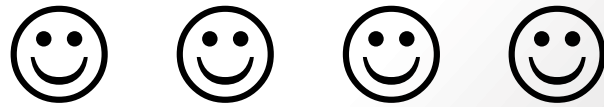


# TURBO TALKS



# Molecular Detection of eukaryotic pathogens in esophageal cancer

Jianzhen Xu, Shantou University medical college, China

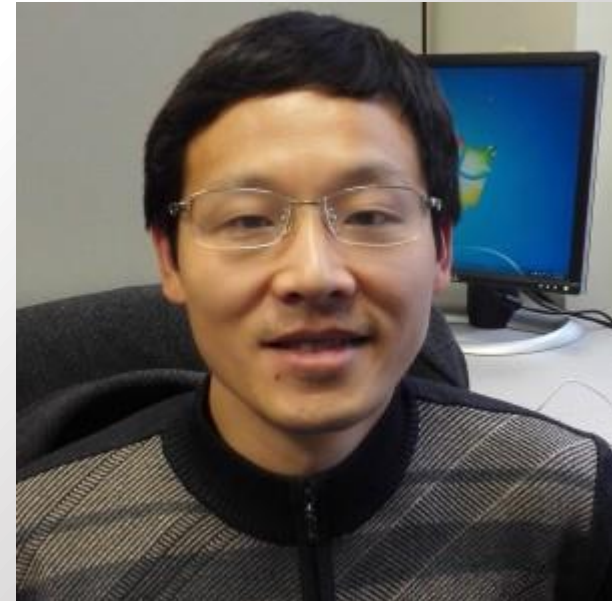
**Research goal:** To investigate whether or not eukaryotic pathogen infection play a role in esophageal cancers

**How?** using next-generation sequencing through a polymerase chain reaction (PCR)-based analysis of 16S rRNA genes(metagenomics)

**Samples/Model System:** biopsy

**The challenge:** bioinformatics analysis

**Workshop goals:** To learn how EuPathDB can assist in designing the project and analyzing the data





# Characterization of *Toxoplasma gondii* Tgj1 Type I Hsp40

Jonathan Munera-Lopez, National University of General San Martín (Argentina)

**Research goal:** Identify the biological role of Tgj1 in *Toxoplasma gondii*

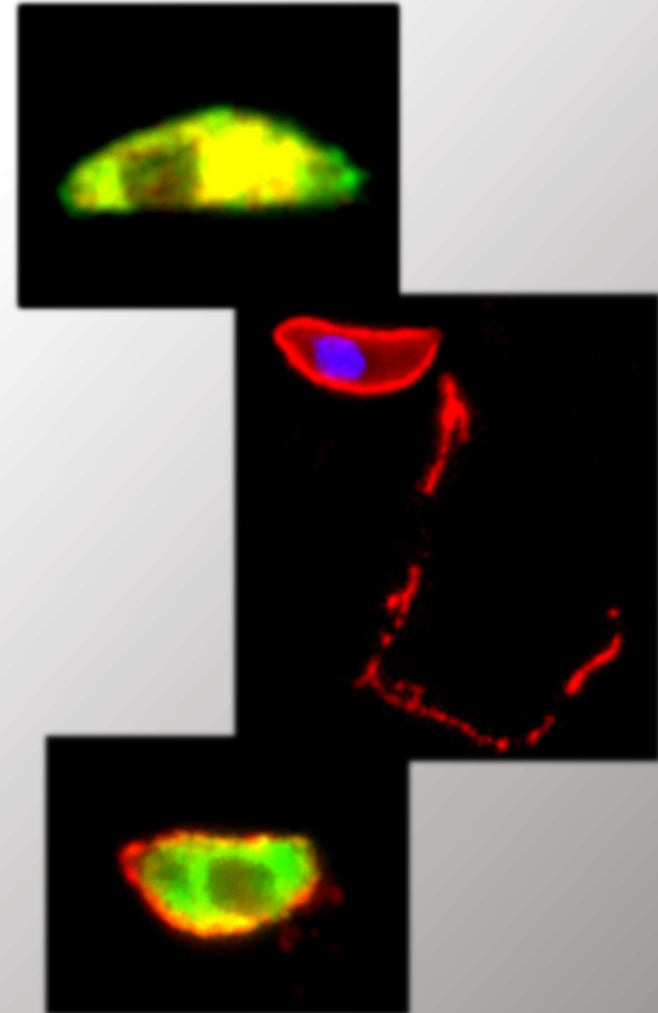
**How?** Localization and functional studies by endogenous tagging, CRISPR Knock-outs and invasion assays.

**Samples/Model System:**

*Toxoplasma gondii*

**The challenge:** Determine if Tgj1 is involved in invasion.

**Workshop goals:** Develop efficient search strategies and analysis of the outcome.



# Epidemiology and Population Biology of Grape Downy Mildew in Georgia

Cheng-Fang Hong, University of Georgia

**Research goal:** Monitor downy mildew epidemics and clarify the importance of sexual reproduction and population biology of downy mildew pathogen in GA.

**How?** CAPS analysis of ITS and  $\beta$ -tubulin gene and SSR markers.

**Samples:** Vineyard field samples, e.g. infected tissues, leaf litters.

**The challenge:** Integrate and interpret information obtained from experiments and translate into knowledge.

**Workshop goals:** To learn how EuPathDB can assist in analyzing my results.





# Grapevine downy mildew: population diversity and role of sexual reproduction in epidemic dynamics in subtropical regions

Meyrielle Pires de Camargo, University of São Paulo/University of Georgia

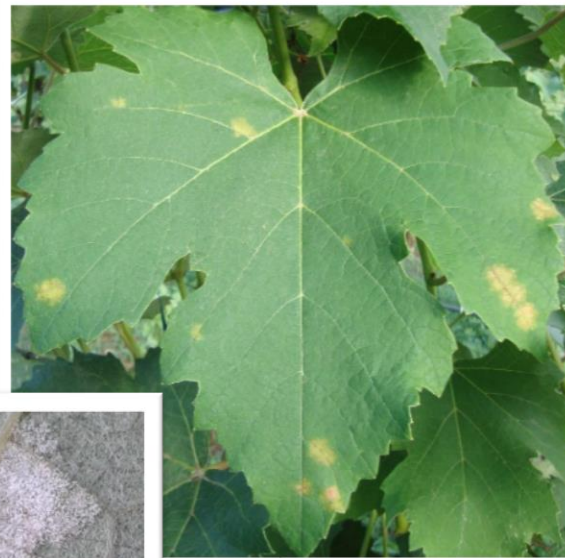
**Research goal:** Investigate the population diversity of *P. viticola* from GA-USA and SP-BR, to understand the role of primary and secondary infections in downy mildew epidemics and verify the presence of cryptic species of *P. viticola*.

