Twenty Sixth Annual

Biotechnology Training Retreat

Saturday,
March 18, 2017

Christian Brothers Retreat & Conference Center

Twenty Sixth Annual Biotechnology Training Retreat

Co-sponsored by:

NIH Training Program in Biomolecular Technology (NIH-T32-GM08799)

UC Davis Designated Emphasis in Biotechnology Graduate Program (DEB)
UC Davis Biotechnology Program

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2017 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 26th anniversary of the Biotechnology Training Retreat. I have attended 22 of these wonderful events. This annual event honors our **2016-17 Fellows and their preceptors**, as well as **our industry affiliates**. In addition, our other DEB students are showcasing their research in the poster session. We have a new website to showcase our Fellows. Check it out: http://www.NIHT32.ucdavis.edu. 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), **Jacqueline Phillips (**Program Assistant), and our Associate Director, **Dr. Denneal Jamison-McClung, who will present the bioethics question.** Our BTP director, Kent Leach, cannot be with us today but we are grateful to associate directors, **Joanna Chiu** and **Luis Carvajal Carmona,** for chairing the morning and afternoon sessions today**.**

It is a pleasure to introduce our current Biotechnology Fellows. The **NIH Fellows** include: **Karan Agrawal,** Pharmacology & Toxicology (preceptor is John Newman); **Jasmine Corbin,** Chemical Engineering (preceptor is Karen McDonald); **Linda Su Feher** Biochemistry, Molecular, Cellular & Developmental Biology (preceptor is Alex Nord); **Maika Malig,** Integrative Genetics and Genomics (preceptor is Frédéric Chédin); **Sana Vaziri,** Computer Science (preceptor is Sharon Aviran) and **Cody Yothers,** Chemistry (preceptor is Annaliese Franz). Our four **Biotechnology Fellows** (industry and campus fellowships) include: **Akhila Bettadapur,** Biochemistry, Molecular, Cellular & Developmental Biology (preceptor is Katherine Ralston); J**oshua Cohen,** Food Science (preceptor is Daniela Barile); **Amanda Dang,** Materials Science (preceptor is Tonya Kuhl); and **Daniel Lewis**, Integrative Genetics and Genomics (preceptor is Cheemeng Tan).

As many of you know, we submitted a 5 year competitive renewal of the NIH T32 BTP last May. We were excited to receive a site visit last October. Thanks to all who participated. We received a score but were not funded for 2017. We are addressing the reviewers' concerns and will resubmit in September of this year. We feel confident that we can be successful. In the meantime, we are trying to obtain bridge funds from campus to support 3-4 current fellows, as well as keep some of the programs going, albeit at a

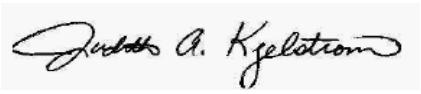
reduced level. Unfortunately, we will not be able to host the retreat in Napa next year, but we hope to return again in the future.

In regard to DEB internships, we placed **40** students in 2015/2016. Included are: **Allergan,** Inc., Irvine, CA – Angela Papalamprou; **Allied Minds,** Boston, MA – Garrick Yuen; **Amyris Biotechnologies**, Emeryville, CA – Amelia Manlove; **Teaching Science-American River College**, Sacramento, CA – Amanda Fox Xu; **Astrona,** SF, CA (Bryce Falk startup) – Marc Pollack; **ARIZ,** Davis, CA- Jon Flynn; **BASF,** Tarrytown, NY– Scott Strobel; **Bayer HealthCare**, Berkeley, CA – Doug Gettel; **BioMarin**, San Rafael, CA – Anna Marie Tuazon; **CA Family Health Council (CFHC), Research Division,** Berkeley, CA – Esther Shin Patchin; **Celgene SF** - Brian Avanzino; **Chr. Hansen**, Hoersholm, Denmark – Xiaochen (Ellie) Yin; **Desktop Genetics,** London, UK – Keith Dunaway; **Genentech,** SF, CA – Samantha Feng, Stefanos Kalomoiris, Angela Monterrubio, Juan Reyes, Tang Tang, Elyse Towns; **General Automation Lab Technologies (GALT) Inc.**, SF, CA – Rita Luu; **Gilead,** San Diego, CA – Nicole Nuñez (nee Chaffee); **HM Clause**, Davis,CA – Nicholas Thomas; **IBM, Almaden Research Center**, Palo Alto, CA-Luiz Irber; **Innovation Access,** UCD- Aiza Cathe Go, Özge Polat (nee Kurtuluş); **Intrexon,** Davis, CA- Mark Lemos; **Lawrence Livermore National Labs**, Livermore CA - Chris Chapman; **Monsanto**, Woodland, CA-Jenna Gallegos; **NASA Johnson Space Center,** Houston Texas – Forrest Ryan Dowdy; **Notable Labs**, SF CA- Jordan Mancuso; **Novozymes,** Davis CA – Akshata Mudinoor; **NSF** Resource Fellowship Foothill Oaks & AM Winn Elementary – Ingrid Leth; Office of Corporate Relations, UCD – Elizabeth Edmiston (nee Fox); **OncoMed Pharmaceuticals, Inc.**, Redwood City, CA – Sum Ying (Annie) Chiu, Malgorzata "Gosia" Liro, Rosanna Kwok; **REG Life Sciences**, South SF, CA – Shuchi Desai; Teaching Science-**Sac City College**, Sacramento, CA – Andrew Burch; **Starkey,** Berkeley, CA – Britt Yazel; **Stem Cell Partners LLC**, Sacramento, CA – Johnathon Anderson. We could not run our Training Grant and DEB graduate program without our partners! Thanks so much.

Forty two DEB students graduated in 2016 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 **2016 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 an MCB 294 seminar: **Zane Starkewolfe** (UC Davis Venture Catalyst); **Gian Oddone** (Marrone Bioinnovations); **Gina MacBarb** (S.I. Bone); **Johnathan Anderson** (UCDMC Institute of Regenerative Cures). 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

NIH Training Program in Biomolecular Technology
(NIH-1-T32-GM08799)

J. Kent Leach, Director
Joanna Chiu, Associate Director
Luis Carvajal-Carmona, Associate Director

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Director

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Marianne Hunter; Assistant Director, Administration
Jacki Balderama; Event Manager
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UC Davis Twenty Sixth Annual Biotechnology Training Retreat
March 18, 2017
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Morning Schedule

6:45 am – Bus departs Davis, Parking Lot #41

8:00 – 8:30 am	**Registration/Continental Breakfast**
8:30 – 8:45 am	**Welcome** **Joanna Chiu, PhD** Associate Director, NIH Training Grant in Biomolecular Technology
8:45 – 12:00 pm	**Morning Session Chair** **Joanna Chiu, PhD** Assoc. Director; NIH Training Grant in Biomolecular Technology
8:45 – 10:20 am	**Presentations** 8:45 am Karan Agrawal ..... *Mentor: John Newman* 9:10 am Jasmine Corbin..... *Mentor: Karen McDonald* 9:35 am Maika Malig..... *Mentor: Frédéric Chédin* 10:00 am **Fiore Cattaruzza, PhD**..... ***OncoMed Pharmaceuticals***
10:20 – 10:45 am	**Break / Poster Viewing**
10:45 – 12:00 pm	**Presentations** 10:45 am Linda Su-Feher..... *Mentor: Alex Nord* 11:10 am Cody Watson Yothers ..... *Mentor: Annaliese Franz* 11:35 am Denneal Jamison-McClung, PhD ..... *Bioethics Question (Handout)*

Afternoon Schedule

12:00 – 1:00 pm	**Lunch / Poster Viewing**
1:00 – 1:20 pm	**Photo Taking for NIH/Biotech Trainees**
1:20 – 5:00 pm	**Afternoon Session Chair** **Luis Carvajal-Carmona, PhD** Assoc. Director; NIH Training Grant in Biomolecular Technology
1:20 – 3:15 pm	**Presentations** 1:20 pm Denneal Jamison-McClung, PhD ..... *Bioethics Question (Discussion)* 1:40 pm Sana Vaziri..... *Mentor: Sharon Aviran* 2:05 pm **Abigail Yu, PhD** ..... ***Sutro Biopharma, Inc. (DEB & NIH BTP Grad)*** 2:25 pm Akhila Bettadapur..... *Mentor:Katherine Ralston* 2:50 pm Joshua Cohen..... *Mentor: Daniela Barile*
3:15 - 3:30 pm	**Short Break (15 min)**
3:30 – 5:00 pm	**Presentations** 3:30 pm **Herta Steinkellner, PhD**..... ***BOKU, Vienna, Austria*** 3:50 pm Amanda Dang ..... *Mentor: Tonya Kuhl* 4:15 pm Daniel Lewis..... *Mentor: Cheemeng Tan* 4:40 pm **Lonnie Bookbinder, MBA, PhD** . ***ARIZ Precision Medicine***
5:00 pm	**Closing Remarks** Joanna Chiu, PhD Assoc Director, NIH Training Grant in Biomolecular Technology

5:20 pm – Bus departs Napa

For social media, use #BiotechRetreat

2017 Poster Titles

A. "Sebum Lipid and Lipid Mediator Profiling: A Non-Invasive Approach for Cutaneous Research"

Karan Agrawal*[1,2], Lauren A. Hassoun[3], Negar Foolad[3], Raja K. Sivmani[3], John W. Newman[1,2,4]
[1]Department of Nutrition, University of California, Davis
[2]NIH West Coast Metabolomics Center, Davis, California
[3]Department of Dermatology, University of California, Davis Medical Center, Sacramento,
[4]USDA-ARS, Western Human Nutrition Research Center, Davis, California

B. "Purification of *Nicotiana bethamiana* Based Human Recombinant Butyrylcholinesterase Protein"

Salem Alkanaimsh[1], Jasmine M. Corbin*[1], Kalimuthu Karuppanan[1], Raymond L. Rodriguez[2,3,] Somen Nandi[2,3], and Karen A. McDonald[1,3]
[1]Department of Chemical Engineering, University of California, Davis
[2]Department of Microbiology and Molecular Genetics, University of California, Davis
[3]Global HealthShare Initiative, University of California, Davis

C. "Revisiting the Immunogenicity (or Tolerogenicity) of Poly (Lactic-Co-Glycolic-Acid)"

Riley Allen*, Jeff Ma, Jamal Lewis
Department of Biomedical Engineering, University of California, Davis

D. "Aerosol Emission During Human Speech"

Sima Asadi*[1], Anthony S. Wexler[2,3,4,5], Christopher D. Cappa[4], Nicole Bouvier[6], Santiago Barreda-Castanon[7], and William D. Ristenpart[1]
[1]Department of Chemical Engineering, University of California, Davis
[2]Department of Mechanical and Aerospace Engineering, University of California, Davis
[3]Air Quality Research Center, University of California, Davis
[4]Department of Civil and Environmental Engineering, University of California, Davis
[5]Department of Land, Air and Water Resources, University of California, Davis
[6]Department of Microbiology, Icahn School of Medicine at Mt. Sinai, New York, NY
[7]Department of Linguistics, University of California, Davis

E. "PH-Induced Vomocytosis for Intra-Lymph Nodal Delivery of Microparticle Vaccines"

Amir Bolandparvaz*, Jeffrey Ma, Annie Zhou, Jamal S. Lewis
Department of Biomedical Engineering, University of California, Davis

F. "Investigations into the Localization and Function of Sr35, a Wheat CC-NBS-LRR Protein that Confers Resistance to Race TTKSK (Ug99) of *Puccinia graminis* f. sp. *tritici*"

Stephen Bolus*[1], Gitta Coaker[2], Jorge Dubcovsky[1]
[1]Department of Plant Sciences, University of California, Davis
[2]Department of Plant Pathology, University of California, Davis

G. "Methods for Rapid and Scalable Quality Assessment of RNA Structure Probing Data"

Krishna Choudhary*, Huan Chen, Luyao Ruan, Nathan P. Shih, Fei Deng, and Sharon Aviran
Department of Biomedical Engineering and Genome Center, University of California, Davis

H. "Building A Next Generation Chimeric Antimicrobial Protein to Provide Rootstock-Mediated Resistance to Pierce's Disease in Grapevines"

Aaron Jacobson, Sandeep Chatkraborty, Hossein Gouran*, My Phu, Ana M. Ibanez, Basuthkar J. Rao, and Abhaya M. Dandekar
Department of Plant Sciences, University of California, Davis

I. "Predicting Combination Therapies to Target Genetic Vulnerabilities in Cancer"

Nelson Johansen*[1], Gerald Quon[2]
[1]Department of Computer Science, University of California, Davis
[2]Department of Molecular and Cellular Biology, University of California, Davis

J. "Expression, Purification, and Biophysical Characterization of a Secreted Anthrax Decoy Fusion Protein in *Nicotiana benthamaiana*"

Kalimuthu Karuppanan[1], Sifti Dhura-Gill[1], Muchena J. Kailemia[2], My L. Phu[3], Carlito B. Lebrilla[2,5], Abhaya M. Dandekar[3], Raymond L. Rodriguez[4], Somen Nandi[4], and Karen A. McDonald[1]
[1]Department of Chemical Engineering, University of California, Davis
[2]Department of Chemistry, University of California, Davis
[3]Department of Plant Science, University of California, Davis
[4]Department of Molecular & Cellular Biology, University of California, Davis
[5]Department of Biochemistry and Molecular Medicine, University of California, Davis

K. "Interplay Between Signaling and Adhesion Controls the Microgeography of Microbial Aggregates"

Daniel Lewis*, Cheemeng Tan
Department of Biomedical Engineering, University of California, Davis

L. "Stretching of RBCS at High Strain Rates"

Jordan E. Mancuso* and William D. Ristenpart
Department of Chemical Engineering, University of California, Davis

M. "Bioreactor Culture Duration of Engineered Constructs Influences Bone Formation Potential *In Vivo*"

Debika Mitra*[1], Osamu Yasui[1], Jacklyn Whitehead[1], J. Kent Leach[1,2]
[1]Department of Biomedical Engineering, University of California, Davis
[2]Department of Orthopaedic Surgery, School of Medicine, University of California, Davis, Sacramento

N. "WGBS Reveals Autism-Associated Hypomethylation and Differentially-Methylated Regions in Umbilical Cord Blood Samples from the Prospective MARBLES Study"

Charles E. Mordaunt*, Keith W. Dunaway*, Yihui Zhu, Rebecca J. Schmidt, Cheryl K. Walker, Sally Ozonoff, Irva Hertz-Picciotto, and Janine M. LaSalle
Department of Medical Microbiology and Immunology, Genome Center, MIND Institute, Center for Children's Environmental Health, University of California, Davis

O. "Role of Argininosuccinate Synthase in Pierce's Disease Development in Grapevines"

Cintia H.D. Sagawa*, Hossein Gouran*, Aaron Jacobson, and Abhaya M. Dandekar
Department of Plant Sciences, University of California, Davis

P. "Utilization of Metabolomics for Epimetabolite Discoveries in Stemness, from Stem Cells to Cancer Cells"

Megan Showalter*[1], Tomas Cajka[1], Luis Valdiviez[1], Henrik Sperber[2], Julie Mathieu[2], Kacey Vandervorst[3], Johnathon Anderson[4], Randy Carney[3], Hannele Ruohola-Baker[2], Jan Nolta[4], Kit Lam[3], Kermit Carrway[3], and Oliver Fiehn[1]
[1]West Coast Metabolomics Center, University of California Davis
[2]Institute for Stem Cell and Regenerative Medicine, University of Washington
[3]Department of Biochemistry and Molecular Medicine, University of California, Davis
[4]Stem Cell Program and Institute for Regenerative Cures, University of California Davis Health System

Q. "Production and Preliminary *In Vitro* Evaluation of a Plant-Made, Oxidation Resistant Alpha-1 Antitrypsin"

David Z. Silberstein*[1], Kalimuthu Karuppanan[1], Hnin Hnin Aung[2], Ching-Hsien Chen[2], Carroll E. Cross[2], and Karen A. McDonald[1]
[1]Department of Chemical Engineering, University of California, Davis
[2]Department of Internal Medicine, University of California, Davis

R. "Transient Production of a Recombinant Anthrax Receptor Fusion Protein in *Nicotiana benthamiana* Plant Cell Suspension Culture"

Sara C. Sukenik*[1] and Karen A. McDonald[2]
[1]Department of Biomedical Engineering, University of California, Davis
[2]Department of Chemical Engineering, University of California, Davis

S. "Analysis, Validation and Deregulation of RNAi-Mediated Crown Gall Resistant Walnut Rootstock J1 1A"

Sriema L. Walawage*, Brad Hanson, Greg Bowne, Charles A. Leslie, Michael Braverman, Abhaya Dandekar
Department of Plant Sciences, University of California, Davis

T. "Molecular Profiling of Grapevine Response to Pierce's Disease Provides Insights into the Invasion Biology of *Xylella Fastidiosa*"

Paulo A. Zaini*, Rafael Nascimento, Hossein Gouran, Dario Cantu, Sandeep Chakraborty, My Phu, Luiz Ricardo Goulart, Abhaya M. Dandekar
Department of Plant Sciences, University of California, Davis

U. "Placental DNA Methylation in Relation to Maternal Periconceptional Prenatal Vitamin Use and Child Outcomes in the MARBLES Prospective Autism Study"

Yihui Zhu*, Diane Schroeder, Charles Mordaunt*, Paula Krakowiak, Keith Dunaway*, Florence Crary, Cheryl Walker, Sally Ozonoff, Irva Hertz-Picciotto, Rebecca Schmidt, Janine LaSalle
Department of Medical Microbiology & Immunology, Genome Center, MIND Institute, University of California, Davis

V. "Cell-Secreted Extracellular Matrix, Independent of Cell Source, Promotes the Osteogenic Differentiation of Human Stromal Vascular Fraction"

