concern, several genes associated with resistance to antibiotics were differentially expressed after exposure to biocides, such as the multidrug efflux protein acrA. The close inspection of the transcriptomic data allowed us to identify a cluster of genes regulated by the zinc-binding regulator zur, which were upregulated after exposure to sodium hypochlorite and peracetic acid. Further analysis of individual knockout mutants for such genes with growth curves and exposure assays validated their role in resistance to these biocides. Future work will include the study of resistant strains and the identification of cross-resistance key players.

***DEB Graduate Student**

Q. PARALLEL ENHANCER ANALYSIS IN MOUSE BRAIN TO CHARACTERIZE REGULATORY VARIANTS

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Genomic enhancers play critical roles in the regulation of gene expression during brain development. Sequence variation in enhancers is hypothesized to contribute to genetic risk for neurological disorders such as epilepsy and schizophrenia. The advancement of massively parallel reporter assays, which can screen thousands of DNA sequences for enhancer activity, has enabled the functional characterization of enhancers in both in vitro and in vivo models, but few of these assays have been applied to the brain. We adapted an enhancer reporter assay known as STARR-seq, in which the candidate sequence is placed in the 3' untranslated region of a reporter gene, for in vivo delivery into the mouse brain. We developed a pilot library of genomic candidates containing common non-coding sequence variants, including those associated with epilepsy and schizophrenia, in order to identify whether these variants contribute to altered gene expression in the brain. Results from preliminary deliveries of this library to the postnatal mouse brain via adeno-associated virus suggest that this method is able to identify sequences capable of acting as enhancers. We validated a schizophrenia-associated regulatory element and show that it drives reporter gene expression in developing mouse brain. Utilizing this approach works toward understanding how non-coding sequence variation in human populations contributes to brain development and neurological disorders.

***DEB Graduate Student**

R. TRANSIENT RECOMBINANT PROTEIN IN PRODUCTION IN GLYCOENGINEERED PLANT CELL SUSPENSION CULTURES

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In emergency situations, such as an infectious disease outbreak or bioterrorist attack, rapid production of novel protein-based drugs or vaccines could save lives. We are developing a transient expression platform which uses genetically engineered *Agrobacterium tumefaciens* to deliver DNA encoding a protein of interest to plant cells in suspension culture. Various proteins could be made using this system simply by using different *Agrobacterium* vectors. Compared to stable transgenic cell lines which take months to develop and screen, these *Agrobacterium* vectors can be made in as little as two weeks, decreasing the lead time required before large-scale production of novel recombinant proteins can begin. Using this platform, we have successfully produced a recombinant anthrax toxin receptor-Fc fusion protein (referred to as CMG2-Fc) by co-culturing *Agrobacterium* with plant cell suspension cultures. A potential concern with using plant-made proteins as human therapeutics is that plants produce slightly different glycosylation patterns than mammalian systems, which could lead to adverse immune responses in patients. To reduce the presence of plant-specific glycans on CMG2-Fc, β(1,2)-xylosyltransferase and α(1,3)-fucosyltransferase knockdown *Nicotiana benthamiana* cell suspension cultures were used. Compared to CMG2-Fc produced in wild type *Nicotiana benthamiana* plants, CMG2-Fc produced in the glycoengineered transient cell culture system had dramatically reduced levels of plant-specific glycans. In summary, this data demonstrates a new method for rapid, scalable production of glycoengineered protein therapeutics using plant cell suspension cultures.

***DEB Graduate Student**

S. MOLECULAR DYNAMICS SIMULATION OF TOLL-LIKE RECEPTOR 4 (TLR) ECTODOMAIN

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Toll-like receptors (TLRs) have a central role in both the innate and adaptive immune systems. These proteins recognize pathogen-associated molecular patterns and induce the release of the effector molecules of the immune system. The dysregulation of the TLR system may cause various autoimmune diseases and septic shock. TLR4 was identified as the signaling receptor for lipopolysaccharide which is responsible for the endotoxic shock, a severe inflammatory disease that leads rapidly to multi organ failure and death. Moreover, several studies suggest a possible role for TLR4 in cancer, cardiovascular disease, Alzheimer's, obesity, and diabetes. Recent advances in crystallography and *in silico* techniques provide promising opportunities for TLR4 investigations and drug design. Recently the X-ray structures of the extracellular domain (ECD) of mouse-TLR4 in ligand-bound (PDB 5IJC and 5IJD) and unbound (PDB 5IJB) states have been resolved. The TLR4 ECD contains leucine rich repeats that folds into a characteristic horseshoe-like structure and with the aid of its co-receptor (MD-2) is responsible for ligand recognition. We used multiple long-timescale (1.2 μs) molecular dynamics simulations on these structures to investigate TLR4 ECD conformational changes and interaction sites for its potential roles in signaling mechanism. All simulations were done in an explicit-water model with AMBER force field on graphics processing units (GPUs). Compared to earlier simulations done by others using a different force field that showed a highly dynamic TLR4 with an overall RMSD of 10 Å (de Aguiar *et al*, Proteins: Struct., Funct., Bioinf. 2015), our simulations showed that TLR4 structure was well maintained. Further analysis showed that the interface was also stable. Comparison of the ligand-bound and unbound structures shows the function of the MD-2 co-receptor and ligands in stabilizing the structure of TLR4 ECD.

T. PURIFICATION, FUNCTIONAL STUDY AND N-GLYCOSYLATION MODIFICATION OF A PLANT-MADE ANTHRAX DECOY PROTEIN (CMG2-Fc)

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We are interested in utilizing plants as bioreactors for biopharmaceutical production. Specifically, I am working on transient expression, purification and protein functional study of an Fc-fusion bioscavenger (CMG2-Fc) against anthrax disease in *Nicotiana benthamiana* plants through agrobacterium-medicated gene transfer. This whole plant transient expression system allows large scale biopharmaceutical production within brief time frame without requiring high-cost maintenance as cell culture does, which cuts the time and cost to bring critical medication to the market during a pandemic. To separate CMG2-Fc from a large pool of plant native proteins, I developed a two-step chromatography procedure (protein A column followed by hydrophobic interaction column), which enriched and purified CMG2-Fc with over 70% yield and 95% purity free of degraded fragments and aggregation. To validate protein function, I studied CMG2-Fc binding kinetics and affinity against protective antigen of anthrax utilizing surface plasmon resonance and biolayer interferometry. The data suggested that CMG2-Fc binds rapidly and tightly to protective antigen with sub-nM affinity, thus can be used as both preventive and post-exposure treatment against anthrax biological weapon to protect soldiers. One concern about plant-made biopharmaceutical is the presence of plant-specific glycans as they may lead to potential safety issues such as hypersensitivity or allergy, as plant-specific α(1,3)-fucose and β(1,2)-xylose are known to be important IgE binding determinants of plant allergens. To solve this issue, I developed a bioprocessing method to avoid plant-specific N-glycans through kifunensine (5.4μM) addition during transient vacuum agroinfiltration. Comparing CMG2-Fc N-glycan pattern with and without kifunensine addition, the relative abundance of plant-specific N-glycan shifted from 97.7% (no kifunensine treatment) to 1.8% (kifunensine treatment) without compromising protein yield or modification of the primary sequence. Oligomannose glycans are great precursors for in vitro enzymatic modification to produce more human-like N-glycans, and are preferred for HIV-1 viral vaccine and certain monoclonal antibodies.