**How?** SSR analysis; CAPS and DNA sequencing (ITS,  $\beta$ -tubulin);

**Samples/Model System:** single-lesions of *P. viticola* from grapevine leaf tissues

**The challenge:** Data analysis and interpretation of results

**Workshop goals:** Acquire knowledge of different database resources to improve data analysis of my research



# Aflatoxin biosynthesis in *Aspergillus flavus* and its relationship to environmental oxidative stress.

Jake Fountain, University of Georgia

Dr. Gaurav Agarwal, University of Georgia

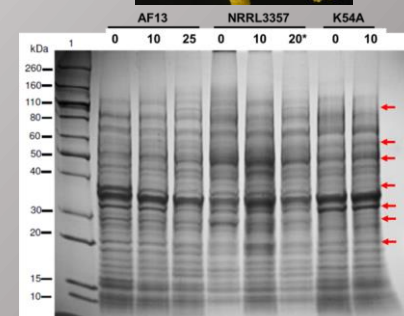
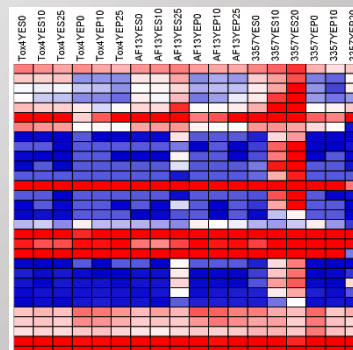
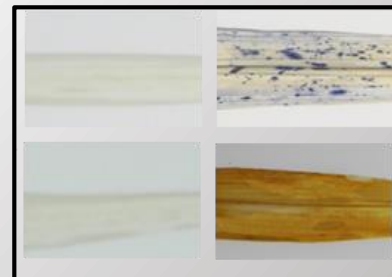
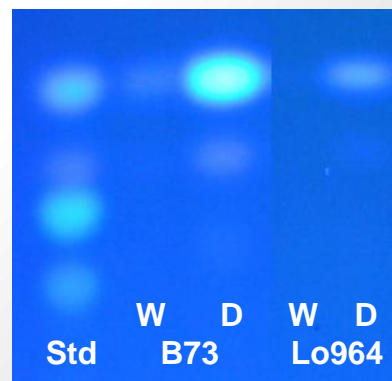
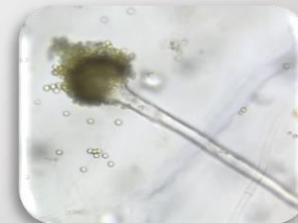
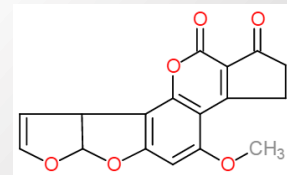
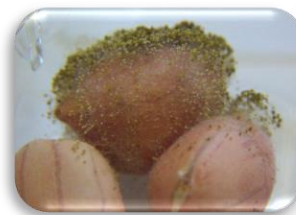
**Research goal:** Investigate the biological role of aflatoxin biosynthesis, particularly under environmental stress conditions, and to examine host plant responses to drought stress.

**How?** RNA sequencing and iTRAQ proteomics of the pathogen under increasing levels of stress. Metabolomics of host plant tissue.

**Samples/Model System:** *A. flavus* mycelia and maize kernel tissues.

**The challenge:** Identifying connections between pathways to determine coordinated responses to stress.

**Workshop goals:** To learn how EuPathDB and FungiDB can assist in analyzing my results and informing my research.







# Streamlined Deletion of *Toxoplasma* Glycogenes Using CRISPR/Cas9

H. Travis Ichikawa, University of Georgia

**Research goal:** Establish an efficient and cost effective method to generate a deletion mutant library of *Toxoplasma gondii* for the community.

**How?** Predict *Toxoplasma gondii* glycogenes and delete them by CRISPR/Cas9 system.

**The samples:** Lab strains of *Toxoplasma gondii*, Type I, II and III.

**The challenge:** Accurate prediction of glycogenes and development of an efficient and cost effective method for deletion mutagenesis.

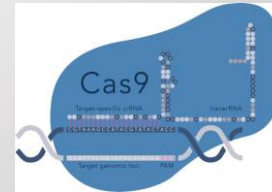
**Workshop goals:** To learn how EuPathDB can assist in understanding predicted glycogenes better and further developing the project to ask formulated biological questions.



Glycogenes prediction

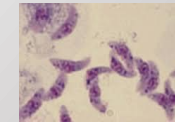


gRNA/Cas9 plasmid designing

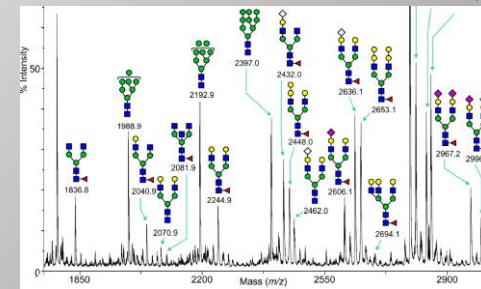
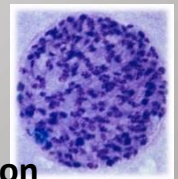


Deletion mutagenesis

Cloning of mutants



Brdyzoite differentiation



Glycomics analysis

# Investigating *C. albicans* genome plasticity during growth within the host, Jen Mason, Emory University

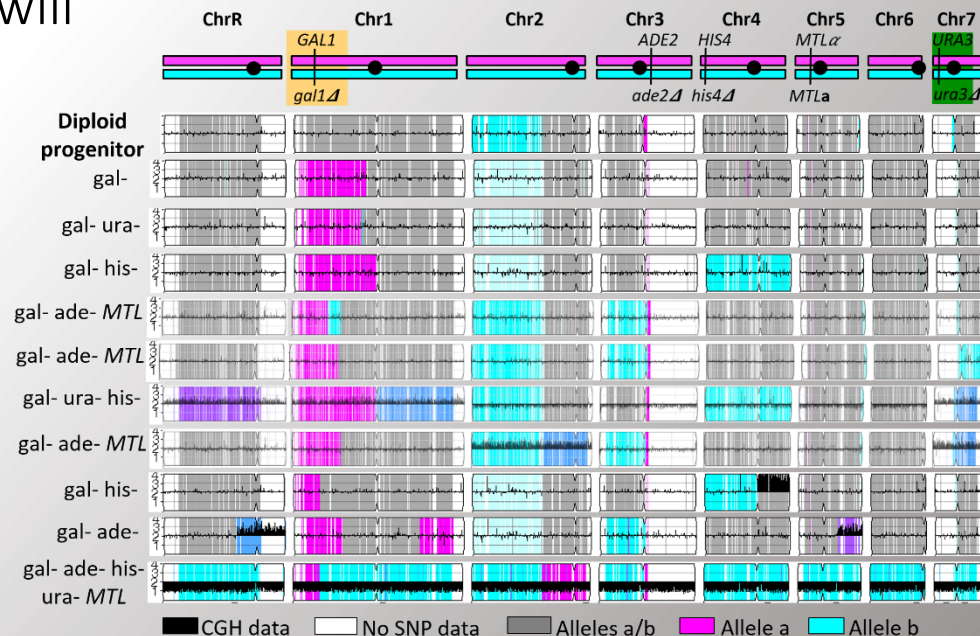
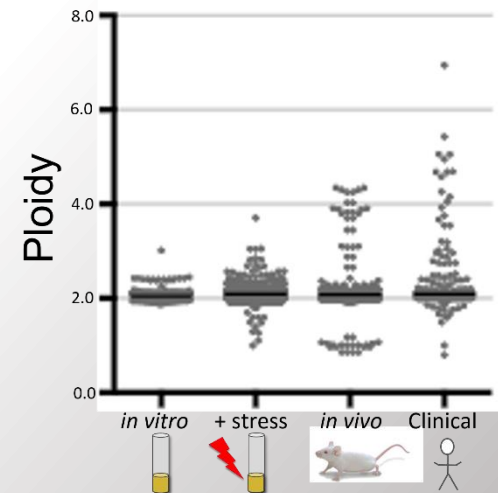
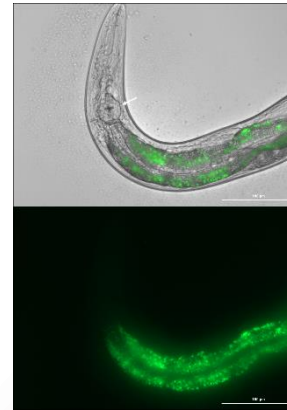
**Research goal:** Determine how growth within the host influences *C. albicans* genome plasticity in comparison to what is detected *in vitro*