Jenna N. Harvestine*[1], Hakan Orbay[2], Jonathan Y. Chen[1], David E. Sahar[2], J. Kent Leach[1,3]
[1]Department of Biomedical Engineering, University of California, Davis
[2]Department of Surgery, Division of Plastic Surgery, UC Davis Medical Center, Sacramento, California
[3]Department of Orthopaedic Surgery, School of Medicine, UC Davis Medical Center, Sacramento, California

W. "Nucleobase Analogs as Probes for Substrate Recognition and Repair by DNA Glycosylase MutY"

Chandrima Majumdar*, Amelia H. Manlove*, Paige L. McKibbin, Sheila S. Davis
Department of Chemistry, University of California, Davis

X. "Delivery of Biomolecules into Solid-Supported Lipid Bilayers Using Nanolipoprotein Particles"

Amanda T. Dang*
Department of Department of Materials Science and Engineering, University of California, Davis

Y. "Identification and Characterization of High-Mannose-Type N-Glycan Modification Enzymes for *in vitro* Enzymatic Glycan Modification of Glycoproteins"

Yanhong Li[1], Jing Wang[1], John Kailemia Muchena[1], Kalimuthu Karuppanan[2], Carlito Lebrilla[1], Karen McDonald[1,2], Xi Chen[1]
[1]Department of Chemistry, University of California, Davis
[2]Chemical Engineering & Materials Science, University of California, Davis

***DEB Graduate Student**

2017 Presentation Titles

1. **"The Sweat Mediator Lipidome is Affected by Stimulation Technique but not Sampling Location"**
   Karan Agrawal[1,2]*, Justin D. Waller[3], Man Van La[4], Ellen L. Bonnel[1], John W. Newman[1,2,3]
   [1]Department of Nutrition, University of California, Davis
   [2]NIH West Coast Metabolomics Center, Davis, California
   [3]USDA-ARS, Western Human Nutrition Research Center, Davis, California
   [4]Department of Environmental Toxicology, University of California, Davis

2. **"An Integrated Bioprocess for Production of Recombinant Butyrylcholinesterase from Transgenic Rice Cell Suspension Cultures"**
   Jasmine Corbin*[1], Muchena J. Kailemia[2], Salem Alkanaimsh[1], Kalimuthu Karuppanan[1], Raymond L. Rodriguez[3,4], Carlito B. Lebrialla[2,5], Karen A. McDonald[1,4], and Somen Nandi[1,3,4]
   [1]Department of Chemical Engineering, University of California, Davis
   [2]Department of Chemistry, University of California, Davis
   [3]Department of Molecular and Cellular Biology, University of California, Davis
   [4]Global HealthShare Initiative, University of California, Davis
   [5]Department of Biochemistry and Molecular Medicine, University of California, Davis

3. **"Developing Novel Genomic Tools to Characterize RNA:DNA Hybrid Formations on Mammalian Genomes"**
   Maika Malig*, Stella Hartono, Jenna Giafaglione, Lionel Sanz, And Frédéric Chedin
   Department of Molecular and Cellular Biology, University of California, Davis

4. **"Targeting Cancer Stem Cells"**
   Fiore Cattaruzza, Pete Yeung,Randall Hemer,Gilbert O'Young, Belinda Cancilla, Chun Zhang, John Lewicki, Austin Gurney, Tim Hoey, Ann Kapoun
   Department of Translational Medicine, Oncomed Pharmaceuticals, Inc., Redwood City, CA

5. **"Single Cells and Genetic Labeling in the Developing Brain"**
   Linda Su-Feher*[1], 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

6. **"Inducing the Production of Bioactive Lipid Derivatives in Microalgae"**
Cody Watson Yothers*, Annaliese Franz
Department of Chemistry, University of California, Davis

7. **"Who's Been Peeking at Your Genes? Genetic Privacy in the Age of Personal Genomics"**
Ethics Discussion
Denneal Jamison-McClung, PhD

8. **"Improved RNA Structure Analysis from Sequence and Probing Data"**
Sana Vaziri*[1], Fei Deng[1], Mirko Ledda[1], Robert Gysel[2], Sharon Aviran[1]
[1]Department of Biomedical Engineering, University of California, Davis
[2]Department of Computer Science, University of California, Davis

9. **"XpressCF: A Scalable Biochemical Protein Synthesis Platform for Designing and Manufacturing a New Generation of Biotherapeutics"**
Abigail Yu*, Cristina Abrahams, Millicent Embry, Xiaofan Li, Gang Yin, Alex Steiner, Toni Kline, Alice Yam, Ryan Stafford, Trevor Hallam
Sutro Biopharma, Inc., South San Francisco, CA

10. **"A Small Molecule Screen for Novel Inhibitors of Amoebic Trogocytosis"**
Akhila Bettadapur*, Katherine S. Ralston
Department of Microbiology and Molecular Genetics, University of California, Davis

11. **"Immobilization of a Recombinant *N*-Glycosidase for Isolation of Bioactive Glycans from Dairy Processing Co-Products"**
Joshua L. Cohen*, Juliana MLN de Moura Bell, and Daniela Barile
Department of Food Science and Technology, University of California, Davis

12. **"Antibodies Produced in Plants: Glycan-Engineering and Modulation of Functional Activities"**
Herta Steinkellner, PhD
Department of Applied Genetics and Cell Biology University of Natural Resources and Life Sciences, Vienna, Austria

13. **"Delivery of Biomolecules into Solid-Supported Lipid Bilayers Using *Nanolipoprotein* Particles"**
Amanda Dang* and Tonya Kuhl
Department of Chemical Engineering & Materials Science

14. **"Interplay Between Signaling and Adhesion-Controls: The Microgeography Of Microbial Aggregates"**
Daniel Lewis*, Cheemeng Tan
Department of Biomedical Engineering, University of California, Davis

15. "Designing and Developing Revolutionary Drugs Targeting Cancer at the Root Cause"

Lonnie Bookbinder, MBA, PhD
ARIZ Precision Medicine, UCD-HM Claus Life Sciences Innovation Center, Davis, California

***DEB Graduate Student**

Oral Presentation Abstracts

1. NIH FELLOW: Karan Agrawal

THE SWEAT MEDIATOR LIPIDOME IS AFFECTED BY STIMULATION TECHNIQUE BUT NOT SAMPLING LOCATION

Presenter: Karan Agrawal*

Authors: **Karan Agrawal*** [1,2], Justin D. Waller[3], Man Van La[4], Ellen L. Bonnel[1], John W. Newman[1,2,3]

Affiliations
[1]Departments of Nutrition, University of California, Davis
[2]NIH West Coast Metabolomics Center, Davis, California
[3]Department of Dermatology, University of California, Davis
[4]USDA-ARS Western Human Nutrition Research Center, Davis, California

Preceptor: John Newman

Recent interest in sweat as a non-invasive biological matrix has led to several characterizations of the sweat metabolome and proteome using both pharmacological and physiological sweat stimulation from various anatomical sites. However, no direct comparisons exist between different methods of sweat stimulation or site of collection. This study addresses this knowledge gap by comparing the lipid mediator profile of eccrine sweat: 1) collected from the volar forearm following pilocarpine iontophoresis (pharmacological) or moderate exercise (physiological) stimulation; and 2) from the volar forearm, anterior distal thigh and lower back following pharmacological stimulation. Healthy male subjects (n = 7, age = 27.2 ± 1.8yr, BMI = 25.0 ± 3.2 kg/m^2) were sampled, and collected sweat was analyzed for over 150 lipid mediators including oxygenated lipids, endocannabinoids and ceramides/sphingoid bases using liquid chromatography-tandem mass spectrometry. Detected sweat lipid mediators were unaffected by sampling site, though only four subjects produced sweat from either the lower back or thigh, but all produced sweat from the forearm. In comparison to exercise-induced sweat, pilocarpine iontophoresis-induced sweat contained increased concentrations of 39 lipid mediators including those derived from 5- and 12/15-lipoxygenase, cytochrome P450, soluble epoxide hydrolase, diacylglycerol lipase and ceramide synthase, all of which are major cutaneous enzyme pathways. Results indicate that pharmacologically inducing sweat enriches the secretion in multiple sweat lipid mediators, while anatomical site of sampling does not,

though the volar forearm provides the most consistent source of sweat. Therefore, it would appear that care must be taken when comparing sweat metabolomics data obtained by different stimulation techniques, whereas sweat metabolomics data obtained from different anatomical sites may be more readily compared.

***DEB Graduate Student**

2. NIH FELLOW: Jasmine Corbin

AN INTEGRATED BIOPROCESS FOR PRODUCTION OF RECOMBINANT BUTRYLCHOLINESTERASE FROM TRANSGENIC RICE CELL SUSPENSION CULTURES

Presenter: Jasmine M. Corbin*

Authors: **Jasmine M. Corbin[1*]**, Muchena J. Kailemia[2], Salem Alkanaimsh[1], Kalimuthu Karuppanan[1], Raymond L. Rodriguez[3,4], Carlito B. Lebrilla[2,5], Karen A. McDonald[1,4], and Somen Nandi[1,3,4]

Affiliations: [1]Department of Chemical Engineering, University of California, Davis
[2]Department of Chemistry, University of California, Davis
[3]Department of Molecular and Cellular Biology, University of California, Davis
[4]Global HealthShare Initiative, University of California, Davis
[5]Department of Biochemistry and Molecular Medicine, University of California, Davis

Preceptor: Karen McDonald

Plant cell suspension cultures have the potential to be a disruptive technology due to their inherent biosafety, controllability, reproducibility, conformance to cGMP requirements, capacity to perform complex glycosylation, and ability to grow in simple, low-cost, chemically defined, animal component-free medium. We have demonstrated use of this alternative expression platform by producing a recombinant form of butyrylcholinesterase (BChE) in a transgenic rice cell suspension culture. BChE is a complex and highly glycosylated human enzyme that has been studied as a therapeutic and prophylactic treatment against organophosphate poisoning and cocaine toxicity. However, widespread use of BChE has been limited because of the difficulty in producing such a large (~340kDa) and complex tetrameric molecule, as well as the prohibitively high costs of its upstream and downstream bioprocessing. The plant cell suspension culture is well-suited to address these specific needs at both the laboratory and industrial scale.

In this transgenic rice cell suspension culture, BChE is expressed under the control of a metabolically regulated promoter along with a secretion signal peptide that enables secretion out of the cell. These features enable the use of a semicontinuous operational strategy that allows for independent optimization of growth and production phases, reduces the need for longer seed trains, and minimizes turn-around time, CIP and SIP operations, chemicals, and energy. Our data demonstrate that BChE can be produced through multiple cycles of growth and BChE expression at varying process scales.

We are developing a downstream processing scheme including techno-economic analysis that illustrates how recombinant proteins produced in plant cell suspension culture can be harvested and purified using standard, linearly scalable methods (including tangential flow filtration, DEAE, and affinity chromatography) to obtain high purities, yields and cost effectiveness. We will also present some selected data on characterization of the recombinant BChE and compare it to its native BChE counterparts. These data include the relationship between recombinant BChE activity, temperature, and pH, amino acid sequence coverage, and the structure and abundance of N-glycans.

***DEB Graduate Student**

3. NIH FELLOW: Maika Malig

DEVELOPING NOVEL GENOMIC TOOLS TO CHARACTERIZE RNA:DNA HYBRID FORMATIONS ON MAMMALIAN GENOMES

Presenter:	Maika Malig
Authors:	**Maika Malig***, Stella Hartono, Jenna Giafaglione, Lionel Sanz, and Frédéric Chedin
Affiliations:	Department of Molecular and Cellular Biology, University of California, Davis
Preceptor:	Frédéric Chedin

Maintaining proper gene expression and genome stability is critical for normal human development and cellular homeostasis. The Chedin lab has recently identified a new type of non-B DNA structure called R-loops that form during transcription in mammalian genomes. R-loops form upon invasion of the duplex DNA by the newly transcribed RNA, resulting in a three-stranded structure composed of an RNA:DNA hybrid and a displaced loop of single-stranded DNA. Genome-wide R-loop mapping shows that these structures are prevalent and form over conserved hotspots. Accumulating evidence further suggests that R-loops play key roles in controlling gene expression and that deregulation of R-loop metabolism leads to genomic instability, a phenomenon linked to a growing number of human disorders. This study aims to increase our understanding of R-loop formation in normal human cells and disease states through the development of novel genomic and computational technologies.

We have made considerable progress in developing a high-throughput, high-resolution R-loop footprinting method by leveraging third generation single-molecule, real-time (SMRT) sequencing. This is applied to a variety of R-loop forming hotspots enables us to have the first and most comprehensive characterization of R-loops at the single-molecule level. Preliminary data shows that the method was highly successful. Long, contiguous C to T footprints have been observed specifically on the looped out strand but not on the RNA-paired DNA strand, as expected. Importantly, this data confirms that R-loop hotspots identified through bulk genome-wide methods are robust but revealed that these often large hotspots are due to the “piling-up” of smaller individual R-loops over larger R-loop-prone regions. For the first time

we can now systematically annotate the starts and stops of individual R-loops on thousands of individual molecules. We hope to leverage R-loop footprinting technology to identify the distinguishing molecular features of R-loops formed in cellular models of amyotrophic lateral sclerosis and Fragile-X syndrome. Both are neurological disorders implicated with R-loop dysfunction.

***DEB Graduate Student**

4. COMPANY AFFILIATE: OncoMed Pharmaceuticals, Inc.

TARGETING CANCER STEM CELLS

Presenter:	Fiore Cattaruzza, PharmD, PhD
Authors:	**Fiore Cattaruzza,** Pete Yeung, Randall Hemer, Gilbert O'Young,Belinda Cancilla, Chun Zhang, John Lewicki, Austin Gurney, Tim Hoey, Ann Kapoun
Affiliations:	OncoMed Pharmaceuticals, Inc., Redwood City, CA

OncoMed Pharmaceuticals is a clinical-stage biotechnology dedicated to discovery and development of novel therapeutics for the treatment of cancer based on our understanding of cancer stem cell pathways and immuno-oncology targets. We will present predictive and pharmacodynamic biomarker data of vantictumab in breast cancer. Vantictumab blocks canonical WNT/β-catenin signaling through binding of five Fzd receptors (1, 2, 5, 7, 8) and has demonstrated evidence of Wnt pathway modulation in both preclinical and clinical studies. In preclinical studies, this antibody was shown to inhibit the growth of several patient derived xenograft (PDX) tumor types, including breast, pancreas, colon and lung. Furthermore, it was observed that vantictumab reduces cancer stem cell frequency, exhibits synergistic activity with standard-of-care chemotherapeutic agents, promotes differentiation and inhibits metastasis. Pharmacodynamic biomarkers of vantictumab in a Phase 1b study show target engagement with downregulation of WNT genes and cancer stem cell genes. Predictive biomarkers are central to maximizing clinical benefit by targeting breast cancer patients most likely to respond to vantictumab. Using microarray gene expression data from 8 minimally passaged breast cancer xenograft models we generated a 6-gene biomarker signature that achieved the best performance of sensitivity, specificity, and positive and negative predictive values. We observed a strong correlation between the gene biomarker signature and the tumor volume observed in the breast xenograft experiments. The identified 6-gene biomarker signature was used to predict the response to vantictumab in combination with paclitaxel in 8 additional, HER2-negative breast cancer xenograft models. The efficacy in all 8 models was predicted correctly by the biomarker. The 6-gene biomarker signature has been evaluated in a Phase 1b study of vantictumab in combination with paclitaxel in patients with locally recurrent or metastatic HER2-negative breast cancer and identified patients with better progression free and overall survival in response to vantictumab in combination with paclitaxel.

5. NIH FELLOW: Linda Su-Feher

SINGLE CELLS AND GENETIC LABELING IN THE DEVELOPING BRAIN

Presenter:	Linda Su-Feher*
Authors:	**Linda Su-Feher*[1]**, 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

Complex genomic signaling pathways control the specification and differentiation of inhibitory interneurons, which arise in the embryonic basal ganglia (BG) during early brain development. Investigating the processes underlying interneuron specification may provide insight into brain development and the pathology of neurodevelopmental disorders associated with interneuron dysfunction. Current methods to classify and study interneuron subtypes fail to give critical information about how these subtypes develop. We performed single-cell RNA-sequencing at embryonic day 11.5 on dissociated mouse BG, incorporating a novel genetic labeling strategy to mark transient cell populations. Profiled cells labeled with our novel reporters represent transient developmental states of GABAergic interneuron progenitors. These results suggest that single-cell RNA-sequencing can be used to characterize labeled cell populations *in vivo*, enabling us to study transient populations of interest in the brain that were previously inaccessible to investigation. Additionally, we are working to improve single-cell RNA-sequencing technologies, enabling us to more efficiently detect and characterize these transient cell states. By building an atlas of interneuron lineage specification during early development using genetic labeling, we hope to examine functional changes in interneuron specification in pathogenic brain development as well as develop new cellular markers for future studies.

***DEB Graduate Student**

6. NIH FELLOW: Cody Watson Yothers

INDUCING THE PRODUCTION OF BIOACTIVE LIPID DERIVATIVES IN MICROALGAE

Presenter: Cody Watson Yothers*

Authors: **Cody Watson Yothers*** and Annaliese Franz

Affiliations Department of Chemistry, University of California, Davis

Preceptor: Annaliese Franz

Physiologically active natural products derived from the oxidation of poly unsaturated fatty acids (oxylipins) are expensive to produce using current methods. This work describes the use of hydrogen peroxide as a chemical trigger to increase the accumulation of oxylipins in oleaginous microalgae for application as an oxylipin production system. The synergistic stressors of nitrogen limitation and hydrogen peroxide treatment significantly increases the accumulation of neutral lipids in the industrially relevant marine diatom *Phaeodactylum tricornutum*, as determined by fatty acid methyl ester (FAME) analysis. Additionally, using a newly developed method for oxylipin analysis in microalgae via UHPLC-MS/MS, we found that under these conditions the concentration of oxylipins increased up to 800% over the control. The most abundant oxylipin species, EPA derived hydroxyl-oxylipin (5-HEPE), increased by >1000% over the control and made up 15% of the oxylipin profile. Current work has focused on using *Phaeodactylum tricornutum* to produce known oxylipin species, and additional studies are underway with other PUFA producing species such as *Tetraselmis suecica*. Future directions will include measuring the bioactivity of these oxylipin profiles and investigating the production of novel oxylipin species. This work demonstrates the use of chemical triggers in microalgae for the sustainable production of oxylipins for nutritional and therapeutic applications.