***DEB Graduate Student**

U. $GABA_A$ RECEPTOR SUBTYPE SELECTIVITY OF CHEMICAL THREAT AGENTS PICROTOXIN AND TETS IN LARVAL ZEBRAFISH

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It has previously been reported that $GABA_A$ receptor ($GABA_AR$) antagonists, including pentylenetetrazole (PTZ), tetramethylenedisulfotetramine (TETS), and picrotoxin (PTX), which are potent convulsants in mammalian models, trigger seizure-like behavior in zebrafish (*Danio rerio*) larvae. Extracellular field potential recordings obtained from the optic tectum of 5 days post-fertilization (dpf) zebrafish confirmed that acute exposures to all three $GABA_AR$ antagonists elicited extracellular spiking patterns consistent with seizure activity. However, the pattern of electrical activity varied between the individual $GABA_AR$ antagonists, which is consistent with data from primary mammalian neuronal cell cultures and rodent models of TETS and PTX-induced seizures. Collectively, these data suggest the possibility of differential $GABA_AR$ subunit profile binding for each convulsant. To address this question, genetic knockdown using morpholinos (MO) targeting $GABA_AR$ subunit-specific mRNA was used to delineate the full receptor subunit profile critical for TETS- and PTX-induced seizures. At 3 dpf, tropical 5D wildtype zebrafish injected with MO were acutely exposed to seizure-causing concentrations of TETS or PTX added to fish water. Behavior was recorded for 20 min post-exposure using the Noldus automated tracking system to determine whether MO knockdown prevented chemical-induced seizure behavior. Based on these experiments, a differential $GABA_AR$ subunit binding profile was identified for TETS vs. PTX. The subunits $\alpha 2$, $\beta 2$, and extrasynaptic δ are essential for the seizure-inducing activity of both TETS and PTX, whereas $\alpha 1$ and $\beta 3$ are important for TETS but not PTX-induced seizures, while $\gamma 2$ is uniquely important for PTX-induced seizures. Phylogenetic analyses demonstrate homologous subunits between ebrafish and mammalian $GABA_AR$, suggesting that these findings are relevant to understanding the differential effect of these chemicals on seizure behavior in mammalian systems, including humans. The study was supported by the NIH CounterACT grant # NS079202 and National Center for Advancing Translational Sciences, NIH award TL1 TR000133.

***DEB Graduate Student**

V. UTILIZING CRISPR/Cas9 TECHNOLOGY TO KNOCKOUT JUNO IN THE PIG GENOME

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Fertilization involves the fusion of egg and sperm to re-constitute a diploid genome and initiate the development of new progeny. To achieve successful fertilization, sperm undergo an acrosome reaction, penetrate the zona pellucida, bind to the oocyte's plasma membrane, and finally, fuse with this plasma membrane. Inoue et al. demonstrated that Izumo1, a protein present under the acrosomal cap of sperm, is essential for sperm-egg fusion in the mouse. The murine oocyte surface receptor for Izumo1, folate receptor 4 (Folr4, also known as Juno), was recently discovered. Bianchi et al. demonstrated (1) that Juno interaction with Izumo1 is conserved across several mammals including the pig, (2) that Juno is essential for fertility in female mice, and (3) that Juno is rapidly shed from the plasma membrane of fertilized eggs, suggesting Juno may also have a role in blocking polyspermy. Our study aims to determine whether or not Juno is essential for fertilization in the pig by creating a gene knockout via a CRISPR/Cas9 system. Guide RNA (gRNA) were designed to target exon regions within the FOLR4 gene. To observe Cas9's targeting and DNA cutting ability, parthenogenetically activated embryos were microinjected with Cas9/gRNA complexes and sequenced at blastocyst stage. One-cell embryos flushed from gilts were also microinjected and transferred to recipient sows with the goal of producing FOLR4 knockout offspring. By injecting gRNA/Cas9 complexes into one-cell embryos, Cas9 localizes to the target sequence, creates a double strand break, and disrupts FOLR4. This knockout will demonstrate whether or not FOLR4 is essential for fertilization in swine. If FOLR4's function in the pig is demonstrated to be similar to that of the mouse, chances of similar protein function in other mammals increase significantly. Lack of function during fertilization would also be noteworthy, as it would emphasize species-specific molecules during gamete recognition.

***DEB Graduate Student**

W. INVESTIGATING PLACENTAL DNA METHYLATION AT AUTISM SPECTRUM DISORDER IN THE MARBLES PROSPECTIVE AUTISM STUDY

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Autism spectrum disorder (ASD) is a group of neurodevelopmental disorders, currently affecting 1 in 68 children in the United States. There is currently no genetic or molecular test for ASD until age three. Most ASD cases appear to be multifactorial, involving genetics variation and periconceptional nutrition. Epigenetic modifications such as DNA methylation open a unique window to study the interface of both aspects. Prenatal vitamins contain folic acid and other methyl donors which interact with DNA methylation to reduce risk of severe language delay and ASD. Placental tissue, usually discarded at birth, is a potentially rich source for studying DNA methylation patterns similar to oocytes and pre-implantation states of development. The MARBLES (Markers of Autism Risk in Babies-Learning Early Signs) study recruits mothers of at least one child with ASD who are planning additional pregnancies. Mothers were interviewed about prenatal vitamin intake during pregnancy. Offspring were followed until they were three years old and clinically diagnosed with ASD or typical development (TD).

In order to find regions that show significant differences between ASD and TD placental samples, WGBS was performed on DNA isolated from 20 ASD and 21 TD placental samples using Illumina next-generation sequencing. There is no statistically significant difference on global CpG methylation between ASD and TD. Then, I identified differential methylated regions (DMR) using the DMR finder approach based on the bsseq R package with more than a 10% methylation difference between ASD and TD placental samples. Two DMRs showed significant differences after a permutation test to calculate the family-wise error rate (FWER) based on WGBS data (correlated $p < 0.05$). In addition to these two "gold" DMRs, there were 352 DMR identified in ASD and TD comparison. 553 genes were assigned to those DMRs using the Genomics Region Enrichment of Annotation Tool (GREAT) with the default association settings. I replicated the methylation results of the both gold DMR by the independent method of pyrosequencing and still maintained the significant difference between ASD and TD. In a preliminary examination of methylation difference associated with prenatal vitamin use, there was no significant difference between prenatal vitamin use in the first month of pregnancy on the global level of DNA methylation. However, using the DMR finder, I identified 587 genes associated with 377 P1 prenatal vitamin DMRs. There are 50 genes that overlap between ASD-associated and P1 prenatal vitamin associated DMRs. Pyrosequencing results of percent methylation at the second DMR demonstrated that both ASD samples and samples without maternal P1 prenatal vitamin use showed higher methylation. Pyrosequencing results of

percent methylation at DMR Two demonstrated that both ASD samples and samples without maternal P1 prenatal vitamin use showed higher percent methylation. I also explore the association between common genetic variants within ASD-associated DMRs and their DNA methylation levels. I did some analysis on known SNP, *MTHFR*. MTHFR is a known SNPs related with both autism and folic acid intake. The MTHFR enzyme regulates folate availability. Mothers had the MTHFR 677 TT genotype had significant higher chances of having an ASD child with 60% reduced enzyme activity. From DMR Two percent methylation and MTHFR genotype, there is a significant association between percent methylation and MTHFR genotype.

These results suggest that additional DMRs may vary with both diagnosis and prenatal vitamin use that may direct our studies to gene loci relevant to the protective effects of prenatal vitamins in ASD risk, similar to the second DMR. This relatively small study of DNA methylation differences in placental samples from the MARBLES prospective study identified two high confidence DMRs that could be useful in assessing risk for ASD at birth and determining the impact of maternal prenatal vitamin usage on ASD occurrence in offspring.