**How?** LOH, SNP/CGH arrays, flow cytometry, sequencing

**Samples/Model System:** *C. albicans* will be propagated in a *C. elegans* host

**The challenge:** Developing the *C. elegans* system to model host interactions with *C. albicans*

**Workshop goals:** To learn new tools/technologies that can assist in data collection and analysis



■ CGH data    □ No SNP data    ▒ Alleles a/b    ■ Allele a    ■ Allele b

# Enhanced *Cryptosporidium hominis* genome annotation

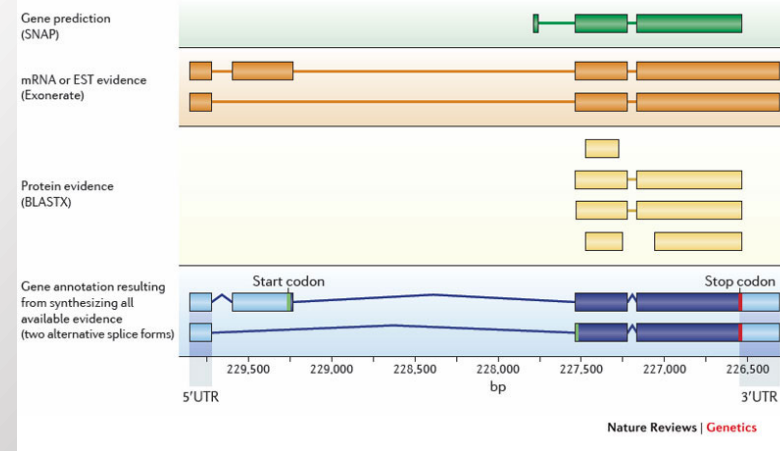
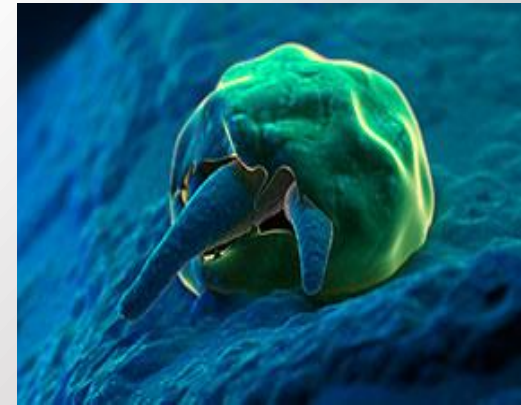
## Yiran Li, University of Georgia

**Research goal:** Generate new annotations for *Cryptosporidium hominis* and provide enhanced functional and metabolic resources for other downstream analysis.

**How?** Use available experimental data as evidence to generate new annotation for newly sequenced genomes.

**The challenge:** Lack of physical map and expression data

**Workshop goals:** To learn how data are organized in EuPathDB and how to dig informative data for my research



# Evolution of Multi-copy Gene Families (Dyneins and Sugar Transporters) in the Apicomplexa

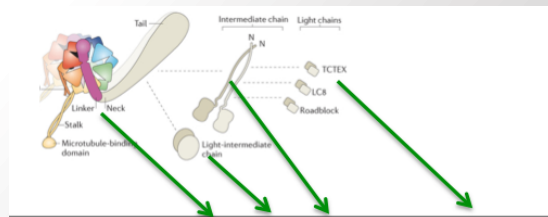
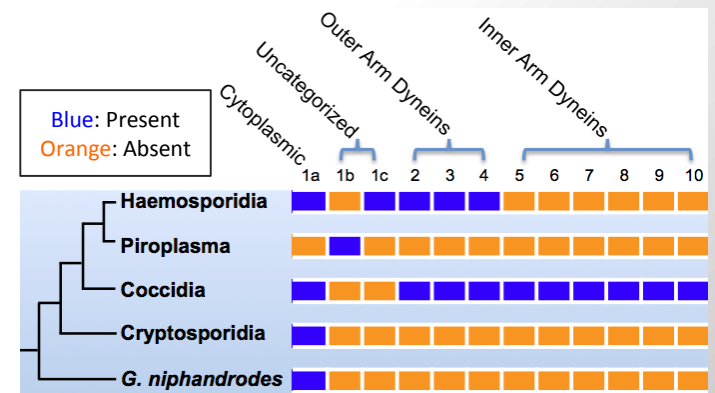
Ousman Mahmud, University of Georgia

**Research goal:** Characterize gene gain and loss patterns within the Apicomplexa and the biological significances of these patterns

**How?** Evolutionary analyses: Orthology clustering, Phylogenetics, etc. Data mining of functional data. Wet bench: Epitope Tagging

**Samples/Model System:** NGS datasets: genomes, transcriptomes, proteomes, etc. Wet bench: *Toxoplasma gondii*

**Workshop goals:** Learn about the latest EuPathDB tools and datasets that may be of use to my research



Species	DHC	DLIC	DIC	DLC		
				LC8	Roadblock	TCTEX
<i>P. berghei</i>	6	1	3	4	2	4
<i>P. cynomolgi</i>	6	1	3	4	2	4
<i>P. falciparum</i>	6	1	3	4	2	4
<i>P. knowlesi</i>	6	1	3	4	2	4
<i>H. tartakovskyi</i>	6	1	3	3	2	3
<i>B. bovis</i>	1	nf	nf	1	nf	nf
<i>B. bigemina</i>	1	nf	nf	1	nf	nf
<i>B. microti</i>	nf	nf	nf	1	nf	nf
<i>T. annulata</i>	1	nf	nf	1	nf	nf
<i>T. parva</i>	1	nf	nf	1	nf	nf
<i>T. equi</i>	1	nf	nf	1	nf	nf
<i>T. orientalis</i>	nf	nf	nf	1	nf	nf
<i>E. tenella</i>	10	1	3	5	2	2
<i>N. caninum</i>	10	1	3	6	2	3
<i>T. gondii</i>	10	1	3	6	2	4
<i>H. hammondi</i>	10	1	3	6	2	3
<i>S. neurona</i>	9	1	3	6	2	4
<i>C. muris</i>	1	1	1	1	1	1
<i>C. parvum</i>	1	1	1	1	1	1
<i>C. hominis</i>	1	1	1	1	1	1
<i>G. niphandrodes</i>	1	nf	nf	3	nf	1
<i>C. vella</i>	12	1	8	6	3	5
<i>V. brassicaformis</i>	15	2	8	9	2	5