***DEB Graduate Student**

Bioethics Discussion

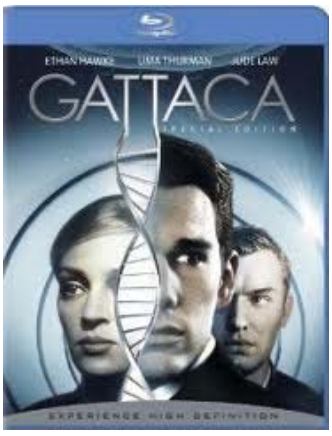
ETHICS QUESTION

"WHO'S BEEN PEEKING AT YOUR GENES? GENETIC PRIVACY IN THE AGE OF PERSONAL GENOMICS"

Written and Presented by

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

Who's Been Peeking at Your Genes? Genetic Privacy in the Age of Personal Genomics



Personal genomics and genetic genealogy have exploded in recent years, with millions of people opting to have their single nucleotide polymorphisms (SNPs) chip sequenced by direct-to-consumer genetic testing companies, such as 23andme and AncestryDNA.

Currently, 23andme is an industry leader in engaging customers in survey-based research that may lead to the identification of disease-related alleles and potential therapeutic targets via genome wide association studies (GWAS) and phenome wide association studies (PheWAS). About 80% of 23andme's 1.2 million customers participate in phenotype surveys via their research survey platform. Since 2011, the company has enrolled over 11,000 Parkinson's disease patients in the largest ever cohort for studying gene variants related to the disease, identifying six new risk loci in 2014 (published in Nature Genetics).

The 1996 Health Insurance Portability and Accountability Act (HIPAA) allows patient health information, including genetic data, to be sold by companies if "anonymized". Under HIPAA, 23andme has shared customer genetic data (banked whole genome samples) with several pharmaceutical companies, academic research groups and non-profit research foundations, including a $10 million deal with Genentech. AncestryDNA, best known for genetic genealogy, has recently entered the health information space and is collaborating with Calico, a biotech company interested in understanding genetic variants associated with human lifespan.

Discussion Questions

Customers are asked by companies to formally consent to personal genomics research participation and current models of genetic data sharing and selling are legal. However…

1. Recent studies have shown that anonymized patient medical records can be de-anonymized in many cases. Are personal genomics companies downplaying future genetic privacy risks associated with sharing "anonymized" customer data?

2. Is it important for customers to understand all potential uses of their genetic data/biological sample upon consenting to one specific use (e.g. SNP data vs. whole genome/banked biological sample data)? Should the personal genomics industry be required to develop dynamic consent tools prior to sharing customer data with third party research organizations?

3. Do personal genomics companies have any obligation (not legal, but ethical or moral) to return additional benefits to their customers if analysis of aggregate genetic data results in an approved therapeutic (e.g. discount on/priority access to therapeutic treatments, access to whole genome sequence data or other test results performed with personal samples, information on medically relevant personal findings, genetic counseling, etc.)?

Genetic Privacy in Families – What's Yours is Mine!

Angela and Erica are identical twins. Angela is interested in personal genomics and would like to submit her sample to a direct-to-consumer personal genomics company (e.g. 23andme), while Erica is concerned about finding out worrisome, non-actionable health information (e.g. ApoE alleles that may be correlated with higher Alzheimer's risk).

Photo credit: http://identity-mag.com/pros-and-cons-of-having-an-identical-twin-brothersister-in-egypt/

Erica worries that the privacy of Angela's genetic data cannot be guaranteed long term and, given their identical twin relationship, Angela's decision to participate in personal genomics research could negatively impact Erica's ability to maintain genetic privacy.

Discussion Questions

1. In families, do individuals have a responsibility or ethical obligation to protect the genetic privacy of extended family members? How should disagreements on genetic data sharing be approached? What measures can be taken to protect broader familial genetic privacy?

2. In medical settings, parents often consent to collect, analyze and share the genetic data of their children, including diagnostic gene or whole genome sequencing. Should there be any limits to parental rights in discovering or disclosing a child's genetic data? Phrased differently... do all people have an inherent, inborn right to genetic privacy?

Genetic Privacy Online Resources and Articles

23andme's statement on genetic privacy (https://www.23andme.com/research/) and research consent documentation (https://www.23andme.com/about/consent/)

Pitts, Peter (February 15, 2017) The Privacy Delusions of Genetic Testing, Forbes Op-Ed https://www.forbes.com/sites/realspin/2017/02/15/the-privacy-delusions-of-genetic-testing/2/#4a2af28f89c8

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Erlich, Yaniv and Narayanan, Arvind (June 2014) Routes for Breaching and Protecting Genetic Privacy, *Nature Reviews – Genetics*, v. 15 pp. 409-421. doi:10.1038/nrg3723

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8. NIH FELLOW: Sana Vaziri

IMPROVED RNA STRUCTURE ANALYSIS FROM SEQUENCE AND PROBING DATA

Presenter:	Sana Vaziri*
Authors:	**Sana Vaziri*[1]**, Fei Deng[1], Mirko Ledda[1], Robert Gysel[2], Sharon Aviran[1]
Affiliations	[1]Department of Biomedical Engineering, University of California, Davis [2]Department of Computer Science, University of California, Davis
Preceptor:	Sharon Aviran

The diverse functionality of RNA can largely be attributed to its ability to fold into a variety of structures. Determining its base-pairing pattern, or secondary structure, from sequence alone remains a challenging and important problem. A breadth of high-throughput approaches to structure analysis that couple chemical modification strategies with DNA sequencing have recently emerged. These experiments produce nucleotide-level measurements on RNA structure in a massively parallel fashion. While this data can be used to improve the accuracies of current computational structure prediction methods, significant errors remain. We implemented a recently outlined probabilistic framework for data-directed secondary structure prediction[1]. The statistically sound integration of chemical modification measurements in this model allows for easy adaptability to various probes and has the potential to elucidate complex interpretations of structural information. Through a systematic analysis of pre-processing effects on prediction accuracies, we gain insights into how the statistical properties of the data drive results.

Beyond data incorporation, an alternative avenue to improving prediction accuracy is to account for suboptimal structures. RNA realistically exists as an ensemble of co-occurring folds. To characterize the entire landscape of possible folds, we are interested in obtaining a compact set of structural patterns representing critical folds. This poses a significant challenge due to the combinatorial explosion in the ensemble size with sequence length. Inspired by a

recent study[2], we explore the problem of denoising a large-scale stochastic sample of the ensemble to mine a set of meaningful patterns. We examine the reproducibility of mining results and describe metrics to determine what constitutes a representative sample of the ensemble.

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1. Eddy 2014, Computational analysis of conserved RNA secondary structure in transcriptome and genomes. Annual Rev Biophys 43: 433-456
2. Rogers 2014, Profiling small RNA reveals multimodal substructural signals in a Boltzmann ensemble. Nucleic Acids Research, 2014,Vol. 42, No. 22: 1-10

***DEB Graduate Student**

9. COMPANY AFFILIATE: Sutro Biopharma, Inc.

XpressCF: A Scalable Biochemical Protein Synthesis Platform for Designing and Manufacturing a New Generation of Biotherapeutics

Presenter: Abigail Yu, PhD

Authors: **Abigail Yu***, Cristina Abrahams, Millicent Embry, Xiaofan Li, Gang Yin, Alex Steiner, Toni Kline, Alice Yam, Ryan Stafford, Trevor Hallam

Affiliations: Sutro Biopharma, Inc.
South San Francisco, CA

Sutro's XpressCF™ technology platform is made possible by the separation, into an extract, of the cellular components required to produce proteins from the process of protein generation itself. The extract includes all the necessary biochemical components for energy production, transcription and translation, and can be used to support cell-free biochemical protein synthesis by the addition of the specific DNA sequence for the desired protein. The process produces single proteins at g/L yields in 8-10 hours at any scale.

A wide variety of protein products have been produced using Sutro's platform. These range from small peptides to multimeric complex mammalian proteins such as monoclonal antibodies. The synthesis of many novel therapeutic proteins and families of proteins that are challenging by cell-based expression systems is now feasible, for example: difficult-to-fold proteins, cytotoxic molecules, and non-natural amino-acid containing proteins. Proteins can be rapidly engineered and optimized by producing many variants in parallel in 96-well plates from DNA libraries. Producing large quantities of a particular protein can be accomplished days from first DNA synthesis, allowing large animal pharmacology and safety assessments to be performed during the design and discovery phase of development.

*DEB and NIH BTP Trainee Graduate

10. NIH FELLOW: Akhila Bettadapur

A SMALL MOLECULE SCREEN FOR NOVEL INHIBITORS OF AMOEBIC TROGOCYTOSIS

Presenter:	Akhila Bettadapur*
Authors:	**Akhila Bettadapur***, Katherine S. Ralston
Affiliations	Department of Microbiology and Molecular Genetics, University of California, Davis
Preceptor:	Katherine S. Ralston

Entamoeba histolytica is a microbial eukaryote and causative agent of the diarrheal disease amoebiasis, which has high prevalence in developing nations. Pathogenesis is associated with profound damage to human tissues, and treatment options are limited. We recently discovered *E. histolytica* cells ("amoebae") attack and kill human cells through a novel cell-nibbling process that we named trogocytosis (*trogo-:* nibble). We showed that small molecules that block trogocytosis inhibit host cell death and tissue invasion, suggesting that trogocytosis presents a new target for therapeutic intervention. I aim to identify novel small molecule inhibitors of trogocytosis through a collaboration with the Small Molecule Discovery Center (SMDC) Screening Core at UCSF. To this end, I have developed two complementary high-content screens to determine trogocytosis inhibition based on high human cell viability. In the first microscopy-based screen, I will use two fluorescent stains that differentiate live verses dead human cells. Quantitative image analysis of small molecule treated amoebae reveals fewer dual stained dead human cells during coincubation, compared to control amoebae. My secondary screen uses CellTiterGlo, a luminescent readout for cellular ATP levels and a proxy for cell viability. Trogocytosis inhibited amoebae yield quantitatively higher luminescent values compared to control amoebae when coincubated with human cells. I have optimized the conditions and validated the accuracy of the readouts for both screens, demonstrating that amoebae treated with known trogocytosis inhibitors lead to a nearly 50% decrease in human cell death after a 45-minute incubation compared to control amoebae. I will now determine if these assays present the necessary statistical robustness, and then begin to screen for novel inhibitors.

After validating promising trogocytosis inhibitors, I will identify their targets using a cross-disciplinary approach with the SMDC Chemistry Core. These small molecules will be candidate therapeutics as well as tools for chemical genetic delineation of the trogocytosis mechanism. This work will improve understanding of amoebiasis pathogenesis, while developing new candidate therapies.

***DEB Graduate Student**

11. BIOTECH FELLOW: Joshua L. Cohen

IMMOBILIZATION OF A RECOMBINANT *N*-GLYCOSIDASE FOR ISOLATION OF BIOACTIVE GLYCANS FROM DAIRY PROCESSING CO-PRODUCTS

Presenter:	Joshua L. Cohen*
Authors:	**Joshua L. Cohen***, Juliana MLN de Moura Bell, and Daniela Barile
Affiliations:	Department of Food Science and Technology, University of California, Davis
Preceptor:	Daniela Barile

Complex glycans in human milk have putative prebiotic, immunomodulatory, and anti-pathogenic roles in infant development. Our lab isolates milk glycans from dairy co-products in a multifaceted attempt to improve nutrition for infants worldwide whilst adding economic value to currently underutilized waste streams. We have successfully developed several methods for isolation of bovine milk oligosaccharides at pilot scale using fermentation, nanofiltration, and enzymatic treatment. To capture a glycan pool that more closely resemble those found in human milk, we have explored the use a recombinant enzyme, called Endo BI-1, cloned from a commensal gut bacterium (*Bifidobacterium longum* subsp. *infantis*). We have leveraged the peculiar ability of this enzyme to cleave a wider variety of N-linked glycans from glycoproteins compared to existing commercial enzymes, and its unique stability to heat treatments. Isolation and use of the cloned enzyme was thus far limited to small-scale glycan capture; however, to advance this field and examine the multifaceted biological functionality of the glycans released from bovine whey glycoproteins using Endo BI-1, the scale of enzymatic release must be increased. We have now evaluated a variety of immobilization resins in order to optimize and scale up glycan release and overall process dynamics. Analytical methods including cutting-edge LC/MS and MALDI-ToF MS have informed developments in glycan release. Concurrent with the development of immobilization techniques to facilitate scaling, we have produced sufficient amounts of purified N-glycans for further screening of *in vitro* models including pathogen adhesion to intestinal epithelial cells and immunomodulatory activity.

***DEB Graduate Student**

12. CAMPUS GUEST: Herta Steinkellner, PhD

ANTIBODIES PRODUCED IN PLANTS: GLYCAN-ENGINEERING AND MODULATION OF FUNCTIONAL ACTIVITIES

Presenter: Herta Steinkellner

Authors: **Herta Steinkellner**

Affiliations: Dept. of Applied Genetics and Cell Biology, University of Natural Resources and Life Sciences, Vienna, Austria

Human immunoglobulins (which exist as 5 isotypes IgG, IgM, IgE, IgD and IgA) circulate as highly heterogeneously glycosylated mixture of otherwise homogeneous protein backbones. Due to recent breakthrough observations demonstrating glycosylation dependent immune-modulatory effects of antibodies, glycobiology has become of special interest in immunology. However, our limited technology in producing complex proteins such as antibodies, with defined glycan structures hamper in depths studies.

This presentation focuses on the ability of plants being used for the expression of human antibodies with targeted glycosylation profiles and how this (and other) post translational modifications impact functional activities. The approach relies on the use of stably transformed glycoengineered *Nicotiana benthamiana* plants in combination with transient expression modules. Importantly, harvesting of recombinant proteins one week post DNA construct delivery allows high speed and flexibility. Major achievements include the production of anti-viral antibodies that show, by the depletion of a single sugar residue (i.e. core fucose), increased antiviral activities. Notably, such glyco-engineered IgGs were successfully applied during the last EBOLA virus outbreak 2014 (Qiu et al., 2014 Nature, 514:47-53). Similarly, by engineering two posttranslational modifications (i.e. tyrosine sulfation and glycosylation) broadly neutralizing HIV IgG antibodies were produced that exhibited enhanced anti-viral effector function (Loos et al., PNAS USA 2015, 12:12675-80) and thus provide a novel strategy to develop efficient drugs against AIDS.

Other antibody formats that were also produced by the plant based expression platform are IgMs and IgAs, both harbor unusual features. With their pentameric structure IgMs belong to the most complex human proteins. Notwithstanding, functionally active therapeutically interesting monoclonal anti-cancer IgM was produced in *N. benthamiana*. Moreover, sophisticated glycan engineering resulted in the generation of targeted sialylated structures, one of the most complex human glycan formations. The approach required the synchronized expression of up to 13 different foreign genes in a single plant cell. Another peculiarity is the presence of O-glycans on serum IgA. We succeeded in the engineering of this unusual glycan formation on plant produced IgA. Collectively the plant based approach allows the efficient generation of different antibody formation with targeted glycosylation profiles thus offering an efficient approach to generate antibodies with optimized functions thus contributing to the development of novel antibody based drugs.

13. BIOTECH FELLOW: Amanda T. Dang

DELIVERY OF BIOMOLECULES INTO SOLID-SUPPORTED LIPID BILAYERS USING *NANOLIPOPROTEIN* PARTICLES

Presenter: Amanda T. Dang*

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

Affiliations: Department of Chemical Engineering

Preceptor: Tonya Kuhl

The folding of an integral membrane protein (IMP) depends strongly upon on the complex interplay of intermolecular interactions facilitated with its host biomembrane environment, making it difficult to ascertain functional conformations in non-native settings. Accordingly, for *in vitro* IMP studies, there exists a need for an experimental platform that can mimic the conditions of the biological membrane in a well-defined, modular fashion. Solid-supported lipid bilayers (SLBs) emulate biological membranes in several key respects, thereby demonstrating considerable promise in meeting this demand. The goal of this project is to develop a broadly applicable method for incorporating properly folded IMPs into SLB platforms. Preliminary experiments on optimization of SLB architecture led to the incorporation of a functional polymer cushion and a micropatterned substrate in the platform design. During evaluation of the feasibility of using nanolipoprotein particles (NLPs) as vehicles for delivery of biomolecules into the bilayer, results from epifluorescence microscopy experiments indicated that lipids and the receptor tyrosine-protein kinase, ErbB2/HER2, transferred spontaneously from NLPs to polymer-cushioned SLBs. In concurrent studies on the fundamental mechanisms of interaction between NLPs and a SLB, atomic force microscopy (AFM) was used to probe the morphology of a mica-supported membrane with NLPs tethered to the surface. AFM topography scans revealed that NLPs bound stably to the surface, albeit in aggregate form. The question of why aggregation occurred is one of many being investigated in the ongoing scope of this work. Altogether, insights gathered from preliminary experiments encourage further research into the nature of NLP-SLB interactions as well as the efficacy of NLP-mediated transport of biomolecules into SLB platforms.