***DEB Graduate Student**

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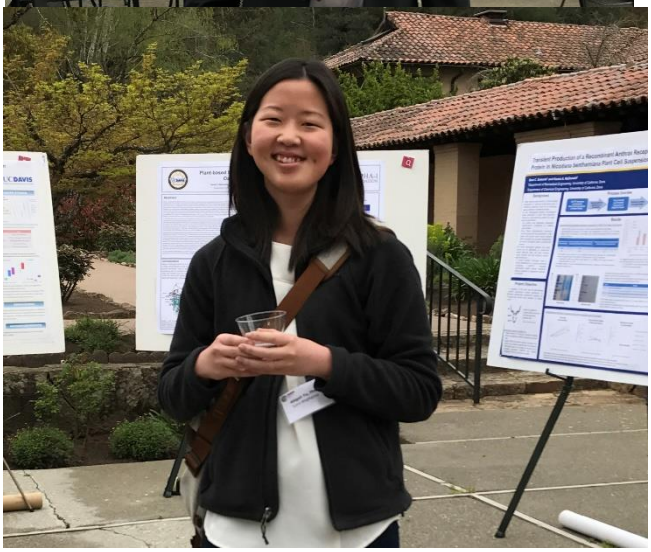

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Monsanto Company – Woodland and Davis Campuses

Contact:
Jose Prado, Ph.D.

37437 State Highway 16
Woodland, CA 95965
(530) 668-8268
www.monsanto.com

Calgene was founded in 1980 and is perhaps best known for the development of the first commercialized genetically engineered food, the FLAVR SAVR tomato. Monsanto acquired Calgene in 1997 and it became a research and development unit within Monsanto Technology. In 2011, the team became a part of Monsanto Chemistry Technology leveraging its plant biological sciences expertise for agricultural innovations. The Woodland and Davis Chemistry Technology teams are focused on delivering novel technology approaches through Biologicals for broad agricultural utility. A key area of the Biologicals focus is the BioDirect platform. To advance BioDirect discovery and Biologicals research into product development and agricultural products, the Chemistry Technology teams work across disciplines and use a variety of tools from biotechnology, molecular biology, biochemistry, genomics, formulations and analytical chemistry. Using these tools, the team is focused on developing BioDirect opportunities for protecting yield by controlling crop pests and improving other crop agricultural characteristics.

Monsanto provides a wide array of integrated solutions and is developing new technology platforms to help meet 21st century challenges to food production through meeting the needs of growers, commercial customers, and consumers in sustainable systems.

Novartis AG (formerly Chiron Corporation)

Contact:
Matthew Coleman, Ph.D., Scientist, Manufacturing Technology

4560 Horton Street
Emeryville, CA 94608-2916
(510) 655-8730

www.novartis.com

Mission
Novartis strives to be a leading biotechnology company by creating products that transform human health worldwide. We aim to prevent and treat diseases and improve people's lives.

Leadership Strategy
We will accomplish our mission through technological leadership, product-oriented research, superior manufacturing, and commercial strategies that create and expand markets.

Ethical Standards
We adhere to the highest legal and ethical principles in the conduct of all aspects of our business. We are committed to adhering to proven standards of financial and operational performance.

Values
Our purpose is to find solutions to human suffering caused by disease. Because disease does not wait for solutions, we are driven by a sense of urgency. As a result, our environment is intense, challenging, and focused on creating value for those who use our products and delivering sustained profitable growth for those who invest in our company.

Quality
Our goal at Novartis is to deliver quality products and services on time to all customers, internal and external. We provide employees with training and resources to meet or exceed customer requirements. We monitor processes and products to identify opportunities for continuous improvement.

Novozymes, Inc.

Contact:
Debbie Yaver, Ph.D., Director

1445 Drew Ave.
Davis, CA 95616
(530) 757-8100
www.novozymes.com

Enzymes are the natural solution to industrial problems. With enzymes we can reduce the consumption of water, energy and harmful chemicals and still make production more efficient. Novozymes is the world leader in enzyme solutions. Based on an advanced biotech platform we produce and sell more than 500 enzyme products in 120 countries. Since 1941 Novozymes has introduced almost every new industrial enzyme on the market, making us the world's largest manufacturer of enzymes today. With our minds set on innovation, we will continue to be so in the future.

Novozymes has introduced, with few exceptions, every new enzyme to the industry, from lipases, which remove grease stains during washing, to amylases, which are used to manufacture sweeteners. In our work we use the following technologies: microbiology, bioinformatics, gene technology, protein chemistry, computer chemistry, directed evolution, fermentation and recovery technology.

OncoMed Pharmaceuticals, Inc.

Contact:
Paul Hastings, Ph.D., President and CEO
John Lewicki, Ph.D., Executive Vice President and Chief Scientific Officer

800 Chesapeake Drive
Redwood City, CA 94063
(650) 995-8200
www.oncomed.com

OncoMed Pharmaceuticals is a biotechnology company dedicated to improving cancer treatment, by developing monoclonal antibodies that target the biologic pathways critical to tumor initiating cells, also known as “cancer stem cells”. We are leveraging our understanding of these tumor initiating cells to discover and develop novel therapeutics that could provide important alternatives for the treatment of cancer.

Tethys Bioscience, Inc.

5858 Horton Street, Suite 550
Emeryville, CA 94608
(510) 724-3260
www.tethysbio.com/index.html

Tethys Bioscience is dedicated to the discovery, development and commercialization of novel biological markers — biomarkers — that provide a practical tool to address the growing global challenge of chronic metabolic diseases such as diabetes.

By developing new tests that use protein and other bloodborne biomarkers to identify people at high risk for devastating and preventable diseases, we can arm patients and physicians with knowledge they can use to help prevent disease progression. These biomarkers give a snapshot of an individual's current risk, which may be modifiable. Our goal is to provide clinicians with an objective and convenient means to risk-stratify their patients and help them focus appropriate intervention strategies on those most likely to benefit. Our research strategies lead to sets of biomarkers that can be used to quantify the level of an individual's risk.

We approach the market with a unique combination of strengths:

- A research, management and commercialization team with extensive experience in diagnostic innovation
- Alliances with world-class researchers and partners
- A solid financial foundation

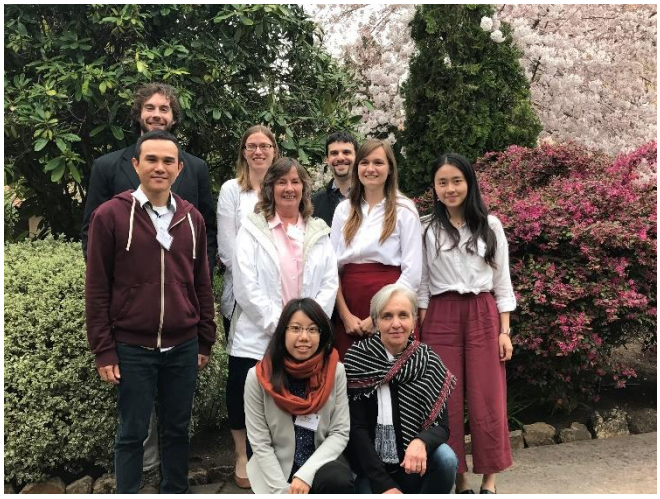
The company has become a pioneer in the discovery, development and value creation of novel biological markers for the clinical diagnostics marketplace: ***Biomarkers***. The company believes there is a large unmet need in both the discovery of potentially important biomarkers and the eventual use of them in routine clinical practice for many significant diseases.

Tethys Bioscience has built expertise, created significant intellectual property, and is executing its business plan around three key areas: ***Biomarker Discovery, Clinical Validation and ValueCreation***. Tethys is focused upon introducing products that yield significant savings to the health care system and improve the quality of life for patients.

- Biomarker discovery efforts are focused on applying advanced research tools to identify important biomarkers associated with diseases that affect many people and are very costly to health care systems throughout the world today.

- Clinical validation involves a complex process that results in defining a set of new biomarkers and the application of the resulting test to enhance current clinical practice.
- Value creation encompasses the use of sophisticated health economic analyses to define appropriate performance criteria for new biomarkers and the execution of market development strategies to drive the adoption of new biomarkers in clinical practice.