Illustration of Apicomplexan Dynein Heavy Chain Phylogeny

Apicomplexan Dynein Subunit Copy Number



# Genomics-based laboratory surveillance and reference diagnosis for *Cyclospora cayetanensis*

Yvonne Qvarnstrom, CDC

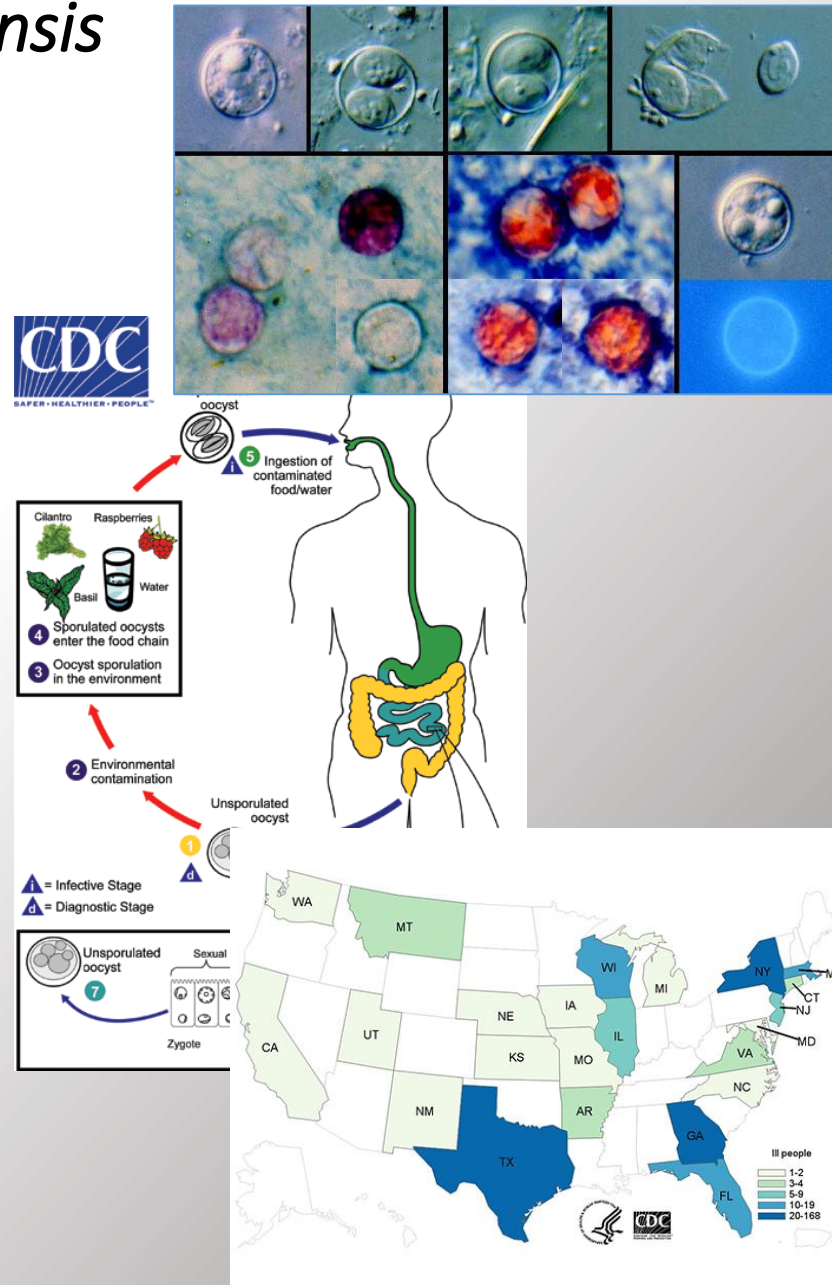
**Research goal:** Develop a typing method and better diagnostic tests to improve outbreak response

**How?** Genomics, transcriptomics and proteomics

**Samples:** Oocysts purified from human stool samples

**The challenge:** No reference genome available. Extremely little material to work with.

**Workshop goals:** To learn how EuPathDB works and if it could be a platform for the *Cyclospora* data.





# Acquisition and Utilization of Host Macromolecular Nutrients by *Toxoplasma gondii*

Paige Teehan, Clemson University

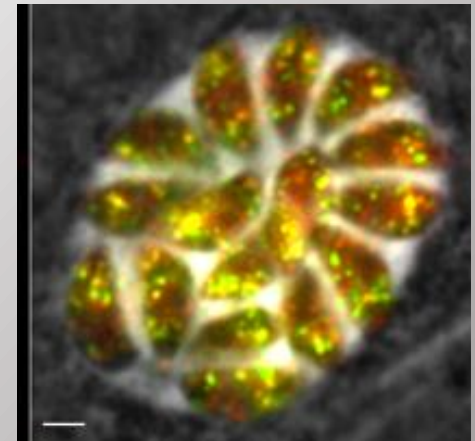
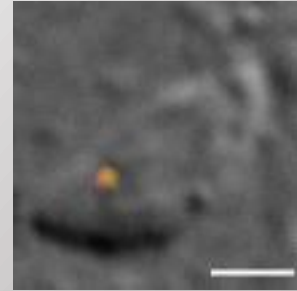
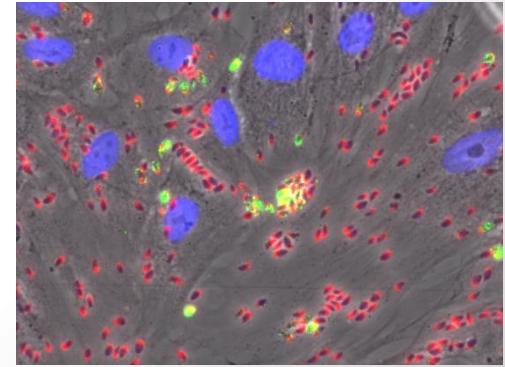
**Research goal:** Characterize the central role of the VAC/PLV in the utilization of host nutrients