***DEB Graduate Student**

14. BIOTECH FELLOW: Daniel Lewis

INTERPLAY BETWEEN SIGNALING AND ADHESION CONTROLS THE MICROGEOGRAPHY OF MICROBIAL AGGREGATES

Presenter: Daniel Lewis

Authors: **Daniel Lewis***, Cheemeng Tan

Affiliations: Department of Biomedical Engineering, University of California, Davis

Preceptor: Cheemeng Tan

Chemical signals and cell-cell adhesion modulate micro-scale geography of yeast-bacterial aggregates. The complex feedback between signaling, adhesion, and aggregate structure is difficult to elucidate in natural systems. As a result, the impact of the feedback between these forces on population dynamics remains elusive. Here, we address the challenges of microbial aggregate formation by studying the interplay between signaling, adhesion, and aggregate structure using synthetic biology approaches. We first use mathematical models and synthetic biochemical components to demonstrate how adhesive interactions can control the spatial distribution of microbial aggregates. Next, we demonstrate the link between spatial distribution of yeast-bacteria aggregates and competition using mathematical models, along with an experimental framework for biological validation of these results. This work establishes intercellular adhesion as a fundamental force behind competition between microbes, reveals new principles behind population dynamics in microbial ecosystems, and enriches bottom-up approaches for controlling multi-species aggregates. Our results create a foundation for rational design of new microbiome-associated therapeutics that exploit signaling and adhesion between microbes.

***DEB Graduate Student**

15. COMPANY AFFILIATE: ARIZ Precision Medicine

DESIGNING AND DEVELOPING REVOLUTIONARY DRUGS TARGETING CANCER AT THE ROOT CAUSE

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

ARIZ Precision Medicine is a cancer drug development company that is using targeted drug delivery systems to deliver genetic messages to kill cancer cells selectively. We are targeting the cause of cancer at an early stage to create drugs that are potentially curative and without side effects. Our business strategy is to sell our product candidates to pharmaceutical companies after proving they work in animal models of cancer, that will take us 18-24 months to do.

ARIZ's lab is located in the UCD-HM Clause Life Sciences Innovation Center. Our lab is managed by Dr. Brad Niles, a UC Davis graduate. We have one UCD DEB intern now and four more lined up for summer biobusiness internships.

Poster Abstracts

A. SEBUM LIPID AND LIPID MEDIATOR PROFILING: A NON-INVASIVE APPROACH FOR CUTANEOUS RESEARCH

Karan Agrawal*[1,2], Lauren A. Hassoun[3], Negar Foolad[3], Raja K. Sivamani[3], John W. Newman[1,2,4]
[1]Department of Nutrition, University of California, Davis, CA
[2]NIH West Coast Metabolomics Center, Davis, CA
[3]Department of Dermatology, University of California, Davis Medical Center, Sacramento, CA
[4]USDA-ARS, Western Human Nutrition Research Center, Davis, CA

Sebum is one of two major cutaneous secretions, and the sebum lipidome has been recently characterized to non-invasively identify markers of papulopustular rosacea and juvenile acne. In order to further explore the diagnostic utility of sebum, this study aims to characterize the sebum lipidome and (for the first time) bioactive lipid mediator profile of subjects with and without atopic dermatitis. Sebum was collected from the cheeks of subjects with and without atopic dermatitis (n = 11 and 9, respectively) using Sebutape Adhesive Patches and over 200 sebum fatty acids and bioactive lipid mediators were profiled using gas chromatography-mass spectrometry and liquid chromatography-tandem mass spectrometry, respectively. A total of 79 lipid mediators were detected in the sebum and increases in concentrations of C30-C40 [NS] and [NdS] ceramides, and the cyclooxygenase-, lipoxygenase-, cytochrome P450- and soluble epxoide hydrolase-derived metabolites of the major sebum polyunsaturated fatty acids were observed in the sebum of subjects with atopic dermatitis, and this effect was strongest in women. Analysis of sebum lipidomic data for these subjects is currently in progress and results will be available during the presentation. Our current findings demonstrate the presence of lipid mediators in sebum, and suggest differences in the lipid mediator profile between subjects with and without atopic dermatitis. Sebum lipid and lipid mediator profiling therefore may provide a non-invasive assessment of atopic dermatitis pathogenesis, and aid in novel target elucidation and assessment of therapeutic efficacy.

***DEB Graduate Student**

B. PURIFICATION OF *NICOTIANA BETHAMIANA* BASED HUMAN RECOMBINANT BUTYRYLCHOLINESTERASE PROTEIN

Salem Alkanaimsh[1], Jasmine M. Corbin[*1], Kalimuthu Karuppanan[1], Raymond L. Rodriguez[2,3], Somen Nandi[2,3], and Karen A. McDonald[1,3]
[1]Department of Chemical Engineering, University of California, Davis
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Butyrylcholinesterase (BChE) is a serum glycosylated serine hydrolase shown to protect different animal models against lethal amounts of a variety of cholinesterase-inhibiting organophosphate nerve agents. The supply of plasma-derived butyrylcholinesterase is constrained by the availability human blood which contributes to its high cost, more than $10,000/treatment. Limitations like cost and availability necessitate the development of expression platforms capable of large-scale, low-cost production of a fully active and efficacious recombinant BChE (rBChE) such as *Nicotiana benthamiana* plants. Thus, development of an effective downstream process for purifying rBChE is critical. Traditionally, procainamide affinity chromatography has been the main chromatography method to purify BChE from a variety of sources (human or recombinant). Recently, a more effective affinity chromatography based on potent cholinesterase inhibitor (tacrine-huperzine A hybrid; huperine X termed as Hupresin) was developed, and showed improved yields compared with procainamide. Here, we describe a purification scheme of rBChE protein from *Nicotiana benthamiana* plants that is produced using a *Tobacco Mosaic Virus* (TMV) viral expression vector at a level of 20 mg/kg fresh weight. Different extraction buffers were screened for their ability to extract rBChE and native plant proteins. Citric buffered saline at pH 4 was selected to minimize native plant proteins extracted, and it showed 4.5 folds enhancement in specific activity compared to Tris buffered saline. The extract was concentrated and buffer exchanged using tangential flow filtration (TFF), to 20 mM phosphate buffer, pH 7.4 prior to protein capture using DEAE-Sepharose with a 82.5 % protein yield. DEAE-Sepharose increased the purity of rBChE by (56%) by removing major protein contaminants with a yield of 60%. The rBChE was adsorbed to an affinity hupresin, and purified to homogeneity with an overall yield of 33.4%. Purity was assessed on SDS-PAGE with a one major band with a molecular weight of around 80 kDa. Mass spectroscopy confirmed the protein sequence and its thermal stability analysis was preformed.

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C. REVISITING THE IMMUNOGENICITY (OR TOLEROGENICITY) OF POLY (LACTIC-CO-GLYCOLIC-ACID)

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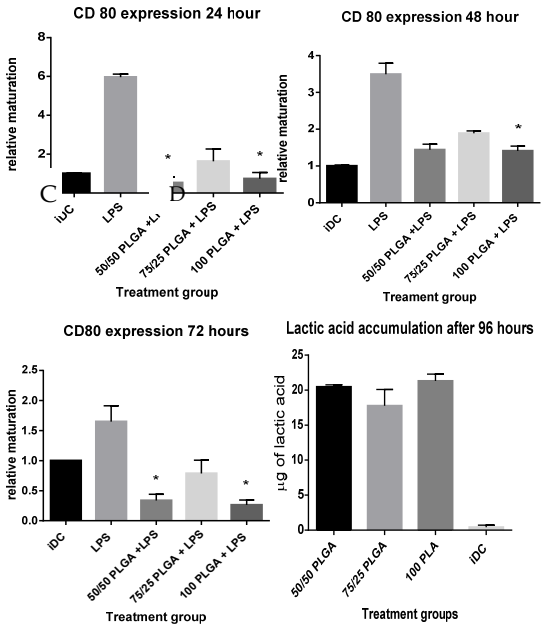
Introduction: One potential avenue for treatment of autoimmune diseases is tolerogenic dendritic cells (tDCs)- live "anti-vaccines". In an attractive method to develop these "anti-vaccines" *in vivo*, phagocytosable and unphagocytosable microparticles (MPs) are loaded with tolerogenic factors and delivered to DCs. Often, a material of choice for this application has been poly (lactic-co-glycolic acid) (PLGA), which has shown enhanced biocompatibility and can be finely tuned to enhance the delivery of tolerogenic factors to DCs. Taken altogether, PLGA MPs may provide an adaptable platform for targeted delivery to immune cells and therefore, autoimmune regulation. However, there have been contradicting reports on the immunogenicity of PLGA. These contradicting results are partly due to the nature in which PLGA immunostimulatory effects have been studied. These studies have assessed immune cell activation over a short time period and mainly considered the contact dependent nature of DC-PLGA interactions. However, following *in vivo* administration, PLGA and its breakdown constituents (glycolic acid/ lactic acid) may be *in situ* for beyond 3 weeks. Therefore, there may be a time dependent effect of this material and its monomers on immune cells. Further, it has been shown that tumor derived lactic acid can inhibit T cell activation, as well as DC cell maturation and antigen presentation. **Our *hypothesis* is that lactic acid, formed from the breakdown PLGA MPs, plays a time-dependent, immunosuppressive role in the development of immunosuppressive DCs.**

Materials and Methods: To test this hypothesis, we used an oil/water emulsion solvent evaporation technique to fabricate PLGA MPs. MPs were fabricated with PLGA (Average Mw~22 kDa) of different ratios of lactic to glycolic acid (100:0, 75:25, 50:50). MPs were incubated with bone marrow-derived DCs at time points ranging from 6-120 hours (10:1 MP to DC ratio). DC immunophenotype (CD80, CD86, MHCII) was assessed by flow cytometry at the end of the incubation period. Maturation resistance (PLGA MP incubation followed by LPS incubation) was studied in a similar manner. Additionally, a mixed lymphocyte reaction (MLR) was used to evaluate the ability of DCs to stimulate T cell proliferation via a BrdU assay. Lactic acid content in the culture media was quantified using a colorimetric assay to correlate DC phenotype to lactic acid content. MP uptake was analyzed using rhodamine 6G encapsulation and flow cytometric analysis.

Results and Discussion: Size of MPs was confirmed using DLS (~1 µm). MP uptake by DCs was confirmed using phase contrast microscopy and there was no significant difference in uptake of different PLGA compositions at the time points assessed (not shown). In general, PLGA either maintains or lowers the expression of positive costimulatory molecules on DCs (not shown). Furthermore, the 75:25 ratio of PLGA is the least effective in lowering DC maturation. This observation is reinforced by results from the maturation resistance study, where the 75:25 ratio shows increased CD80 expression in comparison to the other formulations following LPS stimulation (**Figure 1a-c**). It should be noted that the overall maturation state at longer time points is significantly lower than that of iDCs (**Figure 1c).** After 96 hours of incubation, the 75:25 PLGA MP composition showed a moderate decrease in mean lactic acid concentration in the culture media (**Figure 1d**). In the MLR, the 75:25 treated DCs had the most allostimulatory ability, and the T- cell proliferation in these treatments were the highest (not shown).



Conclusions: Based on preliminary results it is evident that the ratio of lactic to glycolic acid can influence early and late maturation status of DCs. Moreover, the indication is that PLGA may be more immunosuppressive in nature and suppressive ability is dependent on its biodegradability to lactic acid. PLGA is increasingly being researched as an adjuvant for inflammatory applications. Herein we show that careful consideration of PLGA composition may be required for desired immune response.

Figure 1. 75:25 PLGA composition shows the least tolerogenic properties upon maturation resistance at A) 24 hours B) 48 hours and C) 72 hours (* represents a p value less than .05 compared with 75/25 treatment) D) Represents lactic acid accumulation after 96 hours of

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D. AEROSOL EMISSION DURING HUMAN SPEECH

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The physical pathways governing airborne disease transmission between humans are poorly understood. The traditional research has been more emphasized on dramatic expiratory activities such as sneezing and coughing that yield easily visible aerosols. However, some early works identified speaking as an important source of large number of expiratory aerosols that are too small to see with the naked eye, but are nonetheless large enough to carry a variety of pathogens (e.g., influenza virus, 80 – 120 nm in diameter). This observation raises an important question: what types of speech emit the most aerosols? Here we show that the number of aerosols emitted during healthy human speech is correlated with both the amplitude (as a measure of loudness) and type of vocalization. Experimental measurements with an aerodynamic particle sizer indicate that speaking in a loud voice (~98 dBC) yields up to ten times more aerosols than in a quiet voice (~70 dBC). Furthermore, certain 'phones' (the basic units of speech) associated with voiced plosives (e.g., [d]) yield more aerosols than unvoiced fricatives (e.g., [f]) or nasals (e.g., [m]). We interpret these results in terms of the egressive airflow rate associated with the vocalization, which is known to vary significantly with both phonetic structure and overall loudness. The results suggest that individual speech patterns, including choice of language spoken, could affect the probability of airborne disease transmission.

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E. PH-INDUCED VOMOCYTOSIS FOR INTRA-LYMPH NODAL DELIVERY OF MICROPARTICLE VACCINES

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Motivation:

The recent Ebola pandemic devastated many West African countries, including Liberia and Nigeria. The outbreak has led to millions of infections, more than 11,000 deaths, and $2.2 billion lost in gross domestic product due to the burden on the healthcare system and lower economic output. The re-emergence of infectious diseases, such as Ebola, Zika, or West Nile viruses, has prompted the CDC to re-emphasize the need for more potent and efficacious vaccines to combat these diseases. Current vaccination strategies are ineffective, as up to 99% of the vaccine components remain at the site of administration. With this inefficiency in mind, researchers have demonstrated the ability to elicit stronger immune responses by directly injecting vaccines into lymph nodes (LNs)[4]. Moreover, *Jewell et al.* demonstrated that controlled release of vaccine components from polymeric particles at the LNs generates more potent immune responses at significantly lower dosages than conventional vaccines. However, the need for ultrasound-guided tracer dye to locate the LNs, due to their anatomical position and size, has prevented mass translation of this vaccination strategy. Furthermore, the cost and unavailability of required equipment are barriers to access in remote and rural communities. Employing microparticles (MPs) as carriers of drugs has many advantages over traditional vaccine formulations, such as high efficiency, low off-target toxicity, low production cost, controlled-release and long-term stability. My goal is to develop vaccine-loaded polycaprolactone (PCL) MPs which can be transported and deposited into the LNs by phagocytic cells (DCs and macrophages). This will allow controlled release of encapsulated vaccine agents directly at the LNs, thereby achieving greater vaccine efficacy whilst using lower dosages.

Dendritic cells are the sentinels of the immune system and are professional antigen presenting cells (APCs) that process and present antigens to T and B cells to elicit immune responses[5]. Moreover, DCs have demonstrated the ability to phagocytose micron-sized polymeric MPs, loaded with immunomodulatory agents. Upon uptake, researches have shown that DCs travel to the command centers of the immune system, the lymph nodes, to interact with T and B cells. As they traverse to the LNs, materials within the phagolysosome are typically degraded. However, this is not the case when *Cryptococcus Neoformans* are engulfed by phagocytic cells. *Cryptococcus Neoformans*, a type of fungus cell, can evade the phagosomal degradation through a phenomenon known as vomocytosis or non-lytic exocytosis: the escape of *C. Neoformans* from host cell after ingestion. Although the exact mechanism is not known, it has been shown that *C. Neoformans* has the ability to manipulate the acidic environment of the phagolysosome to a more basic pH and this is believed to be integral for

vomocytosis. Moreover, the role of lysosomal and cytosolic pH has been well established in regulation of macrophage lysosomal enzyme secretion. In mimicry of this pathogen, the *long-term goal* of my dissertation is to develop an intelligently-designed, polymeric, microparticle system for direct delivery and controlled release of vaccine agents at the LNs. Herein, *the overall objective* is to induce pH-mediated vomocytosis of MPs from phagocytic cells (DCs and macrophages).

Objective:

I plan to address this overall objective through the following investigative aims: (i) determine the optimal phagosomal pH for and kinetics of induced vomocytosis and (ii) design surface-functionalized MPs for inducing vomocytosis.

Research Plan Overview:

Aim 1: *Determine the optimal phagosomal pH for and kinetics of induced vomocytosis.* The objective of this aim is to determine and measure the optimal pH for vomocytosis of MPs by DCs *in vitro*. Our approach is to conjugate a pH-sensitive dye on surface of MPs to measure the pH within the phagolysosome. Herein, our *working hypothesis* is that increasing phagolysosome pH will activate vomocytosis of MPs. These preliminary studies demonstrate that we can induce vomocytosis of MPs from DCs by increasing the media pH and subsequently phagolysosome pH (**Figure 1A-B**). At this basic pH, the immunophenotypic stability and cellular integrity of DCs are unaffected (**Figure 1C-D**). These results, and reports by others, suggest that manipulation of the phagosomal pH can induce vomocytosis of MPs. Our test conditions will be media at pHs 6, 7.5, and 9. We will find the optimal pH for vomocytosis by investigating output responses, including number of particles expelled. Additionally, we will assess kinetics of MP vomocytosis by analyzing vomocytosis events at incremental time points through flow cytometry and microscopy techniques. Furthermore, we will investigate the mechanistic principles behind pH-dependent vomocytosis of MPs through a collaboration with Dr. Volkmar Heinrich at UC Davis. Utilizing his expertise in optical tweezers, we can closely monitor the biophysical changes of phagocytic cells during vomocytosis.