Participants



Retreat Participants

Biotech Fellows 2017 - 2018	
Amanda Dang	Materials Science & Engineering
Linda Su-Feher	Biochemistry, Molecular & Cellular Developmental Biology
Cody Watson Yothers	Chemistry
Graduate Students/Post-docs	
Sima Asadi	DEB, Chemical Engineering
Katherine Beglinger	DEB, Biochemistry, Molecular Cellular & Developmental Biology
Akhila Bettadapur	DEB, Biochemistry, Molecular Cellular & Developmental Biology
Jonas Calsbeek	DEB, Pharmacology & Toxicology
Takeyah Campbell	DEB, Biomedical Engineering
Nkechinyere Chidi-Ogbolu	DEB, Biomedical Engineering
Savannah Conlon	DEB, Chemistry
Pauline Famy	DEB, Chemical Engineering
Sukriti Gakhar	DEB, Chemical Engineering
Anirudh Gaur	DEB, Biochemistry, Molecular Cellular & Developmental Biology
Noah Goshi	DEB, Biomedical Engineering
Jamie Ho	DEB, Biochemistry, Molecular Cellular & Developmental Biology
Allison Hsia	DEB, Biomedical Engineering
Kalimuthu Karuppanan	Chemical Engineering
Ellen Lai	DEB, Integrative Genetics and Genomics
Kori Lay	DEB, Chemistry
Yixing Lu	DEB, Food Science
Linda Ma	DEB, Biochemistry, Molecular Cellular & Developmental Biology
Kantharakorn Macharoen	Chemical Engineering
Chandrima Majumdar	DEB, Chemistry Dept.
Lauren Matelski	DEB, Immunology
Karen McDonald	DEB, Chemical Engineering
Matt McNulty	DEB, Chemical Engineering
Leanna Monteleone	DEB, Chemistry
Charles Mordaunt	DEB, Biochemistry, Molecular Cellular & Developmental Biology
Katherine Murphy	DEB, Plant Biology
SeHee Park	DEB, Chemistry
Beatriz Pereira	DEB, Microbiology
Trenton Smith	DEB, Chemical Engineering

Sara Sukenik	DEB, Biomedical Engineering
Alireza Tafazzol	DEB, Biomedical Engineering
Sana Vaziri	DEB, Computer Science
Lalani Walawage	Assistant Specialist Plant Sciences (Dandekar lab)
Anita Wen	DEB, Pharmacology & Toxicology
Mary Xiong	DEB, Chemical Engineering
Bianca Yaghoobi	DEB, Pharmacology & Toxicology
Kelly Zacanti	DEB, Animal Biology
Yihui Zhu	DEB, Integrative Genetics and Genomics
UC Davis Faculty	
Joanna Chiu	DEB, Entomology
Abhaya Dandekar	DEB, Plant Sciences
Roland Faller	DEB, Chemical Engineering
Annaliese Franz	DEB, Chemistry/BMCDB
Tonya Kuhl	DEB, Chemical Engineering
Kent Leach	DEB, Biomedical Engineering
Alex Nord	DEB, Center for Neuroscience
William Ristenpart	DEB, Chemical Engineering
Industry	
Alberto Iandolino,PhD	Monsanto, Calgene Campus
Brad Niles,PhD	ARIZ Precision Medicine
Pankaj Pathak, PhD	Marrone Bio Innovations
Guests	
Renata de Almeida Barbosa Assis, PhD	Vising Scholar
Biotechnology Program	
Jacki Balderama	Biotechnology Program, Event Manager
Lorella Gino	Biotechnology Program, Program Associate
Marianne Hunter	Biotechnology Program, Assistant Director Administration
Denneal Jamison-McClung	Biotechnology Program, Associate Director
Judy Kjelstrom	Biotechnology Program, Director

biotech.ucdavis.edu

The Mission of the Biotechnology Program:

The Biotechnology Program was created in 1986, to assist in the organization of university activities related to biotechnology and to coordinate such activities with other efforts on the Davis campus. It is a central facility of the Office of Research. The Program's missions include:

- Promoting and coordinating the development of biotechnology and biotechnology - related research on the campus;
- Assisting with development of new and improved facilities for biotechnology research;
- Promoting research interactions between faculty and private industry and public agencies;
- Recommending and implementing curriculum development and training in biotechnology;
- Serving as an information and education resource on biotechnology for the campus and the public.

The Program serves as the **Administrative Home** for educational programs:

- Designated Emphasis in Biotechnology (**DEB**) graduate program
  deb.ucdavis.edu
- Advanced Degree Program (**ADP**) for corporate employees
  A PhD program for the working professional
- NIH Training Program in Biomolecular Technology for PhD students
- BioTech SYSTEM – K-14 educational consortium

Biotechnology Program Office:

Dr. Judith Kjelstrom - Director
Dr. Denneal Jamison-McClung – Associate Director
Marianne Hunter – Assistant Director, Administration
Jacki Balderama – Event Manager
Jacqueline Phillips – Program Associate
Kelly Meade – Budget Analyst
Office Location: 0301 Life Sciences
Telephone: (530) 752-3260 (main line) FAX: (530) 752-4125
Email: biotechprogram@ucdavis.edu

- The DEB provides a formal accreditation (on diploma & transcript) to reflect interdisciplinary biotechnology training.
- Not all of the DEB students will be funded by the NIH Biotechnology Training Program.

The fellows are a select subset based on a highly competitive nomination & selection process:
1. Nomination by a Faculty Trainer and completion of an application by the student.
2. Ranking by the Executive Committee of the NIH Biotechnology Training Program is
based on: academic merit; quality of the research; interdisciplinary nature of research;
and willingness to complete an internship.

Information about the NIH Biotechnology Training Grant is publicized on the NIH Training Program website: www.niht32.ucdavis.edu/

Designated Emphasis in Biotechnology Program (DEB)

Goals and Mission of the DEB

The Designated Emphasis in Biotechnology (DEB) is an inter-graduate group program that allows Ph.D. students to receive and be credited for training in the area of biotechnology. The DEB provides a nurturing interactive environment to promote integration of multiple disciplinary approaches to the conduct of research and to promote learning in biotechnology. The mission is to prepare well-educated students to approach problems with creativity and flexibility. The program will provide tools for the students to be leaders, visionaries, entrepreneurs, researchers and teachers in the broad area of biomolecular technology.

DEB Mission:

- To provide well-coordinated, cross-disciplinary training of graduate students in critical areas of biomolecular technology research.
- To promote interdisciplinary research environments that integrate basic biological science, engineering and computational disciplines.
- To allow cross-disciplinary training and trainee experience in a biotechnology company or cross-college laboratory.

Students come from a wide array of disciplines: Participating graduate programs currently include **29 programs**: Agricultural & Environmental Chemistry; Animal Biology; Applied Science Engineering; Biochemistry, Molecular, Cellular & Developmental Biology; Biological Systems Engineering; Biomedical Engineering; Biophysics; Chemistry; Chemical Engineering; Civil & Environmental Engineering; Comparative Pathology; Computer Science, Electrical & Computer Engineering; Entomology; Food Science Technology; Genetics; Immunology; Materials Science & Engineering; Mechanical & Aeronautical Engineering; Microbiology; Molecular, Cellular and Integrative Physiology; Neurosciences; Nutritional Biology; Pharmacology and Toxicology; Plant Biology; Plant Pathology; Soils & Biogeochemistry; and Statistics. The DEB program supplements a student's Ph.D. curriculum and those completing the program will obtain an official designation on their diploma & transcript indicating a qualification in biotechnology. Example: **Doctoral Degree in Microbiology with a Designated Emphasis in Biotechnology**

Brief History:

The DEB was formally established in 1997 as an outgrowth of the first NIH Training Grant in Biotechnology (funded in the early 1990s). The DEB became the formal training program for the current NIH Training Grant in Biomolecular Technology (1-T32-GM08799: July 1, 2002-June 30, 2017). The DEB provides a very effective multidisciplinary biotechnology concentration, which includes exposure to bioethics, business and legal aspects of biotechnology as well as a 3-6 month internship in a biotechnology company or research laboratory in another college or national laboratory. As of 2012, the DEB has 29 affiliated graduate groups or departmentally based graduate programs. The number of students in the Designated Emphasis in Biotechnology has increased dramatically over the last several years and now boasts over 230 members, with many being first year students. We have graduated 150 students with a DEB notation on their diplomas as of 2016.