**How?** By using a global epitope tagging strategy to identify more VAC/PLV-associated peptidases

**Samples/Model System:** *T. gondii* grown in HFF cells

**The challenge:** Correctly placing epitope tags to identify new genes without disrupting their function

**Workshop goals:** To learn about features of EuPathDB and ToxoDB that will assist in advancing my research



# How *T. brucei* sense and respond to environmental glucose

Yijian (Evan) Qiu, Clemson University

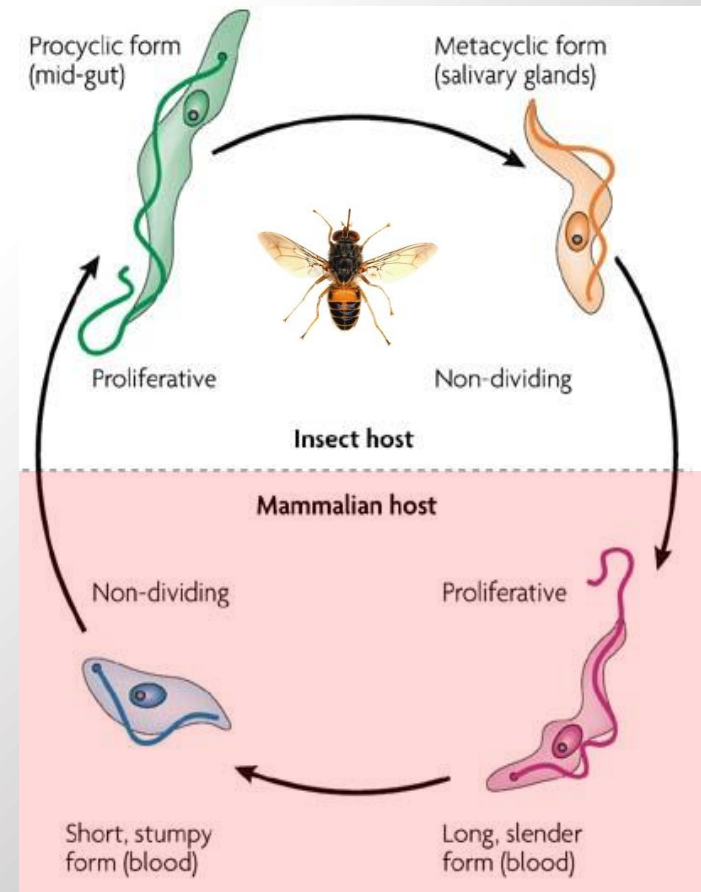
**Research goal:** Study the mechanisms enable the parasites to respond to difference in availability of glucose in the suite of niches they occupy

**How?** Perform RNAseq and RT-PCR on trypanosomes growing in different glucose levels

**The samples:** Cultured blood stream form and procyclic form parasites

**The challenge:** Blood stream form cannot live in the absence of glucose; Metacyclic form not easy to grow

**Workshop goals:** To learn how to EuPathDB to combine different datasets in analyzing my results



Modified from Lee et al., Nature reviews, 2007

# Identification of a Pex3 homolog in *Trypanosoma brucei*

Logan Crowe, Clemson University

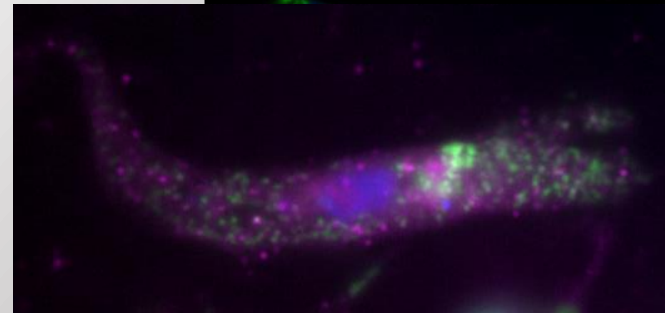
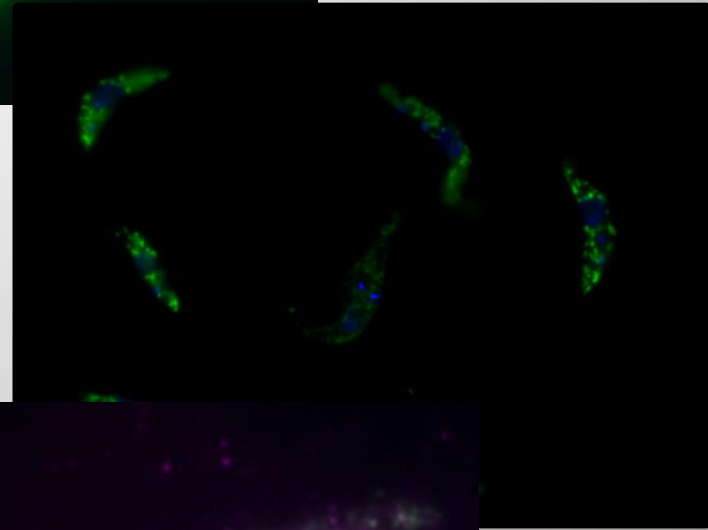
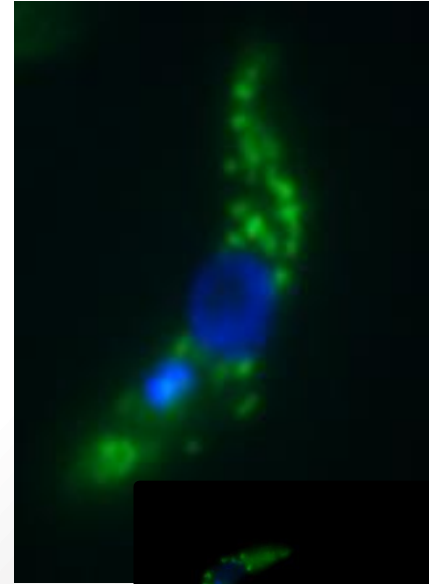
**Research goal:** Identify *T. brucei* Pex3

**How?** Sequence similarity to known Pex3s, functional characterization of putative Pex3, localization

**Samples/Model System:** *Trypanosoma brucei*

**The challenge:** There is low sequence similarity in peroxins, making identification difficult

**Workshop goals:** Learn better methods for identifying genes beyond BLAST



# A DNA Sequence Based Surveillance System for Cryptosporidiosis



**Kevin Tang, CDC, Atlanta, GA**

**Research goal:** Develop DNA sequence based surveillance system to reduce the transmission of Cryptosporidium in the United States

**How?** Use NGS sequencing for Cryptosporidium genotyping and identification.

**The samples:** Stool specimens

**The challenge:** Purification of Cryptosporidium pathogen and differentiating pathogen DNA in clinical samples from host or other contaminated eukaryotic DNA