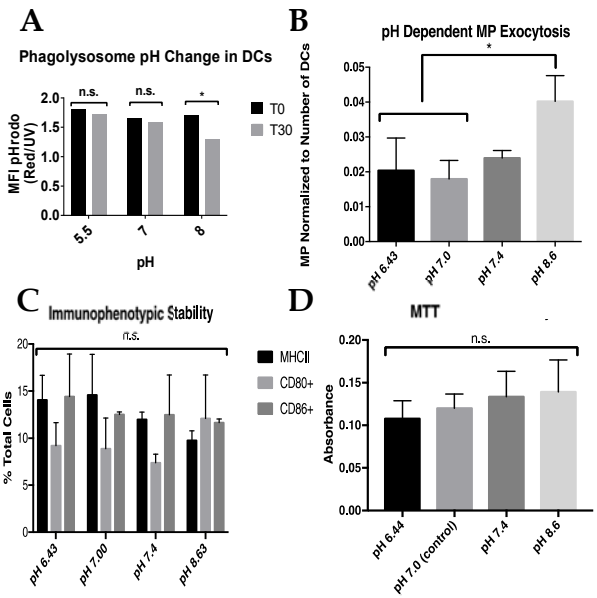
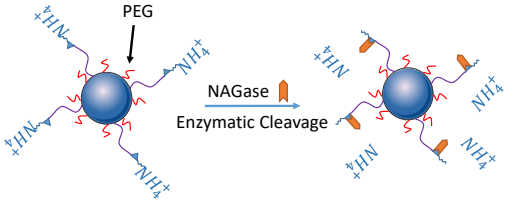


Figure 1: A. Bathing cells in different pH media results in a change in phagolysosome pH **B.** Increased MP vomocytosis from DCs at basic pH. **C.** Immunophenotypic stability unaffected at different pHs. **D.** Verification of cellular functionality at the pHs. ANOVA * symbol ($p<0.05$). **Data shown are preliminary data and further experiments need to be performed to confirm results.**



Aim 2: ***Design surface-functionalized MPs for inducing vomocytosis.*** The objective of this aim to develop MPs surface-tethered with basic molecules to increase the phagosomal pH following internalization by DCs. Basic molecules, such as ammonium chloride or chloroquine, are potential candidates for surface functionalization of MPs, and ultimately induction of MP vomocytosis. To tether these basic molecules to PCL MPs, we will synthesize PCL MPs with a high concentration of surface –COOH groups. Then, we can react ammonium, connected to a NAG linker substrate with nucleophilic groups, through a 1-ethyl-3-(-3-dimethylaminopropyl) carbodiimide hydrochloride (EDC) reaction to conjugate our basic molecule on the surface. Our *working hypothesis* is that the surface functionalized basic molecule will act as a sink to sequester H^+ ions in the phagosome. We will activate the pH-inducing molecules by enzymatic cleavage of a linker substrate using an enzyme, NAGase, that is secreted in the phagolysosome (**Figure 2**). This work is novel, since it is a stimuli-responsive system for a phenomenon that is rarely investigated and is applied towards the next generation of vaccines.

Figure 2: NAGase enzymatic cleavage of pH-modulating NH_4^+ from PCL MPs.

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F. INVESTIGATIONS INTO THE LOCALIZATION AND FUNCTION OF SR35, A WHEAT CC-NBS-LRR PROTEIN THAT CONFERS RESISTANCE TO RACE TTKSK (Ug99) OF *PUCCINIA GRAMINIS* F. SP. *TRITICI*

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Wheat stem rust is caused by the obligate fungal pathogen *Puccinia graminis* f. sp. *tritici*. Since 1999, TTKSK (Ug99) and related races of wheat stem rust have threatened global food security. Among the few genes conferring resistance to these new virulent races, *Sr35* encodes a typical CC-NBS-LRR protein. We characterized Sr35 in the model plant *Nicotiana benthamiana*. Overexpression of *Sr35* in *N. benthamiana* triggers cell death. However, placement of a GFP fluorescent tag on the N-terminus eliminates the ability of Sr35 to trigger cell death in *N. benthamiana* suggesting that the N-terminus is critical for signaling. Nonetheless, overexpression of the CC domain alone was not sufficient to trigger cell death, a result that differs from MLA10 in barley. Results will be presented on Sr35's subcellular localization in both the signaling active and inactive constructs. Future research will focus on identifying Sr35 signaling components in wheat.

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G. METHODS FOR RAPID AND SCALABLE QUALITY ASSESSMENT OF RNA STRUCTURE PROBING DATA

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RNA is a biomolecule that plays an integral role in many biological processes, ranging from adaptive immunity to biocatalysis. In fact, RNAs have been implicated in diseases as well as utilized for their potential in medicine and biotechnology. To serve numerous functional roles, RNA must fold into specific structures. RNA structure has been traditionally studied with crystallography, NMR spectroscopy or phylogenetic analysis but these are costly, labor-intensive, and of limited applicability. Computational methods that make predictions based on sequence information alone are scalable but display poor accuracy. The recent advance of new structure probing techniques coupled with high-throughput sequencing has helped RNA studies expand in scope and depth to *in vivo* genome-wide capabilities. These techniques generate data that have also been utilized to significantly improve accuracy of prediction algorithms.

Numerous probing techniques that differ in protocols and analysis platforms have been recently developed. Despite their differences, most experiments face similar challenges in assessing reproducibility due to the stochastic nature of chemical probing and sequencing. To date, quality of such data is assessed through visual inspection or simple statistical tests, which are often applicable only to specific techniques. However, as protocols expand to genome-wide studies, quality control becomes a daunting task. General and efficient methods are needed to quantify variability and quality in the broad range of existing and emerging techniques.

We recently developed a new method to rapidly and quantitatively evaluate data reproducibility in probing experiments. We used a signal-to-noise ratio concept to evaluate replicate agreement, which has the capacity to identify high-quality data as well as to screen for potential structure differences. We demonstrated efficacy and utility of the method on numerous recently published small and large-scale datasets (Choudhary et al., *Bioinformatics*, 2016). We have found theoretical relationships between noise in structural data and controllable design parameters in probing experiment. Such relationships can guide rational design of experiments to meet desired quality criteria. Additionally, we developed realistic noise models to evaluate sensitivity of secondary structure prediction, which is one of the important applications of structure probing data, to noise in data.

Conclusions from our modeling studies can help biologists set quality criteria for their probing data to meet desired accuracy in structure prediction. Finally, we have refined our methods and integrated them with novel quality summaries in an interactive visualization tool to facilitate smooth transfer to community of biologists.

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H. BUILDING A NEXT GENERATION CHIMERIC ANTIMICROBIAL PROTEIN TO PROVIDE ROOTSTOCK-MEDIATED RESISTANCE TO PIERCE'S DISEASE IN GRAPEVINES

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Xylella fastidiosa (Xf), the causative agent of Pierce's Disease, has a complex lifestyle requiring colonization of plant and insect. Its growth and developmental stages include virulence responses that stimulate its movement *in planta* and its ability to cause disease in grapevines (Chatterjee et al., 2008). Resistance to this pathogen must be multifaceted to block the pathogen at different stages of its complex lifestyle. A key issue is the reservoir of bacterial inoculum already present in California that poses an immediate threat in the presence of a significant insect vector like the GWSS. Chemical pesticides are now used to suppress the GWSS population, which is effective but does not reduce this reservoir of bacterial inoculum. We have previously shown that *Xf* exposed to xylem fluid from resistant lines expressing NE-CB shows significant mortality. Our group has successfully designed and tested a NE-CB chimeric protein that specifically targets *Xf* in plant xylem (the site of infection), rapidly clears the pathogen, and blocks infection (Dandekar et al., 2009, 2012; Kunkel et al., 2007). The protein contains two separate domains. A surface binding domain recognizes outer membrane proteins; we have previously shown that it recognizes and cleaves mopB, a major *Xf* outer membrane protein (Dandekar et al., 2012). This surface binding domain is encoded by a synthetic gene derived from the human innate defense protein neutrophil elastase (NE) (Dandekar et al., 2012; Kunkel et al., 2007). The second, CB domain is a clearance domain, connected with a flexible linker to the C-terminal of NE. This domain is a synthetic gene that encodes an antimicrobial peptide, cecropin B, that specifically lyses Gram-negative bacteria like *Xf* (Andrès and Dimarcq, 2007). The two domains work in tandem to recognize and lyse *Xf*. Our current hypothesis for the mode of action is that NE binds to the surface of Xf via mopB outer membrane protein, bringing the cecropin peptide close to the bacterial surface where it can lyse and kill the pathogen. Transgenic expression of this protein in tobacco and grape has provided phenotypic evidence of bacterial clearance and biochemical evidence of mopB degradation by NE (Dandekar et al., 2012). A major concern is that the presence of a protein of human origin in grapevines is potentially controversial to groups opposed to GMOs. Therefore, substituting plant- or grapevine-NE and CB proteins would be less controversial.

***DEB Graduate Student**

I. PREDICTING COMBINATION THERAPIES TO TARGET GENETIC VULNERABILITIES IN CANCER

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Combinatorial cancer therapy exploits the synergistic effectiveness of combinations of compounds with differing mechanisms of action as compared to their individual prescription. Currently, over 1,300 FDA-approved drugs are available today which provides a large catalog of candidate combinations from which individual treatments can be selected. This motivates the development of an unbiased systematic method for prioritizing the most efficacious combinations. We have formulated the problem of finding such drug combinations as a computational optimization problem where an optimal solution will contain drugs with maximal coverage of identified vulnerable genes, minimal off target effects and distinct mechanisms of action. As such, the therapies derived from the predicted drug set will decrease the likelihood of resistant cancer cell populations, decrease potential toxicity of the constituent drugs through lower dosage and provide effective treatment across a wide spectrum of cancer specific patients. Our work aims to integrate big-data genomic studies to (1) identify consistently vulnerable genetic targets across multiple cancer specific cell lines and (2) infer compound gene targets by utilizing high-throughput cellular perturbation experiments of over 20,000 compounds (including FDA) in order to map compounds to consistently vulnerable genes. Through the mechanistic and unbiased approach of our model, we can identify novel and efficacious combinatorial treatments comprised of compounds we predict should be repurposed for cancer treatment and those already approved by the FDA.

***DEB Graduate Student**

J. EXPRESSION, PURIFICATION, AND BIOPHYSICAL CHARACTERIZATION OF A SECRETED ANTHRAX DECOY FUSION PROTEIN IN *NICOTIANA BENTHAMIANA*

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Anthrax toxin receptor-mediated drug development for blocking anthrax toxin action has received much attention in recent decades. In this study, we produced a secreted anthrax decoy fusion protein comprised of a portion of the human capillary morphogenesis gene-2 (CMG2) protein fused via a linker to the fragment crystallizable (Fc) domain of human immunoglobulin G1 in *Nicotiana benthamiana* plants using a transient expression system. Using the Cauliflower Mosaic Virus (CaMV) 35S promoter and co-expression with the p19 gene silencing suppressor, we were able to achieve a high level of recombinant CMG2-Fc-Apo (rCMG2-Fc-Apo) protein accumulation. Production kinetics were observed up to eight days post-infiltration, and maximum production of 826 mg/kg fresh leaf weight was observed on day six. Protein A affinity chromatography purification of the rCMG2-Fc-Apo protein from whole leaf extract and apoplast wash fluid showed the homodimeric form under non-reducing gel electrophoresis and mass spectrometry analysis confirmed the molecular integrity of the secreted protein. The N-glycosylation pattern of purified rCMG2-Fc-Apo protein was analysed; the major portion of *N*-glycans consists of complex type structures in both protein samples. The most abundant (>50%) N-glycan structure was $GlcNAc_2(Xyl)Man_3(Fuc)GlcNAc_2$ in rCMG2-Fc-Apo recovered from whole leaf extract and apoplast wash fluid. High mannose N-glycan structures were not detected in the apoplast wash fluid preparation, which confirmed the protein secretion. Altogether, these findings demonstrate that high-level production of rCMG2-Fc-Apo can be achieved by transient production in *Nicotiana benthamiana* plants with apoplast targeting.

K. INTERPLAY BETWEEN SIGNALING AND ADHESIONCONTROLS THE MICROGEOGRAPHY OF MICROBIAL AGGREGATES

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Chemical signals and cell-cell adhesion modulate micro-scale geography of yeast-bacterial aggregates. The complex feedback between signaling, adhesion, and aggregate structure is difficult to elucidate in natural systems. As a result, the impact of the feedback between these forces on population dynamics remains elusive. Here, we address the challenges of microbial aggregate formation by studying the interplay between signaling, adhesion, and aggregate structure using synthetic biology approaches. We first use mathematical models and synthetic biochemical components to demonstrate how adhesive interactions can control the spatial distribution of microbial aggregates. Next, we demonstrate the link between spatial distribution of yeast-bacteria aggregates and competition using mathematical models, along with an experimental framework for biological validation of these results. This work establishes intercellular adhesion as a fundamental force behind competition between microbes, reveals new principles behind population dynamics in microbial ecosystems, and enriches bottom-up approaches for controlling multi-species aggregates. Our results create a foundation for rational design of new microbiome-associated therapeutics that exploit signaling and adhesion between microbes.

***DEB Graduate Student**

L. STRETCHING OF RBCS AT HIGH STRAIN RATES

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Most work on the mechanical behavior of red blood cells (RBCs) in flow has focused on simple shear flows. Relatively little work has examined RBC deformations in the physiologically important extensional flow that occurs at the entrance to a constriction. In particular, previous work suggests that RBCs rapidly stretch out and then retract upon entering the constriction, but to date no model predicts this behavior for the extremely high strain rates typically experienced there. In this work, we use high speed video to perform systematic measurements of the dynamic stretching behavior of RBCs as they enter a microfluidic constriction. We demonstrate that the Kelvin–Voigt viscoelastic model captures the observed stretching dynamics, up to strain rates as high as 2000 s^{-1}. The results indicate that the effective elastic modulus of the RBC membrane at these strain rates is an order of magnitude larger than moduli measured by micropipette aspiration or other low strain rate techniques.

***DEB Graduate Student**

M. BIOREACTOR CULTURE DURATION OF ENGINEERED CONSTRUCTS INFLUENCES BONE FORMATION POTENTIAL *IN VIVO*

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Of the 6.2 million bone fractures that occur in the United States every year, up to 10% fail to heal properly. Autograft bone is the current gold standard to repair non-healing bone defects, but this material has numerous shortcomings such as donor site morbidity and limited availability. Tissue engineered constructs offer a promising alternative to autografts and commonly incorporate stem cells, biomaterials, and signaling molecules. Compared to static or dynamic culture, constructs seeded with mesenchymal stem cells (MSCs) and cultured under mechanical stimulation (e.g., media perfusion in bioreactors) exhibit increased nutrient availability, cell growth and survival, and osteogenic differentiation. However, the effect of bioreactor culture duration *in vitro* on the bone forming capacity of MSCs upon transplantation *in vivo* is unknown. While shorter culture durations may be sufficient to prime MSCs towards the osteogenic pathway, longer durations may be necessary to produce a more mature bony construct for implantation. We investigated this phenomenon by culturing MSCs on polymeric scaffolds in flow perfusion bioreactors and characterized DNA content and MSC osteogenic potential *in vitro* for up to 21 days. We detected significant increases in DNA for 14-day culture over 7 day culture, yet no increases were observed for later time points. Gene expression of bone sialoprotein (IBSP), an osteogenic differentiation marker, was significantly increased after 14 days of culture relative to 7 days. Based on these *in vitro* results, we selected 14 days as our longest culture duration for *in vivo* studies. We subcutaneously implanted constructs cultured for 1, 7, and 14 days in eight-week old immunocompromised mice. Acellular scaffolds served as the negative control. Constructs were explanted at 2 and 8 weeks and evaluated for presence of human MSCs and bone formation, respectively. Histological analysis at 2 weeks post-implantation confirmed that human cells were present in all experimental groups. At 8 weeks, constructs cultured for 14 days had the highest bone volume fraction and bone mineral density compared to other experimental groups. The results of this study show that culturing constructs in a flow perfusion bioreactor for longer durations produces a more mature construct that leads to enhanced ectopic bone formation in mice over constructs cultured for shorter times.

***DEB Student**

N. WGBS REVEALS AUTISM-ASSOCIATED HYPOMETHYLATION AND DIFFERENTIALLY-METHYLATED REGIONS IN UMBILICAL CORD BLOOD SAMPLES FROM THE PROSPECTIVE MARBLES STUDY

Charles E. Mordaunt*, Keith W. Dunaway*, Yihui Zhu, Rebecca J. Schmidt, Cheryl K. Walker, Sally Ozonoff, Irva Hertz-Picciotto, and Janine M. LaSalle
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Autism spectrum disorders (ASD) have complex etiologies, likely involving multiple genetic and environmental insults in perinatal life. The epigenetic layer of DNA methylation, at the interface of genetic and environmental risk and protective factors, holds promise for improved understanding of complex ASD etiologies. Currently, ASD is diagnosed behaviorally at two years of age; however, existing interventions are most effective the earlier they are begun. We performed this study to identify DNA methylation biomarkers predictive of ASD diagnosis by age three. The MARBLES (Markers of Autism Risk in Babies - Learning Early Signs) 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) (n = 26 TD, 26 ASD). ASD cord blood samples showed significantly lower global percent CpG methylation compared to typically-developing (TD) controls (ASD 76.6% vs TD 77.4%, p = 0.01). Smaller differentially-methylated regions (DMRs) enriched for CpG islands were also identified in ASD cord blood (5,828 total DMRs). 60% of all DMRs were hypomethylated, but all DMRs that were significant after correction for multiple hypothesis testing were hypermethylated. Methylation at four of the DMRs with genome-wide significance showed a significant positive association with Autism Diagnostic Observation Schedule (ADOS) severity scores. Identified DMRs 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 Graduate Student**

O. ROLE OF ARGININOSUCCINATE SYNTHASE IN PIERCE'S DISEASE DEVELOPMENT IN GRAPEVINES

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Pierce's disease (PD) in grapevines is among several deadly plant diseases caused by strains of the gram-negative bacterium *Xylella fastidiosa* (*Xf*). The analysis of the secretome of wild type *Xf* Temecula1 (WT) revealed LesA and PrtA are among the most abundant secreted proteins that we have shown to be involved in virulence, cell growth, motility, and biofilm formation. Enzymatic activity of LesA protein is closely associated with PD symptoms. *Xf* mutants deficient in *prtA* display an obligate planktonic phenotype, secrete high levels of LesA, are hypervirulent and accumulate high levels of argininosuccinate synthase (ArgG). ArgG is an enzyme involved in arginine biosynthesis and was previously characterized as virulence factor in the rice pathogen *Xanthomonas oryzae* pv *oryzeae* (*Xoo*). High levels of arginine in infected leaves of citrus was also associated with citrus variegated chlorosis caused by *Xf*. We aim to investigate if arginine metabolism that appears to be closely associated with LesA activity contributes to *Xf* growth and PD symptom development. Therefore, *argG* coding sequence in *Xf* WT (PD0291) was disrupted by kanamycin resistance gene in the putative active site of the enzyme through homologous recombination. The disruption on *argG* gene revealed no significant effect on biofilm formation of *Xf* growing *in vitro*. However, grapevines inoculated with *Xf argG*$^{-}$ presented less symptomatic necrotic regions on the edges of the leaves (scorch) compared grapevines inoculated with *Xf* WT after 15 weeks post inoculation. Identifying the relationship of arginine metabolism with PD symptom development and the expression of *lesA* will allow a better understanding of how arginine contributes to *Xf* virulent planktonic phase leading to disease development.