Program Administration:

The administrative home for the DEB and the NIH Training Grant in Biomolecular Technology is the UC Davis Biotechnology Program. Dr. Judith Kjelstrom serves as the DEB and NIH Training Grant program coordinator for the DEB, in addition to directing the Biotechnology Program. She works closely with the DEB chair, Katayoon Dehesh (Department of Plant Biology) and the rest of the executive committee: Karen McDonald (Chemical Engineering), Abhaya Dandekar (Plant Sciences), Robert Rice (Environmental Toxicology) and David Rocke (Applied Science/Biostatistics) to oversee the day-to-day activities of the graduate program.

Course Work:

The DEB has a required core curriculum for students regardless of whether their graduate major is in biological science, engineering, statistics, etc. A key feature of the DEB is its requirement for a research internship at a cooperating biotechnology company or a cross-college site. When the students complete their Ph.D. requirements as well as the DEB requirements, their diploma notes not only their graduate major, but also that they have completed the DEB (e.g., "Ph.D. in Chemical Engineering with a Designated Emphasis in Biotechnology").

We have created a website for the Designated Emphasis in Biotechnology (deb.ucdavis.edu/) to advertise the program as well as the NIH Training Grant. The announcement of the grant is on the site. Program information, forms, pictures and other pertinent information is listed on the site. We have linked the website to graduate home pages of most of the 23 DEB program affiliates in the Division of Biological Sciences, College of Engineering, College of Letters and Science and the College of Agriculture and Environmental Sciences.

1. **Course Requirements**:

a. **DEB 263 (previously MCB 263)** (2 units): Biotechnology Fundamentals and Application (winter quarter, alternate odd numbered years)

An interdisciplinary course which includes: introduction to modern recombinant DNA technology; rate processes of biological systems, optimization of bioreactor performance; practical issues in biotechnology; and some specific case studies of the development of biotechnology products and processes. Grading: Letter grade; two one-hour exams, one

research paper (team project) on a selected topic relevant to biotechnology, and regular reading assignments.

b. **MCB 282** (variable): Biotechnology Internship (may be done any quarter)

The internship will expose qualified graduate students to research activities in a biotechnology company, to company culture, to legal and business aspects of industry, and to another career option. A minimum of 3 months internship at a local biotechnology company or cross college or national laboratory (i.e. Lawrence Berkeley Laboratory, Lawrence Livermore National Laboratory, etc.). S/U grading; research performance (student report) will be evaluated by the professor in charge and in consultation with the company trainer.

c. **MCB/ECH 294** (1 unit): Current Progress in Biotechnology (fall, winter and spring quarters). Three quarters of seminar are required for the DEB Program.

This course is an interdisciplinary seminar, featuring speakers from industry as well as academia. The students will have an opportunity to discuss the seminar topic with the lecturers, to learn about biotechnology research activities at companies and to network with speaker. Grading: S/U grading, attendance is required, and a summary report on the seminars is required at the end of the quarter.

d. **MIC 292** (1 unit): From Discovery to Product - An Introduction to Biotechnology at the Industrial Level. (winter quarter; even numbered years). MIC 292 is an approved **seminar elective** for the DEB program (may substitute for one quarter of MCB/ECH 294).

This course is designed to provide a unique opportunity to gain insight into basic and applied biotechnology at the industrial level. Lectures are presented by senior scientists from Novozymes Biotech, Inc. in Davis California (www.novozymes.com). A tour of the industrial facilities will be arranged. Grading: S/U grading, attendance is required, and a summary report on the seminars is required at the end of the quarter.

e. **GGG 296** (2 units): Scientific Professionalism and Integrity (fall quarter) or approved bioethics course.

The course will allow the student to become familiar with their roles and responsibilities as a professional scientist and/or instructor. While some standards of acceptable scientific behavior will be presented in class, most of the time will be spent discussing various "gray zone" scenarios, in which proper conduct is unclear. Grading: S/U grading; active class participation in class discussions is required. **This course is currently highly recommended, but will be required, pending approval.**

2. **Qualifying Exam Requirements**:

The Ph.D. qualifying exam should demonstrate appropriate knowledge with the area of biotechnology. At least one faculty member of the designated emphasis shall participate in the qualifying examination.

3. **Thesis Requirements**:

The dissertation committee shall include at least one faculty member of the designated emphasis. The major professor must be a participating DEB member.

4. **Additional Requirements**:

Regular attendance at the annual Biotechnology Training retreat and at the informal Pizza Chalk Talk Seminars (talks by students and faculty on current research) is expected.

DEB Program Students as of February 2018

NAME	GRADUATE GROUP/PROGRAM
Hannah Aizad Ledford	Molecular, Cellular & Integrative Physiology
Betsy Alford	Plant Pathology
Chidera Alim	Molecular, Cellular and Integrative Physiology
Riley Allen	Biomedical Engineering
Sonia Allen (Reveco)	Integrative Genetics & Genomics
Leif Anderson	Biomedical Engineering
Rigoberto Arenas	Chemistry
Sima Asadi	Chemical Engineering
Mina Azimi	Biochemistry, Molecular, Cellular & Developmental Biology
Christopher Baehr	Biomedical Engineering
Krithi Bala	Integrative Genetics & Genomics
Douglas Banda	Chemistry
DJ Darwin Bandoy	Integrative Pathobiology
Jed Bassein	Immunology
Katherine Beglinger	Biochemistry, Molecular, Cellular & Developmental Biology
Zachary Bendiks	Microbiology
Anastasia Berg	Biochemistry, Molecular, Cellular & Developmental Biology
	Biochemistry, Molecular, Cellular & Developmental Biology
Amirhossain Bolandparvaz	Biomedical Engineering
Stephen Bolus	Plant Pathology
Casey Boosalis	Molecular, Cellular & Integrative Physiology
Katie Bradshaw	Pharmacology and Toxicology
Glory Bui	Microbiology
Tawni Bull (Middleton)	Horticulture and Agronomy
Andrew Burch	Biochemistry, Molecular, Cellular & Developmental Biology
Jonas Calsbeek	Pharmacology and Toxicology
Takeyah Campbell	Biomedical Engineering
Austin Carroll	Chemistry
Anna Case	Chemistry
Alena Casella	Biomedical engineering
Bardo Castro Esparza	Microbiology
Nkechinyere Chidi-Ogbolu	Biomedical Engineering
Krishna Choudhary	Biomedical Engineering
Angel Cobos	Chemistry

Nicole Coggins	Molecular, Cellular & Integrative Physiology
Joshua Cohen	Food Science
Lisa Cohen	Molecular, Cellular and Integrative Physiology
Morgan Connolly	Microbiology
Adam Contreras	Biochemistry, Molecular, Cellular & Developmental Biology
Luis Eduardo Contreras Llano	Biochemistry, Molecular, Cellular & Developmental Biolog
Jasmine Corbin	Chemical Engineering and Materials Science
Karolina Czarnecki	Plant Biology
Amanda Dang	Material Science and Engineering
Rachel Danielson	Soils & Biogeochemistry
Destiny Davis	Plant Biology
Raquel de Mello e Pinho	Animal Biology
Marcus Deloney	Biomedical Engineering
Pamela Denish	Biophysics
Claire Depew	Immunology
Nithin Dhananjayan	Biophysics
Erin Doherty	Chemistry
Cintia Helena Duarte Sagawa	Plant Biology
Ameen Eetemadi	Computer Science
Nicholas Ellinwood	Pharmacology and Toxicology
Shea Feeney	Biochemistry, Molecular, Cellular & Developmental Biology
Samantha (Chun) Feng	Pharmacology & Toxicology
Michael Fong	Biomedical engineering
Sukriti Gakhar	Materials Science and Engineering - Longo Research Group
Javier Garcia	Biochemistry, Molecular, Cellular & Developmental Biology
Anirudh Gaur	Biochemistry, Molecular, Cellular & Developmental Biology
Donald Gibson	Integrative Genetics & Genomics
Deepshika Gilbile	Chemical Engineering
Eduardo Gonzalez	Pharmacology & Toxicology
Noah Goshi	Biomedical Engineering
Mona Gouran	Plant Biology
Charles Graddy	Microbiology
Brittany Greenwood (nee-Blankenship)	Microbiology
Benjamin Groth	Microbiology
Alex Gulevich	Biochemistry, Molecular, Cellular & Developmental Biology
Orangel Gutierrez	Integrative Genetics & Genomics
Jenna Harvestine	Biomedical Engineering