**Workshop goals:** To learn how EuPathDB can assist in analyzing the sequence data



# Calcium entry and calcium uptake research in *Toxoplasma* calcium stores

## Le Chang, University of Georgia

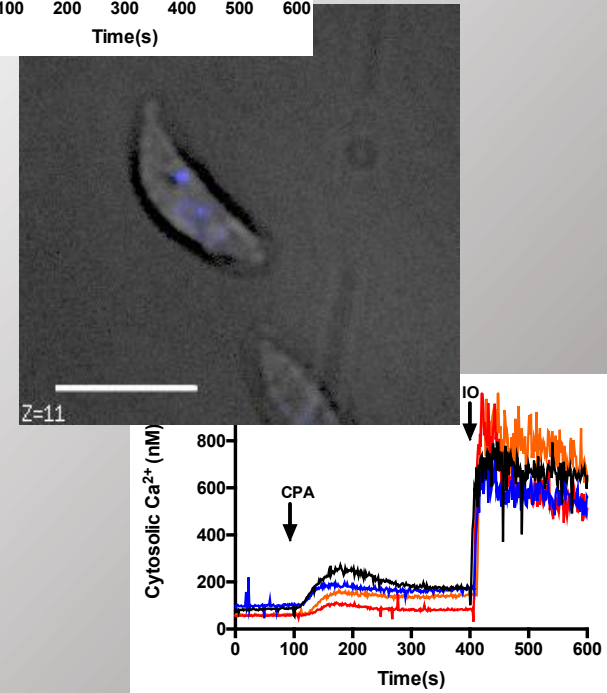
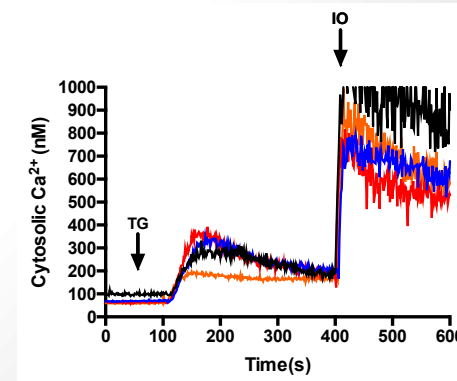
**Research goal:** By measuring calcium indicators fluorescence modification to figure out how calcium entry and calcium uptake in toxoplasma.

**How?** First, to load toxoplasma with different indicators or dyes in different part of the parasite, then use fluorimeter to measure modification of these indicators. Then by adding different chemical reagent to start research.

**Samples/Model System:** toxoplasma

**The challenge:** toxoplasma calcium stores

**Workshop goals:** To learn how to use EuPathDB to search essential gene in a efficiency way to assist my research.





# Discovery and Characterization of Novel Glycosyltransferases that Modify *Toxoplasma* Skp1 in the Cytoplasm (Kazi Rahman)

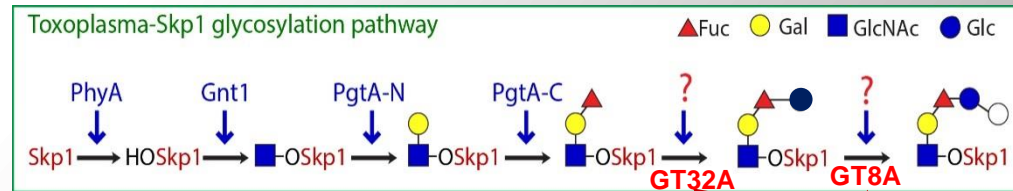
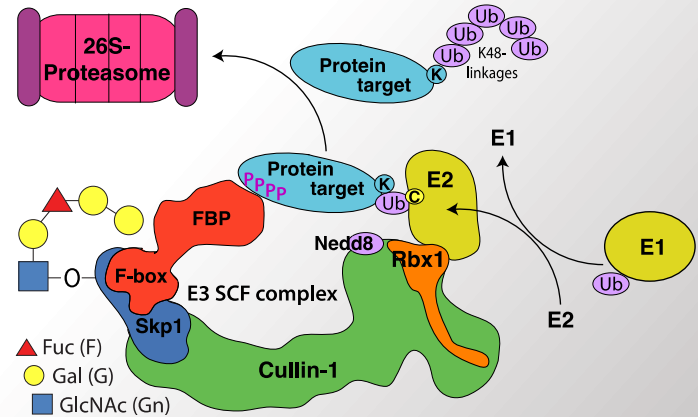
**Research goal:** Identification and Characterization of glycosyltransferases that transfer terminal disaccharide on *Toxoplasma* Skp1.

**How?** Bioinformatics-based prediction of entire glycosyltransferases from *Toxoplasma* and selection of putative Skp1 modifying glycosyltransferases based on evolutionary and functional analysis

**The samples:** *Toxoplasma* tachyzoites

**The challenge:** Prediction of glycosyltransferase domains and their orthologs due to low sequence homology

**Workshop goals:** To learn how EuPathDB can assist in identifying the evolutionary related glycosyltransferases that potentially modifies Skp1 in other organisms.



- Toxoplasma proteome (~8400 proteins)
- Putative Glycosyltransferases (45)
- Cytosolic glycosyltransferases (10)



# CRISPR (clustered regularly interspaced short palindromic repeats)/Cas9 (CRISPR-associated gene 9) system in *Trypanosoma Cruzi*.

Teresa Cruz-Bustos, CTEGD, University of Georgia

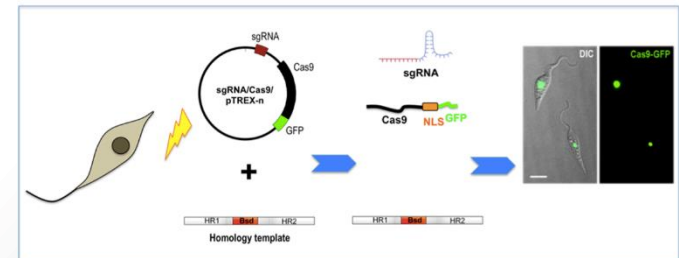
**Research goal:** gene editing using CRISPR/Cas9 system for disrupting genes and the homology recombination technique in *Trypanosoma Cruzi*.

**How?** PCR, cloning, transfection and drugs selection of Parasites

**Samples/Model System:** *Trypanosoma cruzi*

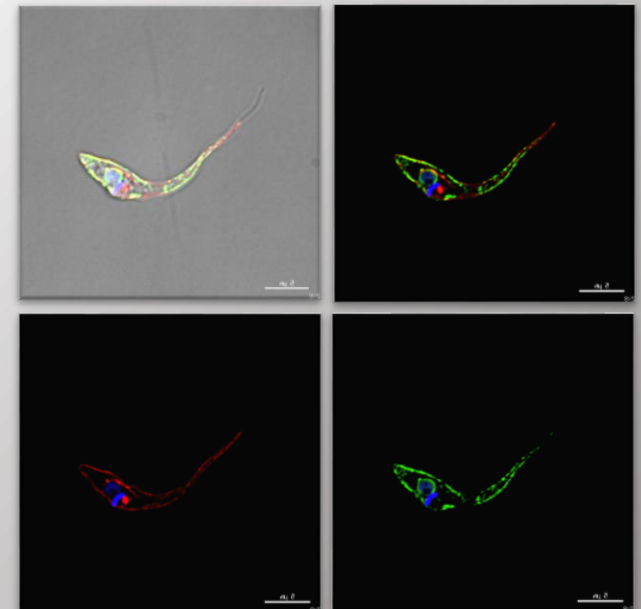
**The challenge:** using CRISPR/Cas9 to silence genes with the purpose of study the functionality of this genes of *T.cruzi* some of them are related with the mechanosensor response and other involved in osmotic response