***DEB Graduate Student**

P. UTILIZATION OF METABOLOMICS FOR EPIMETABOLITE DISCOVERIES IN STEMNESS, FROM STEM CELLS TO CANCER CELLS

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Metabolomics has focused for too long on classic, well-defined pathways of primary metabolites that constitute the major highways in cellular anabolism or catabolism. This biochemical pathway-centric focus has been nurtured by a view that metabolites only rarely act as regulators, isolating well-researched fields as exceptions to the rule rather than as an overarching theme of metabolism in its own right. Enzymatic transformations of primary, canonical metabolites generate active biomolecules that regulate important cellular and physiological processes. We define an epimetabolite as a metabolite removed from its classical function in anabolism or catabolism. These non-canonical metabolites serve a functional role, including but not limited to, regulation, defense, communication, storage or transport functions. Epimetabolites often remain chemically similar to their canonical counterparts and may use simple modifications like methylation or acetylation that can be easily reversed. Shown here are examples from cancer and stem cells of proposed and validated epimetabolites, some with examples of the regulation roles of these metabolites highlighted by further studies. Used here are untargeted and targeted methods for GC-TOFMS, HILIC-QTOFMS and RPLC-QTOFMS with data processed using MS-DIAL software. Statistical analysis and visualization of univariate and multivariate statistical analysis was done using R and DeviumWeb. Network maps of chemical similarities and biochemical connections between metabolites was done using MetaMappR and Cytoscape. We conclude from these examples that metabolomics provides optimal platform for the discovery and study of epimetabolites

***DEB Graduate Student**

Q. PRODUCTION AND PRELIMINARY *IN VITRO* EVALUATION OF A PLANT-MADE, OXIDATION RESISTANT ALPHA-1 ANTITRYPSIN

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Alpha-1 antitrypsin deficiency (AATD) is the best-recognized genetic predispositioning factor to COPD in both smokers and non-smokers. Currently, the only specific treatment for AATD is intravenous replacement therapy with human alpha-1 antitrypsin (AAT) purified from pooled plasma, at a cost of over $100,000 per patient annually. Aerosolized AAT has shown potential for treatment of both AATD and cystic fibrosis; however, when inhaled into a neutrophilic inflammatory oxidative milieu, the oxidative susceptibility of methionine residues at positions 351 and 358 in the reactive site loop potentially leads to oxidative inactivation. Using a novel cucumber mosaic virus-based inducible transient expression system, we have produced a biobetter plant recombinant AAT (prAAT) in *Nicotiana benthamiana*. This variant replaces the oxidation-susceptible methionine residue at position 358 with a valine residue to increase resistance to oxidation.

N. benthamiana plants were vacuum infiltrated as detached leaves with two strains of *Agrobacterium tumefaciens*: one carrying the biobetter AAT gene and one carrying a gene for the tomato bushy stunt virus p19 viral RNA silencing suppressor driven by a constitutive cauliflower mosaic virus 35S promoter. Leaves were incubated in humidity chambers at 20 °C in the dark for 6 days before flash freezing in liquid nitrogen, grinding, and protein extraction in a 20 mM Tris, 150 mM NaCl, and 0.01% (v/v) Tween-80 AAT stability buffer. Purification was achieved using Alpha-1 Antitrypsin Select Affinity Chromatography (GE Healthcare) followed by concentration and diafiltration using Amicon 30 kDa NMWCO spin columns with a 58±8% yield of active AAT.

Purified prAAT was tested against an analytical standard (Calbiochem) and Prolastin-C (Griffols), a common therapeutic formulation of human AAT, to determine its activity and oxidation resistance. 41±11% of purified prAAT and 71.9±5.5% of Prolastin-C showed activity against porcine pancreatic elastase as determined by a residual elastase activity inhibitory assay. Under oxidation with 48.9mM H_2O_2 for 60 minutes at room temperature, prAAT was found to retain 102.8±20.4% of its original anti-elastase activity, while Prolastin-C retained 13.8±5.0% anti-elastase activity.

Under oxidation with 100nM NaOCl for 15 minutes at room temperature, prAAT was found to retain 99.9±9.7% of its original anti-elastase activity, while Prolastin-C retained 34.2±24.1% anti-elastase activity. Human bronchial epithelial cells were grown in a 96 well plate and exposed to human neutrophil elastase and either prAAT or Prolastin-C. After 48 hours of incubation post-exposure, both prAAT and Prolastin-C showed similar protection against elastase-induced cell death.

We are currently investigating our prAAT's resistance to oxidation by hypochlorite. Future work will include optimization of downstream processing and further preclinical studies of prAAT toxicity and efficacy.

***DEB Graduate Student**

R. TRANSIENT PRODUCTION OF A RECOMBINANT ANTHRAX RECEPTOR FUSION PROTEIN IN NICOTIANA BENTHAMIANA PLANT CELL SUSPENSION CULTURE

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Faster production of experimental protein therapeutics or vaccines at a large-scale is needed to respond to emerging infectious disease outbreaks or bioterrorist threats. We are investigating transient protein expression in plant cell suspension culture as a new platform that could be used to rapidly manufacture large quantities of novel protein therapeutics. Plant cells are being explored as an alternative to mammalian expression systems because they can also produce complex proteins, but enhance product safety and efficacy in some cases. Our system uses genetically engineered *Agrobacterium tumefaciens* to mediate transient protein expression in *Nicotiana benthamiana* plant cell suspension culture. A key advantage of our system is that these *Agrobacterium* constructs could be produced in a few weeks while stable transgenic plant or animal cell lines take months to develop and screen. By co-culturing recombinant *Agrobacterium* and *N. benthamiana* in suspension, we have produced an anthrax toxin receptor Fc fusion protein at levels up to 0.7 mg per kg of plant cell fresh weight after 9 days of co-culture. However, reduced intracellular protein levels and evidence of plant cell lysis have also been observed after co-culture with *Agrobacterium*. To increase recombinant protein expression levels in this system, we are testing various strategies to reduce effects on plant cell health associated with *Agrobacterium* infection.

***DEB Graduate Student**

S. ANALYSIS, VALIDATION AND DEREGULATION OF RNAi-MEDIATED CROWN GALL RESISTANT WALNUT ROOTSTOCK J1 1A

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Crown gall disease, caused by *Agrobacterium tumefaciens*, is a significant source of economic loss for growers in California. A crown gall resistant rootstock was developed with the potential solution to this problem. Crown gall resistant paradox rootstock (CGR-PR) lines were created using RNAi technology. These transgenic rootstocks were generated by *Agrobacterium*-mediated plant transformation that express double stranded RNA corresponding to the common and highly conserved *Agrobacterium* genes ipt and iaaM responsible for tumor formation. The genetically engineered rootstocks are able to block the expression of these genes resulting in the suppression of tumor formation. To permit the commercialization of this approach an elite transgenic line J1 1A was identified based on efficacy testing, molecular analysis and horticultural evaluations. Based on consultation with IR4 data packages have been developed to fulfill the documentation of horticultural and molecular information required by federal regulatory agencies (APHS, EPA and FDA) that would enable deregulation necessary to conduct rigorous field testing at multiple locations and eventual commercial release. Material from the clonal line J1 1A was tested as microshoots, as rooted plants in the greenhouse and in the field, to develop the efficacy, molecular and horticultural data. Efficacy testing revealed that the transgenic line J1 1A showed no tumor development when infected with virulent strains of *Agrobacterium tumefaciens* individually or as a mixture. Molecular analysis revealed a single T-DNA insertion event and DNA sequence analysis revealed and intact sequence with no vector sequences at a single location in the walnut genome. Analysis of the products of the inserted T-DNA, RNA proteins and metabolites showed no movement across the graft union when grafted to wild type Chandler scion variety. The introduction of resistance to Agrobacterium did not change its susceptibility to other diseases and pets such as *Phytophthora* species, *Xanthomonas* species, walnut root lesion nematodes and weeds.

T. MOLECULAR PROFILING OF GRAPEVINE RESPONSE TO PIERCE'S DISEASE PROVIDES INSIGHTS INTO THE INVASION BIOLOGY OF *XYLELLA FASTIDIOSA*

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Pierce's disease, a major threat to grapevines and wine production is caused by the bacterium *Xylella fastidiosa*. Although devoid of a type 3 secretion system (T3SS) to deliver effectors inside host cells, this pathogen is able to influence host parenchymal cells from the outside (xylem lumen) by secreting a battery of hydrolytic enzymes. Defining the cellular and biochemical changes induced during disease can foster the development of novel therapeutic strategies, and to this end the we investigated the transcriptional, proteomic and metabolomic responses of diseased *Vitis vinifera* L. c.v. "Thompson Seedless". From the host perspective we found that several antioxidant strategies were induced, including the accumulation of gamma amino butyric acid (GABA), arginine, proline and polyamine metabolism, as well as iron and copper chelation, but insufficient to protect itself from chronic oxidative stress and resulting cell death. Notable upregulation of phytoalexins, pathogenesis-related proteins and various aromatic acid pathway metabolites are part of the host responses observed. Moreover, a very strong upregulation of various cell wall modification enzymes that follow the proliferation of the pathogen within xylem vessels was also detected, consistent with the intensive thickening of vessels' secondary walls. By interpreting the molecular profile changes taking place in symptomatic tissues we report a group of robust molecular markers to aid early disease detection as well as potential therapeutics to breed resistant varieties.

Keywords: defense response, Xanthomonadaceae, plant-bacteria interaction, vascular pathogen, transcriptome, proteome, metabolome.

***DEB Graduate Student**

U. PLACENTAL DNA METHYLATION IN RELATION TO MATERNAL PERICONCEPTIONAL PRENATAL VITAMIN USE AND CHILD OUTCOMES IN THE MARBLES PROSPECTIVE AUTISM STUDY

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Placental tissue, usually discarded at birth, is a potential rich source of for epigenetic biomarkers that the interface of genetic risk and in utero exposures in autism spectrum disorders (ASD). In addition, maternal use of prenatal vitamins containing the methyl donor folic acid could alter placental methylation in persistent ways that influence neurodevelopment. This study was designed to identify regions of differential DNA methylation in placenta from a prospective ASD study in high-risk families. We also studied the relationship between maternal prenatal vitamin use and DNA methylation. MARBLES (Markers of Autism Risk in Babies-Learning Early Signs) mothers who had a child with ASD were interviewed about prenatal vitamin use during a new pregnancy. Placentas were collected for the younger siblings who were followed until they were 3 years old and clinically diagnosed with ASD or typical development (TD). MethylC-seq was performed on DNA isolated from 20 ASD and 21 TD male placentas using Illumina next-generation sequencing on HiSeq 2000 machine with one sample per lane using single-end 100 bp sequencing. We identified differentially methylated regions (DMR) using the DMR finder approach based on bsseq R package. Two DMRs showed significant differences after FDR correction between ASD and TD selected by DMR finder based on MethyC-seq data and validated by pyrosequencing. Both DMRs showed association between prenatal vitamins taken during the first pregnancy month and percent methylation. They were also associated with Mullen Scales of Early Learning on four subscales categories and the Early Learning Composite. This 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.

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V. CELL-SECRETED EXTRACELLULAR MATRIX, INDEPENDENT OF CELL SOURCE, PROMOTES THE OSTEOGENIC DIFFERENTIATION OF HUMAN STROMAL VASCULAR FRACTION

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Cell-secreted extracellular matrix (ECM) is a promising substrate to guide cell phenotype or for use in biomaterial design, yet the instructional capacity of ECMs generated by various cell types is unknown. Lipoaspirates are a heterogeneous cell source of clinical interest for bone repair, collectively referred to as the stromal vascular fraction (SVF), which contain osteoprogenitor cells and other cell populations. To determine whether the bioactivity of cell-secreted ECM was dependent on cell source, we assessed the osteogenic response of human SVF on ECMs secreted by bone marrow-derived mesenchymal stem cells (MSCs), adipose stromal cells (ASCs), and human dermal fibroblasts (HDFs) after decellularizing using a detergent removal method. MSC-derived ECM contained 3-fold and 1.5-fold more protein than ASC- and HDF-derived ECM, respectively, and we observed appreciable differences in ECM composition among cell sources. ECM-coating improved seeding efficiency of SVF compared to tissue culture plastic (TCP). SVF deposited over 4-fold more calcium on ECMs compared to TCP, regardless of ECM source, and this effect was dependent on ECM concentration. When cultured on ECM, CD31+ cells were retained at higher levels than on TCP. Calcium deposition by the heterogeneous SVF was greater than the more homogeneous population of ASCs alone on ECM, confirming a role for retained endothelial cells in osteogenic differentiation. These results support further investigation into the use of cell-secreted ECMs as a biomimetic tool for the cultivation and osteogenic differentiation of SVF.

***DEB Graduate Student**

W. NUCLEOBASE ANALOGS AS PROBES FOR SUBSTRATE RECOGNITION AND REPAIR BY DNA GLYCOSYLASE MUTY

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MutY is a DNA glycosylase responsible for excising adenine (A) base-paired opposite 8-oxo-7,8-dihydroguanine (OG), formed by the oxidation of guanine. If left unrepaired, OG:A mispairs result in the conversion of a G:C base pair to a T:A base pair, causing a point mutation in DNA. The accumulation of mutations in the genome may result in genetic diseases, and in fact the persistence of OG:A mispairs in the *APC* tumor suppressor gene in humans is related to a form of colorectal cancer. Thus, genomic maintenance is of utmost importance for the survival and well-being of a cell. DNA glycosylases, such as MutY, scan the genome for the presence of damaged bases and initiate their cleavage, thereby triggering a cascade of reactions that reinstate the correct base in that location. Some of these miscoding lesions (such as OG) are formed by subtle modifications to the parent base, and our objective is to understand the structural features used by MutY to identify and initiate the repair of its target lesion.

The OG:A mispair is rare and non-helix distorting, therefore presenting a significant challenge to recognition and repair by the enzyme. To determine the features it uses to recognize this mispair, we are using nucleobase analogs of adenine that modify the steric, electronic and hydrogen bonding features of this base. We evaluate the effect of these modifications by incorporating the analog into a DNA duplex and studying its effect on different aspects of the enzymatic reaction. We determine the enzyme-substrate binding affinity, rate of base cleavage and extent of overall repair in a cellular context using a plasmid based bacterial assay. The results we obtained allow us to explore a structure activity relationship (SAR) that provides insight into the structural basis for lesion identification and excision by MutY.

***DEB Graduate Student**

X. DELIVERY OF BIOMOLECULES INTO SOLID SUPPORTED LIPID BILYAERS USING NANOLIPOPROTEIN PARTICLES

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Determination of the native three-dimensional structure of a protein is key to elucidation of its innate functionality. Although advances in NMR spectroscopy, X-ray crystallography, and cryo-electron microscopy have enabled accurate structural characterization of numerous types of proteins, analysis of integral membrane proteins (IMPs) remains challenging due to onerous obstacles associated with obtaining purified IMPs in sufficient yield; conventional methods for extraction and crystallization typically rely on the use of harsh detergents which disturb native IMP structure. In distinction from established protocols in the literature, this project aims to render IMPs amenable to high-resolution structural characterization by delivering them into a polymer-cushioned supported lipid bilayer (SLB) system using nanolipoprotein particles (NLPs). For preliminary experiments, a polyacrylic acid (PAA)-cushioned SLB was utilized because of its robust construction, ease of preparation, and defined pH responsiveness. Moreover, micropatterning the PAA cushion by UV-ozone photolithography prior to lipid bilayer deposition was found to produce unique structural features where the biomembrane bridged across adjacent regions of PAA in some instances. Results from epifluorescence microscopy experiments indicated that lipids and the receptor tyrosine-protein kinase, ErbB2/HER2, transported spontaneously from NLPs into PAA-cushioned SLBs. Interestingly, ErbB2/HER2 only exhibited lateral mobility in SLB regions where biomembrane bridging had occurred. In continuing work, we are investigating NLP-mediated delivery of IMPs to surface-functionalized SLBs.

***DEB Graduate Student**

Y. IDENTIFICATION AND CHARACTERIZATION OF HIGH-MANNOSE-TYPE N-GLYCAN MODIFICATION ENZYMES FOR *IN VITRO* ENZYMATIC GLYCOPROTEINS

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More than two thirds of the therapeutic proteins are N-glycosylated glycoproteins. An increasing body of evidence has shown that appropriate glycosylation is important for pharmacokinetics, cellular distributions, and biological activities of therapeutic glycoproteins. Producing therapeutic glycoproteins with human-like N-glycans for both detailed structure–function relationship studies and therapeutic applications has stimulated an extensive interest in developing various methods for manipulating protein glycosylation, such as specific glycoengineering of host biosynthetic pathways, in vitro chemo-enzymatic glycosylation remodeling, and chemoselective and site-specific glycosylation of proteins. In vitro chemoenzymatic glycan modification of natural and recombinant glycoproteins provides an attractive approach towards the production of glycoproteins with defined glycoforms. Therefore, obtaining large amounts of highly efficient N-glycan modification enzymes is a prerequisite for practical purposes. In this study, several high-mannose-type N-glycan modification enzymes, including three mannosidases and a β1,2-N-acetylglucosaminyltransferase have been successfully cloned and characterized using both oligosaccharides and glycoproteins as substrates.

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We are a recognized leader in protein and pathway engineering. No other biotechnology company offers the breadth of skills and experience that we do to deliver total solutions to a broad array of markets.