Dustin Heeney	Microbiology
Britta Heiss	Microbiology
Carly Hennessey	Molecular, Cellular and Integrative Physiology
Shawn Higdon	Plant Biology
Jamie Ho	Biochemistry, Molecular, Cellular & Developmental Biology
Gena Hoffman (Lurvey)	Plant Biology
Tiffany Hong	Biochemistry, Molecular, Cellular & Developmental Biology
Kayla Horton (Sparks)	Pharmacology and Toxicology
Allison Hsia	Biomedical Engineering
Michelle Hu	Pharmacology and Toxicology
Jessica Huang	Biochemistry, Molecular, Cellular & Developmental Biology
Kuei-Pin Huang	Molecular, Cellular and Integrative Physiology
Alexandria Igwe	Microbiology
Luiz Carlos Irber Jr	Computer Science
Mittal Jasoliya	Integrative Genetics & Genomics
Julia Jennings	Chemistry
Hyunsoo Jin	NOW: Microbiology - WAS: Molecular, Cellular and Integrative Physiology
Nelson Johansen	Computer Science
Daisy Johnson	Microbiology
Shannon Joslin	Integrative Genetics & Genomics
Agya Karki	Chemistry
Prema Karunanithi	Biochemistry, Molecular, Cellular & Developmental Biology
Cindy Khuu	Molecular, Cellular and Developmental Biology
Nicole Kingsley	Integrative Genetics & Genomics
Sophie Kiss	Pharmacology & Toxicology
Hwoi Chan Kwon	Biophysics
Ellen Lai	Integrative Genetics and Genomics
Vu Lam	Entomology
Kori Lay	Chemistry
Mirko Ledda	Integrative Genetics and Genomics
Sharon Lee	Biochemistry, Molecular, Cellular & Developmental Biology
Mark Lemos	Plant Biology
Kyle Lewald	Integrative Genetics and Genomics
Daniel Lewis	Integrative Genetics & Genomics
Johnathon Li	Animal Biology
Riyao Li	Chemistry
Ying Li	Entomology
Jonathan Lin	Microbiology

Yulong Liu	Biochemistry, Molecular, Cellular & Developmental Biology
Furong (Frank) Liu	Plant Pathology
Johnathan Lomas	Biological Systems Engineering
Rachel Lombardi	Food Science
Simon Lopez	Integrative Genetics & Genomics
Elizabeth Lotsof	Chemistry
Yixing Lu	Food Science
Shan Lu	Molecular, Cellular & Integrative Physiology
Linda Ma	Biochemistry, Molecular, Cellular & Developmental Biology
Kantharakorn Macharoen	Chemical Engineering
Chandrima Majumdar	Chemistry
Maika Malig	Integrative Genetics and Genomics
Alice Martinic	Nutritional Biology
Lauren Matelski	Immunology
Morgan Matson	Chemistry
Lucas McKinnon	Plant Biology
Matthew McNulty	Chemical Engineering
Beatriz Merchel Piovesan Pereira	Microbiology
David Merriam	Microbiology
Jessica Mizzi	Microbiology
Leanna Monteleone	Chemistry
Charles Mordaunt	Biochemistry, Molecular, Cellular & Developmental Biology
Katherine Murphy	Plant Biology
Livingstone Nganga	Plant Biology
Alan Nguyen	Immunology
Chuong Nguyen	Pharmacology & Toxicology
Jared Nigg	Microbiology
Jennifer Nill	Chemical Engineering
Glyn Noguchi	Biochemistry, Molecular, Cellular & Developmental Biology
Saghi Nojoomi	Molecular, Cellular and Integrative Physiology
Noah Pacifici	Biomedical Engineering
SeHee Park	Chemsitry
Beau Parry	Microbiology
Monica Pechanec	Animal Biology
Laura Perilla	Plant Pathology
Kevin Pham	Chemistry
Marc Pollack	Microbiology
Ali Rahimian Mashadi	Integrative Pathology
Anita Rajamani	Biomedical Engineering

Abhineet Ram	Biochemistry, Molecular, Cellular & Developmental Biology
Mythili Ramachandran	Pharmacology and Toxicology
Jamie Randol	Integrative Genetics and Genomics
Niknaz Riazati	Molecular, Cellular and Intergartive Physiology
Gabrielle Rossidivito	Plant Biology
Peter Sariano	Biomedical Engineering
Jordan Sayre	Microbiology
Alexander Schaffer	Biochemistry, Molecular, Cellular & Developmental Biol
Aarthi Sekar	Integrative Genetics & Genomics
Rebecka Sepela	Biochemistry, Molecular, Cellular & Developmental Biology
Shanaya Shah	Biochemistry, Molecular, Cellular & Developmental Biology
Kyle Shankle	Plant Biology
Natasha Shroff	Integrative Genetics & Genomics
David Silberstein	Chemical Engineering
Rosalie Sinclair	Plant Biology
Daniel Steele	Plant Biology
Eric Stevens	Microbiology
Allison Stevens	Nutritional Biology
Robert Stewart	Biochemistry, Molecular, Cellular & Developmental Biology
Robert Stolz	Integrative Genetics & Genomics
Linda Su-Feher	Biochemistry, Molecular, Cellular & Developmental Biology
Sara Sukenik	Biomedical Engineering
Rene Suleiman	Microbiology
Alireza (Ali) Tafazzol	Biomedical Engineering
Ruensern Tan	Biochemistry, Molecular, Cellular & Developmental Biology
Srinivas Tapa	Biomedical Engineering
Alexander Thuy-Boun	Chemistry
Connor Tiffany	Immunology
Tina Truong	Immunology
Kim Truong	Pharmacology & Toxicology
Robert Van Ostrand	Chemistry
Kacey VanderVorst	Biochemistry and Molecular Medicine
Sana Vaziri	Computer Science
Gregory Walker	Microbiology
Eric Walters	Microbiology
Marilyn Wang	Immunology
Yaxin Wang	Plant Biology
Kaitlin "Kay" Watt	Integrative Genetics & Genomics
Anita Wen	Pharmacology and Toxicology

Toni West	Biochemistry, Molecular, Cellular & Developmental Biology
Taylor Westmont	Immunology
Jacklyn Whitehead	Biomedical Engineering
Marisol Wolf	Neuroscience
Alonna Wright	Microbiology
Sydney Wyatt	Integrative Genetics and Genomics
Yongao (Mary) Xiong	Chemical Engineering
Ariga Bianca Yaghoobi	Pharmacology & Toxicology
Phoebe Yam	Integrative Genetics & Genomics
Xiaoxiao Yang	Chemistry
Britt Yazel	Neurosciences
Cody Yothers	Chemistry
Annabelle Yu	Microbiology
Kelly Zacanti	Animal Biology
Yue Zhang	Chemistry
Angela Zhang	Chemistry
Jie Zhu	Chemistry
Yihui Zhu	Integrative Genetics and Genomics
Danielle Zumpano	Molecular, Cellular and Integrative Physiology