**Workshop goals:** To learn how EuPathDB can assist in analyzing genes and informing my research



The method was significantly improved after including a homology template for DNA repair

Lander et al., 2015. mBio 6(4): e01012-15



# Effect of Sporulation Conditions on Fitness of *A. fumigatus*

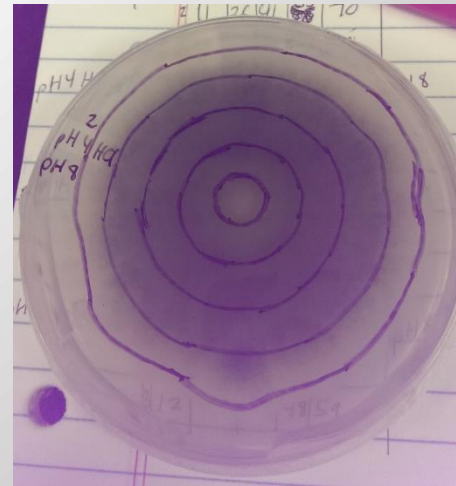
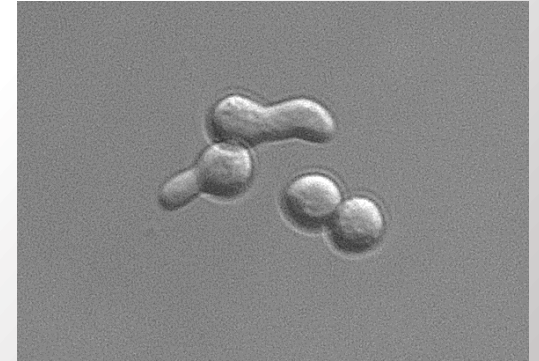
## Rosemary Wills, University of Georgia

**Research goal:** Investigate whether sporulation conditions affect the germination and growth of fungal pathogen *Aspergillus fumigatus*

**How?** Produce conidia under different conditions and assess germination potential, hyphal growth rates, and dormant spore transcriptomes.

**The samples:** *Aspergillus fumigatus* Af293

**Workshop goals:** To learn to use EuPathDB to analyze gene, protein, and transcript sequences.



# Advanced Molecular Techniques Course

## David Peterson, CTEGD, UGA

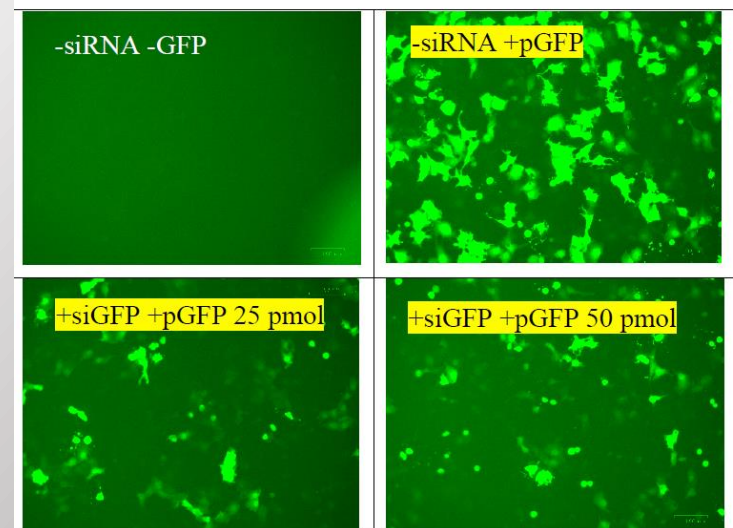
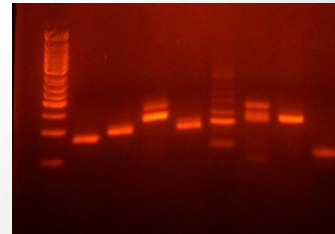
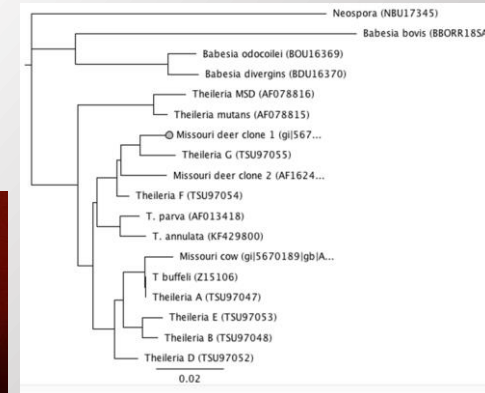
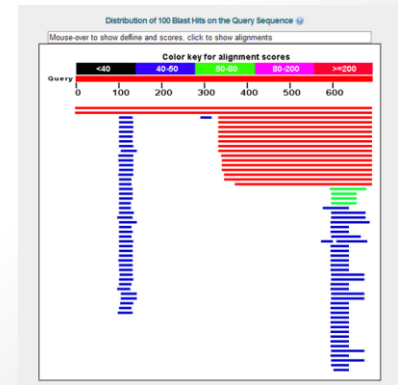
**Teaching goal:** Revise bioinformatics related content in course to keep topics up to date and relevant

**How?** Use examples from published research and online tools that can be adapted to in class exercises

**Samples/Model System:** Anything in EuPathDB that can be used to illustrate solutions to research questions

**The challenge:** Create useful and relevant class exercises that demonstrate the utility of a well designed genomic analysis platform