A catalyst for change
As a Catalyst of the Biobased Economy^{sm}, Genencor is committed to contributing to a sustainable industrial system that relies on renewable resources to produce effective, environmentally friendly products. Our focus on research and development and sustainability is making this happen by driving the application of biotechnology into new areas.

Genentech, Inc.

Contacts:
Benjamin Lin, Ph.D., Senior Researcher, Oncology Biomarker Div. (DEB Graduate)
Melody Trexler Schmidt, Ph.D., Sr. Scientist (DEB Graduate)

1 DNA Way
South San Francisco, CA 94080-4990
(650) 225-1000
www.gene.com

Genentech is a leading biotechnology company that discovers, develops, manufactures, and commercializes biotherapeutics for significant unmet medical needs. A considerable number of the currently approved biotechnology products originated from, or are based on, Genentech science. Genentech manufactures and commercializes multiple biotechnology products directly in the United States and licenses several additional products to other companies. The company has headquarters in South San Francisco, Calif., and is traded on the New York Stock Exchange under the symbol DNA.

Corporate Overview

Genentech, the founder of the biotechnology industry, is a company with a quarter-century track record of delivering on the promise of biotechnology. Today, Genentech is among the world's leading biotech companies, with multiple protein-based products on the market for serious or life-threatening medical conditions and over 30 projects in the pipeline. With its strength in all areas of the drug development process — from research and development to manufacturing and commercialization — Genentech continues to transform the possibilities of biotechnology into improved realities for patients.

Marketed Products:

Delivering innovative medicines to patients with serious or life-threatening medical conditions is what Genentech is all about. Since its beginning in 1976, the company has focused its drug discovery efforts on therapies that would fill unmet needs. Today, Genentech manufactures and commercializes multiple protein-based biotherapeutics for serious or life-threatening medical conditions — giving Genentech one of the leading product portfolios in the biotech industry.

Development Pipeline:
As a biotechnology leader, Genentech has a long-standing tradition of reinvesting a significant percentage of revenues back into research and development — a practice that has proved successful in transforming promising candidates into important new products. With the projects below under way, Genentech's development pipeline has never been more robust and promising. More than half of Genentech's pipeline is composed of potential antibody therapies.

Marrone Bio Innovations, Inc.

Contact:
Pam Marrone, Ph.D., CEO and Founder, Board of Directors

2121 Second Street, Suite 107B
Davis, CA 95618
(530) 750-2800
www.marronebioinnovations.com/index.php

Vision

We will be the world leader in natural product innovation. We will make natural, effective,
safe, environmentally friendly products the mainstream future of pest management.

Values

1. We believe in sustainable business practices economically viable, socially equitable and environmentally responsible.
2. We encourage entrepreneurial attitudes and agility, and believe that ideas, out of the box thinking and creativity are the lifeblood of innovation. Our decisions and products are based on sound science, statistically vetted data, market research, direct contact with customers and good financial analysis.
3. We communicate openly and honestly, respect the views of others and minimize internal politics. Empowered employees, treated fairly, are productive employees. We involve all employees in the company's strategy, goal setting and decision-making.
4. We believe in diversity. A diverse work force and diverse opinions working together in teams result in better decision- making.
5. We have a culture of accountability, continuous learning, coaching, and mentoring for personal and professional growth.
6. We conduct all business dealings with integrity, treating all stakeholders, collaborators and trade partners with respect, fairness and honesty at all times and expect the same in return.

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

NIH Fellows 2016 - 2017	
Karan Agrawal	Pharmacology & Toxicology
Jasmine Corbin	Chemical Engineering
Maika Mailig	Integrative Genetics & Genomics
Linda Su-Feher	Biochemistry, Molecular & Cellular Developmental Biology
Cody Watson Yothers	Chemistry
Sana Vaziri	Computer Science
Biotech Fellows 2016 - 2017	
Akhila Bettadapur	Biochemistry, Molecular & Cellular Developmental Biology
Joshua Cohen	Food Science
Amanda Dang	Materials Science & Engineering
Daniel Lewis	Integrative Genetics & Genomics
Graduate Students/Post-docs	
Salem Alkanaimsh	Chemical Engineering
Riley Allen	DEB, Biomedical Engineering
Sima Asadi	DEB, Chemical Engineering
Amir Bolandparvaz	DEB, Biomedical Engineering
Stephen Bolus	DEB, Plant Pathology
Krishna Choudhary	DEB, Biomedical Engineering
Ryan Dowdy	DEB, Food Science
Sukriti Gakhar	DEB, Chemical Engineering
Jenna Harvestine	DEB, Biomedical Engineering
Carly Hennessey	DEB, MCIP
Jill Hung	Chemical Engineering
Aaron Jacobson	Dandekar Lab Specialist
Nelson Johansen	DEB, Computer Science
Kalimuthu Karuppanan	Chemical Engineering
Kori Lay	DEB, Chemistry
Hannah Ledford	DEB, Molecular, Cellular and Integrative Physiology
Yanhong Li, PhD	Chemistry
Gosia Liro	DEB, BMCDB
Elizabeth Lotsof	Chemistry
Korn Macharoen	DEB, Chemical Engineering
Chandrima Majumdar	DEB, Chemistry
Jordan Mancuso	DEB, Chemical Engineering
Matt McNulty	Chemical Engineering
Debika Mitra	DEB, Biomedical Engineering
Charles Mordaunt	DEB, BMCDB
Nicole Nunez	DEB, Chemistry

Alan Raetz, PhD	David Lab
Cintia Sagawa	DEB, Plant Biology
Housten Saxe	Horticulture & Agronomy
Shanaya Shah	DEB, BMCDB
Megan Showalter	DEB, BMCDB
David Silberstein	DEB, Chemical Engineering
Eric Stevens	DEB, Microbiology
Sara Sukenik	DEB, Biomedical Engineering
Lalani Walawage	Dandekar Lab Manager
Jing Wang, PhD	Chemistry
Jacklyn Whitehead	DEB, Biomedical Engineering
Elyse Wudeck	DEB, MCIP
Mary Xiong	DEB, Chemical Engineering
Paulo Zaini, PhD	Plant Sciences
Yihui Zhu	DEB, Integrative Genetics and Genomics
UC Davis Faculty	
Sharon Aviran	DEB, Biomedical Engineering & Genome Center
Daniela Barile	DEB, Food Science & Technology
Luis Carvajal Carmona	DEB, Biochemistry & Molecular Medicine
Joanna Chiu	DEB, Entomology
Abhaya Dandekar	DEB, Plant Biology
Annaliese Franz	DEB, Chemistry/BMCDB
Jamal Lewis	DEB, Biomedical Engineering
Karen McDonald	DEB, Chemical Engineering
Somen Nandi	Chemical Engineering
John Newman	DEB, Nutrition
Alex Nord	DEB, Center for Neuroscience
Gerald Quon	DEB, Molecular and Cellular Biology
Katherine Ralston	DEB, Microbiology & Molecular Genetics
William Ristenpart	DEB, Chemical Engineering
Allen Rose	DEB, Molecular and Cellular Biology
Cheemeng Tan	DEB, Biomedical Engineering
Industry	
Lonnie Bookbinder, MBA,PhD	ARIZ Precision Medicine
Fiore Cattaruzza, PharmD, PhD	OncoMed Pharmaceuticals
Rashmi Deb, PhD	Monsanto, Calgene Campus
Herta Steinkellner, PhD	BOKU Faculty, Vienna, Austria
Abigail Yu, PhD	Sutro Biopharma, Inc.
Guests	
Sabin Aslam, PhD	Vising Scholar
Mark Winey, PhD	Dean, College of Biological Sciences

Yin Wu	Maxim Integrated
Biotechnology Program	
Jacki Balderama	Biotechnology Program, Event Manager
Marianne Hunter	Biotechnology Program, Assistant Director Administration
Denneal Jamison-McClung	Biotechnology Program, Associate Director
Judy Kjelstrom	Biotechnology Program, Director
Jacqueline Phillips	Biotechnology Program, Program Associate

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/

NIH Training Grant Faculty

Director: J. Kent Leach	
Associate Director: Joanna Chiu	
Associate Director: Luis Carvajal-Carmona	
Athanasiou, Kyriacos	Chair, Distinguished Professor: Department of Biomedical Engineering
Atsumi, Shota	Assoc. Professor, Dept. of Chemistry
Aviran, Sharon	Assistant Professor, Department of Biomedical Engineering
Barile, Daniela	Associate Professor and P.I., Department of Food Science & Technology
Beal, Peter	Professor, Department of Chemistry
Brown, C. Titus	Associate Professor, Population Health and Reproduction: Vet Med
Chédin, Frédéric L.	Associate Professor, Molecular & Cellular Biology
David, Sheila	Professor, Dept. of Chemistry
Dennis, Megan	Assistant Professor. M.I.N.D. Institute; Biochemistry and Molecular Medicine Genome Center. 2016 Sloan Research Fellow in Neuroscience
Facciotti, Marc	Associate Professor, Dept. of Biomedical Engineering
Faller, Roland	Professor, Dept. of Chemical Engineering
Fiehn, Oliver	Professor; Director West Coast Metabolomics Center Department of Molecular & Cellular Biology; Genome Center
Franz, Annaliese	Associate Professor, Dept. of Chemistry
German, J. Bruce	Professor and Food Chemist, Dept. of Food Science & Technology; Director, Foods for Health Initiative
Goldman, Mark	Professor, HHMI Professor, Center for Neuroscience
Griffiths, Leigh	Associate Professor, Medicine and Epidemiology: Vet Med
Hammock, Bruce	Distinguished Professor, Dept. of Entomology and Nematology and UC Davis Comprehensive Cancer Center
Hell, Johannes	Professor, Pharmacology
Hormozdiari, Fereydoun	Assistant Professor, Med: Biochemistry & Molecular Medicine
Koehl, Patrice	Professor, Dept. of Computer Science, UC Davis; Visiting Professor, Department of Biological Sciences National University of Singapore, Founding Director, Data Science Initiative, UC Davis

Korf, Ian	Professor, Dept. of Molecular & Cellular Biology; Associate Professor/Director of Bioinformatics, Genome Center
Kuhl, Tonya L.	Professor, Dept. of Chemical Engineering Professor, Dept. of Biomedical Engineering
Lam, Kit S.	Professor and Chair, MED: Dept. of Biochemistry & Molecular Medicine; Professor, MED: Division of Internal Medicine-Hematology/Oncology
LaSalle, Janine	Professor, MED: Microbiology & Immunology; Associate Director, Genome Center
Lein, Pam	Professor, Molecular Biosciences: Vet Med; Chair, Pharmacology and Toxicology
Lewis, Jamal	Assistant Professor, Biomedical Engineering
Longo, Marjorie	Professor, Dept. of Chemical Engineering
Marco, Maria	Associate Professor and Microbiologist, Food Science & Technology
McDonald, Karen	ProfESSOR Chem Engineering
McPherson, John	Professor, Associate Director, Basic Sciences, UC Davis Comprehensive Cancer Center
Michelmore, Richard	Professor, Dept. of Plant Sciences, MCB, MED: Med Microbiology & Immunology; Director, Genome Center & Bioinformatics Program
Mills, David	Professor, Dept. of Viticulture & Enology
Newman, John	Research Chemist, USDA ARS; Adjunct Assistant Professor, Dept of Nutrition
Nolta, Jan	Director of the Stem Cell Program and Institute for Regenerative Cures; Scientific Director of the GMP Facility for Cell and Gene Therapy; Professor, UCD School of Medicine: Hematology & Oncology, Dept. of Internal Medicine
Nord, Alex	Assistant Professor, CBS, Center for Neuroscience
Pan, Tingrui	Associate Professor, Dept. of Biomedical Engineering; Director, Micro-Nano Innovations (MiNi Lab), UC Davis; Research Director, Global Research in Advanced Technologies Program (GREAT), UC Davis
Panitch, Alyssa	BME Chair (effect 6-30-16)
Parikh, Atul	Professor, Dept. of Biomedical Engineering and Professor, Dept. of Biomedical Engineering
Quon, Gerald	Assistant Prof., Molecular & Cellular Biology
Rauen, Katherine	Chief, Division of Genomic Medicine; Professor, Department of Pediatrics; Albert Holmes Rowe Endowed Chair in Human Genetics II (MD, PhD) – UC Davis Health System

Revzin, Alex	Professor, Dept. of Biomedical Engineering
Ristenpart, William	Associate Prof, Chemical Engineering
Rocke, David	Distinguished Professor, Biomedical Engineering, Public Health Sciences
Segal, David	Professor, UC Davis Genome Center, Department of Biochemistry and Molecular Medicine, Pharmacology, MIND Institute, UC Davis School of Medicine
Seker, Erkin	Assistant Professor, Electrical & Computer Engineering
Siegel, Justin	Assistant Professor, Department of Biochemistry, Chemistry, and the Genome Center
Silva, Eduardo	Assistant Professor. Biomedical Engineering
Simon, Scott I.	Professor, Dept. of Biomedical Engineering
Tagkopoulos, Ilias	Assistant Professor, Dept. of Computer Science
Tan, Cheemeng	Assistant Prof, BME
Yu, Aiming	Associate Professor Director of the PK/PD Bioanalytical Core Facility
Zerbe, Philipp	Assistant Professor, CBS, Plant Biology

NIH Training Program in Biomolecular Technology

The DEB is a **formal training program** for the NIH Training Grant.

The DEB provides **training and a structure for interdisciplinary interactions**, in addition to established graduate programs.

The DEB provides a **formal accreditation** (on diploma & transcript) to reflect interdisciplinary biotechnology training.

Not all of the DEB students will be part of the NIH Biotechnology Training Program. The fellows are a **select subset** based on a highly competitive nomination & selection process:

- Nomination by a Faculty Trainer and completion of an application by the student.

- Ranking by the Executive Committee of the Program based on academic merit, quality of the research, interdisciplinary nature of research, and a willingness to complete an internship.

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 2017

NAME	GRADUATE GROUP/PROGRAM
Karan Agrawal	Pharmacology & Toxicology
Nicholas Aguirre	Neurobiology, Physiology and Behavior
Hannah Aizad Ledford	Molecular, Cellular & Integrative Physiology
Betsy Alford	Plant Pathology
Riley Allen	Biomedical Engineering
Leif Anderson	Biomedical Engineering
Brittany Anderson	Chemistry
Rigoberto Arenas	Chemistry
Sima Asadi	Chemical Engineering
Brian Avanzino	Biochemistry, Molecular, Cellular & Developmental Biology
Mina Azimi	Biochemistry, Molecular, Cellular & Developmental Biology
Christopher Baehr	Biomedical Engineering
Krithi Bala	Integrative Genetics & Genomics
Douglas Banda	Chemistry
Jed Bassein	Immunology
Katherine Beglinger	Biochemistry, Molecular, Cellular & Developmental Biology
Allison Belliveau	Chemical Engineering & Materials Science
Zachary Bendiks	Microbiology
Anastasia Berg	Biochemistry, Molecular, Cellular & Developmental Biology
Akhila Bettadapur	Biochemistry, Molecular, Cellular & Developmental Biology
Matthew Blain-Hartung	Biochemistry, Molecular, Cellular & Developmental Biology
Giselle Blanco	Biochemistry, Molecular, Cellular & Developmental Biology
Brittany Blankenship	Microbiology
Amirhossain Bolandparvaz	Biomedical Engineering
Stephen Bolus	Plant Pathology
Casey Boosalis	Molecular, Cellular & Integrative Physiology
Kevin Bradley	Chemical Engineering
Katie Bradshaw	Pharmacology & Toxicology
Andrew Burch	Biochemistry, Molecular, Cellular & Developmental Biology
Michael Burnside	Chemistry
Timothy Butterfield	Plant Biology
Daniel Caddell	Plant Biology
Austin Carroll	Chemistry
Anna Case	Chemistry
Brian Avanzino	Biochemistry, Molecular, Cellular & Developmental Biology
Christopher Chapman	Biomedical Engineering
Krishna Choudhary	Biomedical Engineering
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
Jasmine Corbin	Chemical Engineering
Ailsa Dalgliesh	Molecular, Cellular & Integrative Physiology
Amanda Dang	Material Science and Engineering
Rachel Danielson	Soils & Biogeochemistry
Destiny Davis	Plant Biology
Kevin De Leon	Molecular, Cellular & Integrative Physiology
Raquel de Mello e Pinho	Animal Biology
Marcus Deloney	Biomedical Engineering
Pamela Denish	Biophysics
Nithin Dhananjayan	Biophysics
Forrest Ryan Dowdy	Food Science
Cintia Helena Duarte Sagawa	Plant Biology
Keith Dunaway	Integrative Genetics & Genomics
Ameen Eetemadi	Computer Science
Nicholas Ellinwood	Environmental Toxicology
Maher Elsheikh	Medical Microbiology and Immunology
Shea Feeney	Biochemistry, Molecular, Cellular & Developmental Biology
Samantha (Chun) Feng	Pharmacology & Toxicology
Jonathan Flynn	Biochemistry, Molecular, Cellular & Developmental Biology
Zachary Fogassy	Microbiology
Michael Fong	Biomedical engineering
Sukriti Gakhar	Materials Science and Engineering
Jenna Gallegos	Plant Biology
Javier Garcia	Biochemistry, Molecular, Cellular & Developmental Biology
Donald Gibson	Integrative Genetics & Genomics
Deepshika Gilbile	Chemical Engineering
Noah Goshi	Biomedical Engineering
Alex Gulevich	Biochemistry, Molecular, Cellular & Developmental Biology
Jisoo Han	Biochemistry, Molecular, Cellular & Developmental Biology
Jenna Harvestine	Biomedical Engineering
Dustin Heeney	Microbiology
Britta Heiss	Microbiology
Carly Hennessey	Molecular, Cellular and Integrative Physiology
Shawn Higdon	Plant Biology
Briana Hill	Chemistry
Pui Yan Ho	Biochemistry, Molecular, Cellular & Developmental Biology
Gena Hoffman (Lurvey)	Plant Biology
Tiffany Hong	Biochemistry, Molecular, Cellular & Developmental Biology
Kayla Horton (Sparks)	Pharmacology & Toxicology