DEB Faculty Trainers as of February 2018

Venkatesh Akella	Electrical & Computer Science
John Albeck	Molecular & Cellular Biology
Rajeevan Amirtharajah	Electrical & Computer Enginering
Paul Ashwood	UCD MIND Institute
Shota Atsumi	Chemistry
Matthew Augustine	Chemistry
Sharon Aviran	Biomedical Engineering
Alan Balch	Chemistry
Enoch Baldwin	Molecular and Cellular Biology Chemistry
Daniela Barile	Food Science & Technology/ Forensics
Nicole Baumgarth	Department of Pathology, Microbiology and Immunology; CCM, Vet Med
Andreas Baumler	Medical Microbiology and Immunology
Peter Beal	Chemistry
Laurel Beckett	Department of Public Health Sciences/Biostatistics
Craig Benham	Biomedical Engineering / Genome Center

Alan Bennett	Plant Sciences, College of Agricultural and Environmental Sciences
Trish Berger	Animal Science
	Pharmacology
Charles L. Bevins	Microbiology & Immunology
David Block	Viticulture & Enology/Chemical Engineering
Eduardo Blumwald	Plant Sciences
Laura Borodinsky	Physiology & Membrane Biology, UCDMC
Alexander (Sandy) Borowsky	Pathology
Julie Bossuyt	Pharmacology, School of Medicine
Richard Bostock	Plant Pathology
Kent Bradford	Plant Sciences, College of Agricultural and Environmental Sciences
Siobhan Brady	Genome Center/ Plant Biology
Nadean Brown	Cell Biology and Human Anatomy, School of Medicine
Titus Brown	Population health and reproduction: Vet Med
Sean Burgess	Molecular & Cellular Biology
Judy Callis	Molecular and Cellular Biology
Kermit Carraway	Biochemistry and Molecular Medicine
Luis Carvajal-Carmona	Genome Center, Biochemistry and Molecular Medicine, School of Medicine Biochemistry and Molecular Medicine, School of Medicine Biochemistry and Molecular Medicine, School of Medicine
Clare Casteel	Plant Pathology
Frederic Chedin	Genome Center, Molecular & Cellular Biology
Chao-Yin Chen	Pharmacology, School of Medicine
Hongwu Chen	Biochemistry & Molecular Medicine
Tsung-Yu Chen	Neurology, Center for Neuroscience
Xi Chen	Chemistry
Xinbin Chen	Comparative Oncology; UCD Cancer Center
Holland Cheng	Molecular & Cellular Biology
Simon Cherry	Biomedical Engineering
Nipavan Chiamvimonvat	Internal Medicine; Division of Cardiovascular Medicine
Joanne Chiu	Entomology and and Nematology
Blaine Christiansen	UCDHS: Orthopaedic Surgery
Gitta Coaker	Plant Pathology
Luca Comai	Plant Biology
Douglas Cook	Plant Pathology
Gino Cortopassi	Molecular Biosciences

Stephen Cramer	Applied Science
Beate Crossley	California Animal Health and Food Safety Laboratory System
Abhaya Dandekar	Pomology/Plant Sciences
Satya Dandekar	MED: Medical Microbiology & Immunology
Sheila David	Chemistry
Cristina Davis	Mechanical and Aeronautical Engineering
Scott Dawson	Microbiology
Wenbin Deng	Cell Biology and Human Anatomy (School of Medicine)
Megan Dennis	Biochemistry & Molecular Medicine
Elva Diaz	Pharmacology
Zhi Ding	Electrical & Computer Engineering
Georgia Drakakaki	Plant Sciences
Jason Eiserich	Nephrology; INT MED
Nael El-Farra	Chemical Engineering
Marc Facciotti	Biomedical Engineering
Robert Fairclough	Neurology: MED
Bryce Falk	Plant Pathology
Roland Faller	Chemical Engineering
Zhiliang (Julia) Fan	Biological & Agricultural Engineering
Katherine Ferrara	Biomedical Engineering
Oliver Fiehn	Molecular and Cellular Biology
Vladimir Filkov	Computer Science
Andrew Fisher	Chemistry
Paul Fitzgerald	MED: Cell Biology & Human Anatomy
Annaliese Franz	Chemistry
Christopher Fraser	Molecular and Cellular Biology
David Furlow	Section of Neurobiology, Physiology, and Behavior
Melanie Gareau	VM Anatomy, Physiol & Cell Bio
Charles Gasser	Molecular & Cellular Biology
Angie Gelli	Pharmacology, SOM
Damian Genetos	Anatomy, Physiology and Cell Biology
Paul Gepts	Plant Sciences
J. Bruce German	Food Science & Technology
Jacquelyn Gervay-Hague	Chemistry
Soheil Ghiasi	Electrical & Computer Engineering
Mark Goldman	Neurobiology, Physiology and Behavior; Ophthalmology and Vision Science
Tom Gradziel	Pomology
Eleonora Grandi	Pharmacology
Jeffrey Gregg	MED: Pathology

Ting Guo	Chemistry
Paul Hagerman	Biochemistry and Molecular Medicine
Fawaz Haj	Nutrition
Bruce Hammock	Entomology & Cancer Center
Stacey Harmer	Plant Biology
Dennis Hartigan-O'Connor	Medical Microbiology and Immunology
Dominik Haudenschild	Orthopaedic Research Labs
Volkmar Heinrich	Biomedical Engineering
Johannes Hell	Pharmacology
Paul Henderson	Internal Medicine: Divison of Hematology and Oncology
Matthias Hess	Animal Science
Wolf-Dietrich Heyer	Microbiology
Fereydoun Hormozdiari	Biochemistry and Molecular Medicine
David Horsley	Mechanical & Aerospace Engineering
You-Lo Hsieh	Textiles & Clothing
Mark Huising	Physiology & Membrane Biology, School of Medicine
Neil Hunter	Microbiology
M. Saif Islam	Electrical & Computer Engineering
Roslyn-Rivkah Isseroff	MED: Dermatology
Tina Jeoh	Biological & Agricultural Engineering
Thomas Jue	MED: Biochemistry
Carl Keen	Nutrition
Darshan Kelley	Western Human Nutrition Research Center, ARS, USDA Dept. of Nutrition
Rick Kiehl	Electrical & Computer Engineering
Dan Kliebenstein	Vegetable Crops & Weed Science
Paul Knoepfler	Cell Biology & Human Anatomy
Anne Knowlton	Cardiovascular Division, Department of Medicine & Department of Medical Pharmacology and Toxicology
Patrice Koehl	Computer Science/Genome Center & Bioinformatics Program
Ian Korf	Molecular & Cellular Biology/Genome Center & Bioinformatics Program
Dietmar Kueltz	Animal Science
Tonya Kuhl	Chemical Engineering
Hsing-Jien Kung	MED: Biochemistry / UC Davis Cancer Center
Anna La Torre	Cell Biology and Human Anatomy

J. Clark Lagarias	Molecular & Cellular Biology
Kit Lam	Biochemistry and Molecular Medicine
Donald Land	Chemistry
Delmar Larsen	Chemistry
Janine LaSalle	MED: Microbiology & Immunology
Jerold Last	Pulmonary / Critical Care Medicine
Kent Leach	Biomedical Engineering
Carlito Lebrilla	Chemistry
Pamela Lein	Molecular Biosciences
Harris Lewin	Evolution & Ecology
Jamal Lewis	Biomedical Engineering
Su-Ju Lin	Center for Genetics & Development & Section of Microbiology - UCD Cancer Center
Bo Liu	Plant Biology
Gang-yu Liu	Chemistry
Marjorie Longo	Chemical Engineering
Angelique Louie	Biomedical Engineering
Paul Luciw	MED: Pathology
Neville C Luhmann, Jr.	Electrical & Computer Engineering
Elizabeth Maga	Animal Science
Maria Marco	Food Science & Technology
Laura Marcu	Biomedical Engineering
Verónica Martínez Cerdeño	Department of Pathology and Laboratory Medicine
Karen McDonald	Chemical Engineering
Richard J. McKenney	Molecular & Cellular Biology
Frank McNally	Molecular & Cellular Biology
John McPherson	Biochemistry and Molecular Medicine
Stephen McSorley	Vet Med: Anatomy, Physiology & Cell Biology
Juan Medrano	Animal Science, , College of Agricultural and Environmental Sciences
Maeli Melotto	Plant Sciences
Richard Michelmore	Plant Sciences
Michael Mienaltowski	Animal Science
Lee Miller	Neurobiology, Physiology and Behavior
Lisa Miller	Department of Anatomy, Physiology and Cell Biology, CNPRC, School of Veterinary Medicine
David Mills	Viticulture & Enology and Food Science & Technology
Maria Mudryj	Medical Microbiology & Immunology
William J. Murphy	Department of Dermatology
James Murray	Animal Science /Department of Population Health and Reproduction, SVM

Florence Negre-Zakharov	Department of Plant Sciences
John Newman	Nutrition & USDA-ARS-WHNRC
Nitin Nitin	Department of Biological and Agricultural Engineering
Stephen Noctor	UCD MIND Institute -Psychiatry and Behavioral Sciences
Jan Nolta	UC Davis Health System - Hematology/Oncology
Alex Nord	Neurobiology, Physiology and Behavior, Center for Neuroscience/Psychiatry and Behavioral Sciences, School of Medicine
Jodi Nunnari	Molecular and Cellular Biology
Anita Oberbauer	Animal Science
Martha O'Donnell	Physiology and Membrane Biology, School of Medicine
Tingrui Pan	Biomedical Engineering
Alyssa Panitch	Biomedical Engineering
Rebecca Parales	Microbiology and Molecular Genetics
Atul Parikh	Biomedical Engineering
Anthony Passerini	Biomedical Engineering
Isaac Pessah	Molecular Biosciences, School of Veterinary Medicine
Ronald Phillips	Chemical Engineering
Kent Pinkerton	Pediatrics, School of Medicine
David Pleasure	Neurology and Pediatrics
Robert Powell	Chemical Engineering
Martin Privalsky	Microbiology
Jinyi Qi	Biomedical Engineering
Gerald Quon	Molecular and Cellular Biology
Katherine Ralston	Microbiology & Molecular Genetics
Katherine Rauen	MED: Pediatrics
Helen Raybould	VM Anatomy, Physiol & Cell Bio
Alexander Revzin	Biomedical Engineering
Crystal Ripplinger	Pharmacology
Subhash Risbud	Materials Science and Engineering
William Ristenpart	Chemical Engineering
David Rocke	MED: Biostatistics, Department of Biomedical Engineering
Jorge Rodrigues	Land, Air and Water Resources
Ray Rodriguez	Molecular & Cellular Biology
Pamela Ronald	Plant Pathology, College of Agricultural and Environmental Sciences
Alan Rose	Molecular and Cellular Biology
Lesilee Rose	Molecular & Cellular Biology
Pablo Ross	Animal Science

John Rutledge	MED: Cardiology
Jon Sack	Anesthesiology and Pain Medicine, Physiology & Membrane Biology
Earl Sawai	Pathology, Microbiology and Immunology, School of Veterinary Medicine
Kate Scow	Land, Air & Water Resources
David Segal	MED: Biochemistry and Molecular Medicine, Pharmacology, MIND Institute, Genome Center
Erkin Şeker	Electrical & Computer Engineering
Barbara Shacklett	Med Microbiology & Immunology, School of Medicine
Frank Sharp	UCD MIND Institute: Neurology
Justin Siegel	Biochemistry, Chemistry, and the Genome Center
Eduardo Silva	Biomedical Engineering
Christopher Simmons	Food Science & Technology
Sergi Simó	Cell Biology and Human Anatomy, School of Medicine
Scott Simon	Biomedical Engineering
Neelima Sinha	Plant Biology
David Slaughter	Biological & Agricultural Engineering
Carolyn Slupsky	Nutrition/ Food Science & Technology
Athena Soulika	Dermatology
Daniel Starr	Molecular & Cellular Biology
Francene Steinberg	Nutrition
Ioannis Steriopoulos	Plant Pathology
Pieter Stroeve	Chemical Engineering
Alexei Stuchebrukhov	Chemistry
Dawn Y. Sumner	Earth and Planetary Sciences
Gang Sun	Textiles & Clothing
Ilias Tagkopoulos	Computer Science
Cheemeng Tan	Biomedical Engineering
Dean Tantillo	Chemistry
Alice Tarantal	Pediatrics and Department of Cell Biology and Human Anatomy
Steven Theg	Plant Biology
Li Tian	Plant Sciences, College of Agricultural and Environmental Sciences
Michael Toney	Chemistry
Jose Torres	Medical Microbiology & Immunology
Renee Tsolis	Medical Microbiology & Immunology: MED
Richard Tucker	Cell Biology & Human Anatomy
Judy Van de Water	Division of Rheumatology/Allergy & Clinical Immunology, GBSF

Alison Van Eene	
Marta Van Loan	
Jean VanderGhe	ral Engineering
Rachel Lee Vann	logy
Mariel Vazquez	lar Genetics
John Voss	lar Medicine
Bart Weimer	lth & Reproduction
Robert H. Weiss	ion of Nephrology, School
Valerie Williamso	logy
David Wilson	Molecular & Cellular Biology
Matthew J. Wood	Environmental Toxicology
Reen Wu	MED: Pulmonary / Critical Care Medicine
Stefan Wuertz	Civil & Environmental Engineering
Heike Wulff	Pharmacology
Kevin Xiang	Pharmacology
Lifeng Xu	Microbiology
Soichiro Yamada	Biomedical Engineering
John Yoder	Plant Sciences
Glenn Young	Food Science & Technology
Aiming Yu	Biochemistry & Molecular Medicine
Philipp Zerbe	Plant Biology
Ruihong Zhang	Biological & Agricultural Engineering

The Value of Internships

Over the last 20 years (even before the formal DEB program was established), we have placed pre-doctoral students in a variety of biotechnology companies for their industrial research experience. They include:

Advanced Micro Devices (AMD)
Agilent Technologies
AgraQuest (a Bayer company)
Alza
Amgen
Amyris
Antibodies, Inc.
Aqua Bounty
Bayer
Berlex Biosciences
BioMarin Pharmaceuticals, Inc.
Carollo
Celera AgGen
Cytokinetics

DuPont
Exelixis
Expression Systems
Genencor
Genentech
Hoffmann Eitle
ICOS
Igenica
Institut Charles Sadron
Marone Bio Innovations
Maxygen
Monsanto, Calgene Campus
Novartis (formerly Chiron)
Novozymes
Nunhems
OncoMed
Scios
Somagenics
Syntex

Recovery Sciences
Roche Biosciences
Sutro Biopharma
State Water Control Resources Board
Tethys Bioscience, Inc.
Unilever
Ventria Biosciences
and others

Industry Partners gain many things from internships:

- Access to highly talented creative researchers
- Opportunity to gain inside track on future employees
- Through students, further collaboration with scientists on campus
- Participate in the annual retreat to meet UC scientists students, potential interns, other company scientists
- Potential to use UC facilities through the collaboration
- Opportunity to participate in weekly campus seminars

Students gain much from internships:

- Ability to work in a highly creative non-academic environment
- Opportunity to participate in focused team approach to defined research goals
- Ability to use equipment and facilities not available on campus
- Discover the type of environment, which suits future career goals
- Participate in industry seminars
- Enhanced curriculum vitae: reference letters and new skills
- Access to potential employment opportunities

Currently, there are over 220 students enrolled, so we need more Academic-Industry Partnerships.