Allison Hsia	Biomedical Engineering
Jessica Huang	Biochemistry, Molecular, Cellular & Developmental Biology
Kuei-Pin Huang	Molecular, Cellular and Integrative Physiology
Hyun Tae Hwang	Pharmacology & Toxicology
Alexandria Igwe	Microbiology
Luiz Carlos Irber Jr	Computer Science
Mittal Jasoliya	Integrative Genetics & Genomics
Julia Jennings	Chemistry
Rogelio Jimenez Espinoza	Chemical Engineering
Hyunsoo Jin	Molecular, Cellular and Integrative Physiology
Daisy Johnson	Microbiology
Shannon Joslin	Integrative Genetics & Genomics
Prema Karunanithi	Biochemistry, Molecular, Cellular & Developmental Biology
Ryan Kawakita	Biological Systems Engineering
Nicole Kingsley	Integrative Genetics & Genomics
Sophie Kiss	Pharmacology & Toxicology
Angelica Kowalchuk	Integrative Genetics & Genomics
James Kurniawan	Chemical Engineering
Hwoi Chan Kwon	Biophysics
Ellen Lai	Integrative Genetics & Genomics
Vu Lam	Biochemistry, Molecular, Cellular & Developmental Biology
Kori Lay	Chemistry
Mirko Ledda	Integrative Genetics & Genomics
Mark Lemos	Plant Biology
Daniel Lewis	Integrative Genetics & Genomics
Johnathon Li	Animal Biology
Ying Li	Entomology
Jonathan Lin	Microbiology
Malgorzata Liro	Biochemistry, Molecular, Cellular & Developmental Biology
Yulong Liu	Biochemistry, Molecular, Cellular & Developmental Biology
Furong (Frank) Liu	Plant Pathology
Johnathan Lomas	Biological Systems Engineering
Simon Lopez	Integrative Genetics & Genomics
Shan Lu	Molecular, Cellular & Integrative Physiology
Kantharakorn Macharoen	Chemical Engineering
Chandrima Majumdar	Chemistry
Maika Malig	Integrative Genetics & Genomics
Jordan Mancuso	Materials Science and Engineering
Alice Martinic	Nutritional Biology
Lauren Matelski	Immunology
Morgan Matson	Chemistry
Shane McInally	Microbiology
Lucas McKinnon	Plant Biology

Amory Meltzer	Integrative Genetics & Genomics
Beatriz Merchel Piovesan Pereira	Microbiology
David Merriam	Microbiology
Tawni Middleton	Molecular & Cellular Biology
Adam Miltner	Biochemistry, Molecular, Cellular & Developmental Biology
Debika Mitra	Biomedical Engineering
Jessica Mizzi	Microbiology
Susan Moenga	Plant Biology
Brian Avanzino	Chemistry
Jessica Moore	Chemistry
Charles Mordaunt	Biochemistry, Molecular, Cellular & Developmental Biology
Marcus Moreno	Biochemistry, Molecular, Cellular & Developmental Biology
Akshata Mudinoor	Biological Systems Engineering
Katherine Murphy	Plant Biology
Kimiko Nakajima	Materials Science and Engineering
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
Nicole Nozzi	Chemistry
Nicole Nuñez (Chaffee)	Chemistry
Neal Oliver	Chemistry
Brian Avanzino	Chemsitry
Mario Parks	Immunology
Kyle Pelot	Plant Biology
Maria Peralta (del Refugio)	Chemistry
Laura Perilla	Plant Pathology
Kevin Pham	Chemistry
Adam Poe	Biochemistry, Molecular, Cellular & Developmental Biology
Marc Pollack	Microbiology
Ali Rahimian Mashadi	Comparative Pathology
Anita Rajamani	Biomedical Engineering
Jamie Randol	Integrative Genetics & Genomics
Sonia Reveco	Integrative Genetics & Genomics
Juan Reyes	Integrative Genetics & Genomics
Jordan Sayre	Microbiology
Aarthi Sekar	Integrative Genetics & Genomics
Rebecka Sepela	Biochemistry, Molecular, Cellular & Developmental Biology
Shanaya Shah	Biochemistry, Molecular, Cellular & Developmental Biology
Guy Shani	Microbiology

Megan Showalter	Biochemistry, Molecular, Cellular & Developmental Biology
Natasha Shroff	Integrative Genetics & Genomics
David Silberstein	Chemical Engineering
Julie Soderlind	Material Science and Engineering
Breanne Sparta	Biochemistry, Molecular, Cellular & Developmental Biology
Daniel Steele	Plant Biology
Eric Stevens	Microbiology and Molecular Genetics
Allison Stevens	Nutritional Biology
Jessica Stolfi	Immunology
Robert Stolz	Integrative Genetics & Genomics
Scott Strobel	Biological Systems Engineering
Linda Su-Feher	Biochemistry, Molecular, Cellular & Developmental Biology
Sara Sukenik	Biomedical Engineering
Rene Suleiman	Microbiology
James Ta	Biophysics
Alireza (Ali) Tafazzol	Biomedical Engineering
Ruensern Tan	Biochemistry, Molecular, Cellular & Developmental Biology
Srinivas Tapa	Biomedical Engineering
Justin Thomas	Chemistry
Alexander Thuy-Boun	Chemistry
George (Kenneth) Todd	Molecular, Cellular & Integrative Physiology
Kim Truong	Pharmacology & Toxicology
Robert Van Ostrand	Chemistry
Kacey VanderVorst	Biochemistry and Molecular Medicine
Sana Vaziri	Computer Science
Erica Vonasek	Biological Systems Engineering
Gregory Walker	Microbiology
Eric Walters	Microbiology
Kening (Connie) Wang	Biomedical Engineering
Yaxin Wang	Plant Biology
Kaitlin "Kay" Watt	Integrative Genetics & Genomics
Toni West	Biochemistry, Molecular, Cellular & Developmental Biology
Donnelly West	Integrative Genetics & Genomics
Samuel Westreich	Integrative Genetics & Genomics
Jacklyn Whitehead	Biomedical Engineering
Damion Whitfield	Microbiology
Marisol Wolf	Immunology
Elyse Wudeck	Molecular, Cellular and Integrative Physiology
Sydney Wyatt	Integrative Genetics & Genomics
Yongao Xiong	Materials Science and Engineering
Phoebe Yam	Integrative Genetics & Genomics
Britt Yazel	Neurosciences
Le Yee (Huwe)	Biomedical Engineering

Xiaochen (Ellie) Yin	Food Science
Brian Avanzino	Chemistry
Annabelle Yu	Microbiology
Yuxuan (Eric) Zheng	Chemistry
Yihui Zhu	Integrative Genetics & Genomics
Steve Zicari	Biological Systems Engineering

DEB Faculty Trainers as of February 2017

Steffen Abel	Plant Sciences
Venkatesh Akella	Electrical & Computer Engineering
John Albeck	Molecular and Cellular Biology
Rajeevan Amirtharajah	Electrical & Computer Engineering
Paul Ashwood	UCD MIND Institute
Kyriacos Athanasiou	Biomedical Engineering
Shota Atsumi	Chemistry
Matthew Augustine	Chemistry
Sharon Aviran	Biomedical Engineering
Alan Balch	Chemistry
Enoch Baldwin	Molecular and Cellular Biology
Diane Barrett	Food Science
Diane Barrett	Food Science & Technology
Peter Barry	Center for Comparative Medicine
Stephen Barthold	Pathology, Microbiology & Immunology
Nicole Baumgarth	Department of Pathology, Microbiology and Immunology; CCM, VetMed
Peter Beal	Chemistry
Laurel Beckett	Biostatistics Department of Public Health Sciences
Craig Benham	Biomedical Engineering / Genome Center
Alan Bennett	Vegetable Crops (Plant Science)
Don Bers	Pharmacology
Charles L. Bevins	Microbiology & Immunology
Linda Bisson	Viticulture & Enology
Caroline Bledsoe	Soils and Biogeochemistry
David Block	Viticulture & Enology/Chemical Engineering & Materials Science
Eduardo Blumwald	Plant Sciences
Laura Borodinsky	Physiology & Membrane Biology UCDMC
Alexander Borowsky	Pathology
Richard Bostock	Plant Pathology
Kent Bradford	Vegetable Crops
Siobhan Brady	Plant Biology and Genome Center
Nadean Brown	Cell Biology and Human Anatomy, School of Medicine

Titus Brown	Population health and reproduction: Vet Med
Christine Bruhn	Food Science & Technology
Alan Buckpitt	VM: Molecular Biosciences
Sean Burgess	Molecular & Cellular Biology
Judy Callis	Molecular & Cellular Biology
Christopher Calvert	Animal Science
Kermit Carraway	Biochemistry and Molecular Medicine
Luis Carvajal-Carmona	Genome Center & Department of Biochemistry and Molecular Medicine
Clare Casteel	Plant Pathology
Fred Chedin	Molecular & Cellular Biology
Chao-Yin Chen	Pharmacology
Hongwu Chen	Biochemistry & Molecular Medicine
Xi Chen	Chemistry
Xinbin Chen	Comparative Oncology
Holland Cheng	Molecular & Cellular Biology
Simon Cherry	Biomedical Engineering
Nipavan Chiamvimonvat	Internal Medicine; Division of Cardiovascular Medicine
Joanna Chiu	Entomology
Blaine Christiansen	UC Davis Health System Department of 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
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:MED
Megan Dennis	Biochemistry & Molecular Medicine
Elva Diaz	Pharmacology
Zhi Ding	Electrical & Computer Engineering
Georgia Drakakaki	Plant Sciences
Don Durzan	Environmental Horticulture
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	Genome Center
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
Charles Gasser	Molecular & Cellular Biology
Angela 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
David Gilchrist	Plant Pathology
Mark Goldman	Neurobiology, Physiology and Behavior; Ophthalmology and Vision Science
Tom Gradziel	Pomology
Jeffrey Gregg	MED: Pathology
Leigh Griffiths	Medicine and Epidemiology
Andrew Groover	Plant Biology
Ting Guo	Chemistry
Paul Hagerman	Biochemistry and Molecular Medicine
Fawaz Haj	Nutrition
Bruce Hammock	Entomology & Cancer Center
Stacy Harmer	Plant Biology
Dennis Hartigan-O'Connor	Medical Microbiology and Immunology
Volkmar Heinrich	Biomedical Engineering
Johannes Hell	Pharmacology
Paul Henderson	Internal Medicine: Division of Hematology and Oncology
Wolf-Dietrich Heyer	Microbiology
Fereydoun Hormozdiari	Biochemistry and Molecular Medicine
David Horsley	Mechanical & Aeronautical Engineering

Krassi Hristova	Soils and Biogeochemistry
You-Lo Hsieh	Textiles & Clothing
Maury Hull	Mechanical Engineering and Aerospace Engineering
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
Richard 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
Ian Korf	Section of Molecular & Cellular Biology
Dietmar Kueltz	Animal Science
Tonya Kuhl	Chemical Engineering
Hsing-Jien Kung	MED: Biochemistry / UC Davis Cancer Center
Tawni Middleton	Cell Biology and Human Anatomy
John Labavitch	Plant Sciences
J. Clark Lagarias	Molecular & Cellular Biology
Kit Lam	MED: Hematology & Oncology
Donald Land	Chemistry
Delmar Larsen	Chemistry
Janine LaSalle	MED: Microbiology & Immunology
Jerold Last	Pulmonary / Critical Care Medicine
Kent Leach	Biomedical Engineering
Julie Leary	Biochemistry & Mass Spectrometry, Dept. of Chemistry
Carlito Lebrilla	Chemistry
Pamela Lein	Molecular Biosciences

Noelle L'Etoile	Center for Neuroscience & Dept. of Psychiatry & Behavioral Sciences
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 & Material Sciences
Angelique Louie	Biomedical Engineering
Paul Luciw	MED: Pathology
Neville 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
Frank McNally	Molecular & Cellular Biology
John McPherson	Biochemistry and Molecular Medicine
Stephen McSorley	Vet Med: Anatomy, Physiology & Cell Biology
Claude Meares	Chemistry
Juan Medrano	Animal Science
Richard Michelmore	Plant Sciences
Lee Miller	Neurobiology, Physiology and Behavior
Lisa Miller	Department of Anatomy, Physiology and Cell Biology, CNPRC, School of Veterinary Medicine
David Mills	Viticulture & Enology
Maria Mudryj	Medical Microbiology & Immunology
William J. Murphy	Department of Dermatology
James Murray	Animal Science / Genetic Engineering Large Animals
Krishnan Nambiar	Chemistry
Lorena Navarro	Microbiology
Florence Negre-Zakharov	Department of Plant Sciences
John Newman	Nutrition & USDA-ARS-WHNRC
Nitin Nitin	Dept. of Food Science & Dept. of Agricultural Engineering
Stephen Noctor	Neuroscience
Jan Nolta	UCDHS: Hematology & Oncology, Dept. of Med

Alex Nord	Center for Neuroscience
Jodi Nunnari	Molecular and Cellular Biology
Robert Stolz	Physiology & membrane Biology; School of Medicine
David Ogrydziak	Food Science & Technology
Tingrui Pan	Biomedical Engineering
Alyssa Panitch	Biomedical Engineering
Rebecca Parales	Microbiology
Atul Parikh	Biomedical Engineering
Anthony Passerini	Dept. of Biomedical Engineering
Timothy Patten	Chemistry
Niels Pedersen	Department of Medicine and Epidemiology
Isaac Pessah	Molecular Biosciences
Ronald Phillips	Chemical Engineering & Material Science
Kent Pinkerton	Pediatrics, School of Medicine
David Pleasure	Neurology and Pediatrics
Ann Powell	Plant Sciences
Jerry Powell	Hemat & Oncol: Med
Robert Powell	Chemical Engineering & Material Science
Martin Privalsky	Microbiology
Jinyi Qi	Biomedical Engineering
Gerald Quon	Molecular and Cellular Biology
Katherine Ralston	Microbiology and Molecular Genetics
Katherine Rauen	MED: Pediatrics
Helen Raybould	VM Anatomy, Physiol & Cell Bio
Subhadip Raychaudhuri	Biomedical Engineering
David Reid	Food Science & Technology
Michael Reid	Environmental Horticulture
Alexander Revzin	Biomedical Engineering
Crystal Ripplinger	Pharmacology
Subhash Risbud	Chemical Engineering & Material Science
William Ristenpart	Chemical Engineering & Materials Science and Dept. of Food Science
David Rocke	Inst. For Data Analysis & Visualization
Jorge Rodrigues	Land, Air and Water Resources
Ray Rodriguez	Molecular & Cellular Biology
Pamela Ronald	Plant Pathology
Alan Rose	Molecular and Cellular Biology
Lesilee Rose	Molecular & Cellular Biology
Pablo Ross	Animal Science
John Rutledge	MED: Endocrinology

Jon Sack	Physiology & Membrane Biology
Earl Sawai	Pathology & Laboratory Medicine
Kate Scow	Land, Air & Water Resources
David Segal	Pharmacology
Justin Seigel	MED: Biochemistry & Molecular Medicine / Chemistry
Earl Sawai	Electrical & Computer Engineering
Barbara Shacklett	Medical Microbiology & Immunology: School of Medicine
Earl Sawai	Neurology
Kazuhiro Shiozaki	Microbiology
Justin Siegel	Chemistry
Eduardo Silva	Biomedical Engineering
Chris Simmons	Food Science & Technology
Sergi Simó	Cell Biol & Human Anatomy
Scott Simon	Biomedical Engineering
Neelima Sinha	Plant Biology
David Slaughter	Biological & Agricultural Engineering
Carolyn Slupsky	Food Science & Technology
Athena Soulika	Dermatology
Daniel Starr	Center for Genetics and Development
Francene Steinberg	Dept. of Nutrition
Ioannis Stergiopoulos	Plant Pathology
Pieter Stroeve	Chemical Engineering & Material Science
Alexei Stuchebrukhov	Chemistry
Gang Sun	Textiles & Clothing
Ilias Tagkopoulos	Computer Science
Cheemeng Tan	Biomedical Engineering
Dean Tantillo	Chemistry
Alice Tarantal	Pediatrics, School of Medicine, CA National Primate Center
Flora Tassone	Biochemistry and Molecular Medicine
Steven Theg	Plant Biology
Li Tian	Plant Sciences
Michael Toney	Chemistry
Jose Torres	MED: Medical Microbiology & Immunology
Renee Tsolis	Med Microbiology & Immunology: MED
Richard Tucker	Cell Biology & Human Anatomy
Judy Van de Water	Division of Rheumatology/Allergy and Clinical Immunology

Alison Van Eenennaam	Animal Science
Marta Van Loan	Nutrition
Jean VanderGheynst	Biological & Agricultural Engineering
Rachel Lee Vannette	Entomology and Nematology
Mariel Vazquez	Microbiology and Molecular Genetics
John Voss	Biochemistry and Molecular Medicine
Bart Weimer	Population Health & Reproduction
Robert Weiss	Internal Medicine: Division of Nephrology, School of Medicine
Valerie Williamson	Nematology
David Wilson	Molecular & Cellular Biology
Matthew 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
Yin Yeh	Applied Science
Tilahun Yilma	VM: Pathology, Microbiology & Immunology
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.

In Memoriam Professor Kentaro Inoue

It is with a heavy heart that the Biotechnology Program says goodbye to an exceptional DEB Faculty Mentor and stellar researcher. Professor Kentaro Inoue passed away Wednesday, August 31st, in a bicycle crash on his way to work from Sacramento to the UC Davis campus.

Kentaro Inoue 47, was a professor in the Plant Sciences department on campus and was very popular among faculty and students alike. Known for his love of biking, research, wine, and hiking, Kentaro was full of life and energy. He leaves behind his wife, Amy Brown, a veterinarian in Roseville.

Goodbye Professor Inoue, you will be missed!