**Workshop goals:** To gain a better understanding of the array of tools within EuPathDB





# Determining the Link between Calcium Influx and Motility in *Toxoplasma gondii*

Stephen Vella, University of Georgia

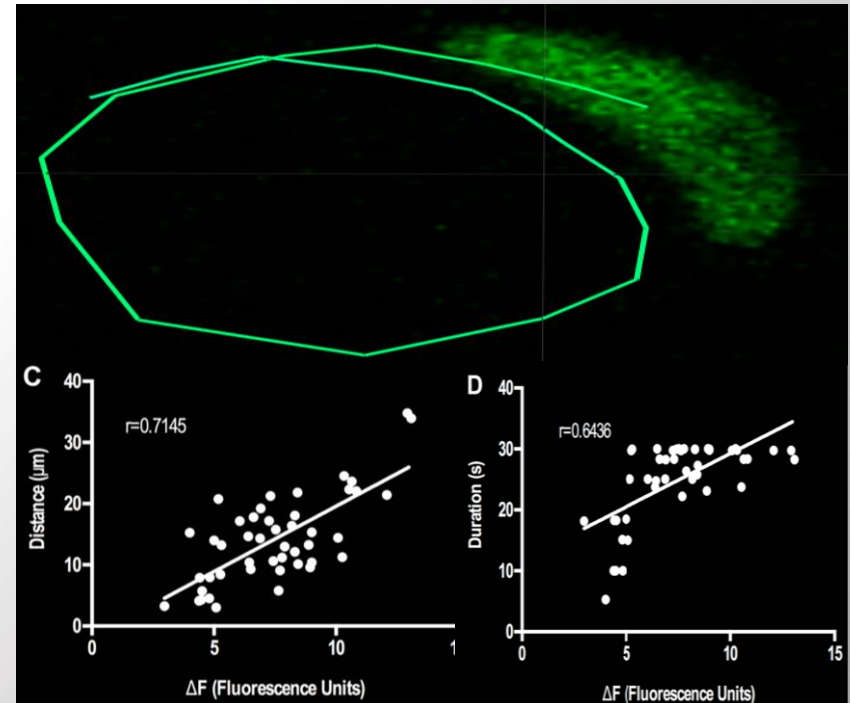
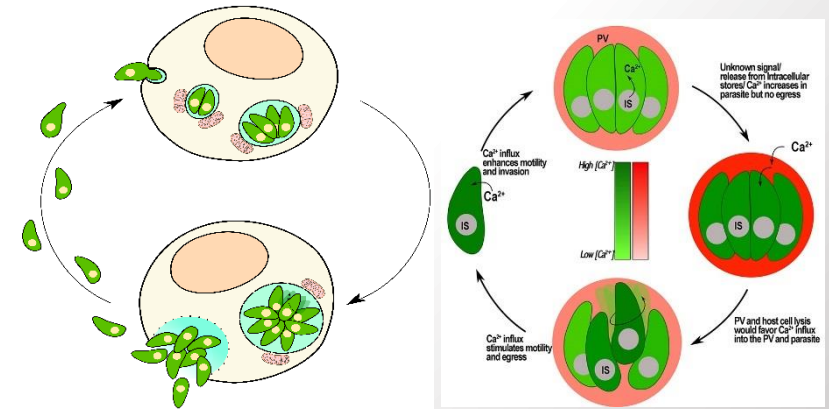
**Research goal:** Determining the role of calcium influx and calcium oscillations in stimulating the switch from a non-motile state to a motile state in *T. gondii*

**How?** Using live-cell imaging and fluorometry determine the contribution of Intracellular Calcium Stores versus Extracellular Calcium Influx in stimulating downstream lytic cycle processes such as motility

**Samples/Model System:** *T. gondii* tachyzoites expressing Genetically Encoded Calcium Indicators and/or loaded with calcium indicators. Calcium release will be stimulated using pharmacological drugs

**The challenge:** The molecules and their role involved in calcium signaling in *T. gondii* are currently unknown.

**Workshop goals:** Learn how to navigate ToxoDB more fluently in search of possible genetic targets.



# Environmental (“E”) effects on vector (“G”) & parasite (“G”) interactions.

Ash Pathak & Courtney Murdock, Dept. of Infectious Diseases, Ecology & the CTEGD, UGA, Athens

**Research goal:** Using next-gen tools such as RNA-seq in combination with hypothesis-driven experiments in the laboratory, but ultimately in field conditions.

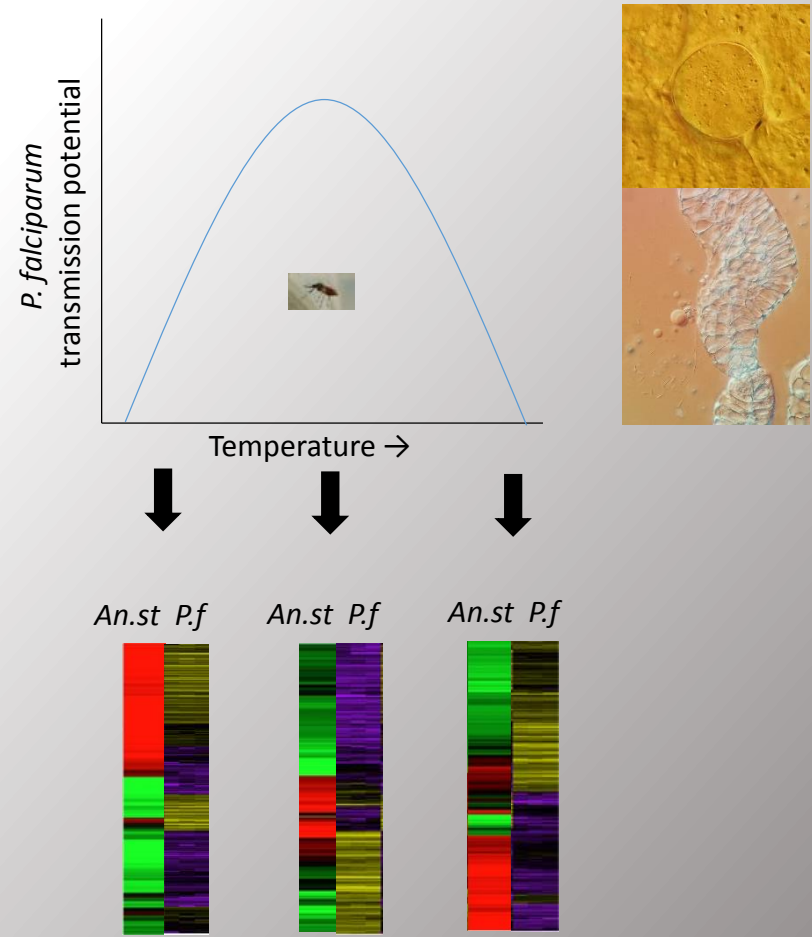
**Samples/Model System:** 1) *An. stephensi* and *P. falciparum*, 2) *Aedes* spp. and arboviruses. Samples: mosquito midguts, salivary glands and whole carcasses.

**The challenge:** 1) Identifying & navigating databases without a degree in bioinformatics or computer science, 2) determining to what extent I trust the outputs and 3) linking individual outputs and/or patterns of outputs to biological function.

**Workshop goals:** 1) to verify that databases aren't rocket science, 2) identify potential gene targets for further validation and functional analyses.



+



# Kristen Knipe, Biotechnology Core Facility Branch Centers for Disease Control and Prevention

**Research goal:** Because I work in the Core Facility, there is no one specific research project. We have customers working with *Plasmodium*, *Leishmania*, and *Cryptosporidium* spp.

**The challenge:** Most of the analysis we do now is with bacterial species.

**Workshop goals:** To enhance my knowledge and understanding of EuPathDB and parasitic genome analysis.



# Annotation of *Cryptosporidium baileyi*

## Shelton Griffith – University of Georgia

**Research goal:** Annotate the *Cryptosporidium baileyi* genome to have a comparative model to compare to human-infecting Cryptosporidiosis because the *C. baileyi* genome can complete its life cycle experimentally tractable chicken eggs unlike *C. parvum/hominis*.

**How?** I will annotate the genome using publically available data found on NCBI and CryptoDB.

**The challenge:** The challenge is getting the most complete annotation possible using the data this is available to me.

**Workshop goals:** To become an expert using CryptoDB.





# Malaria Host-Pathogen Interaction Center (MaHPIC) and Host Acute Models of Malaria to study Experimental Resilience (HAMMER)

Allison Hankus, Emory University

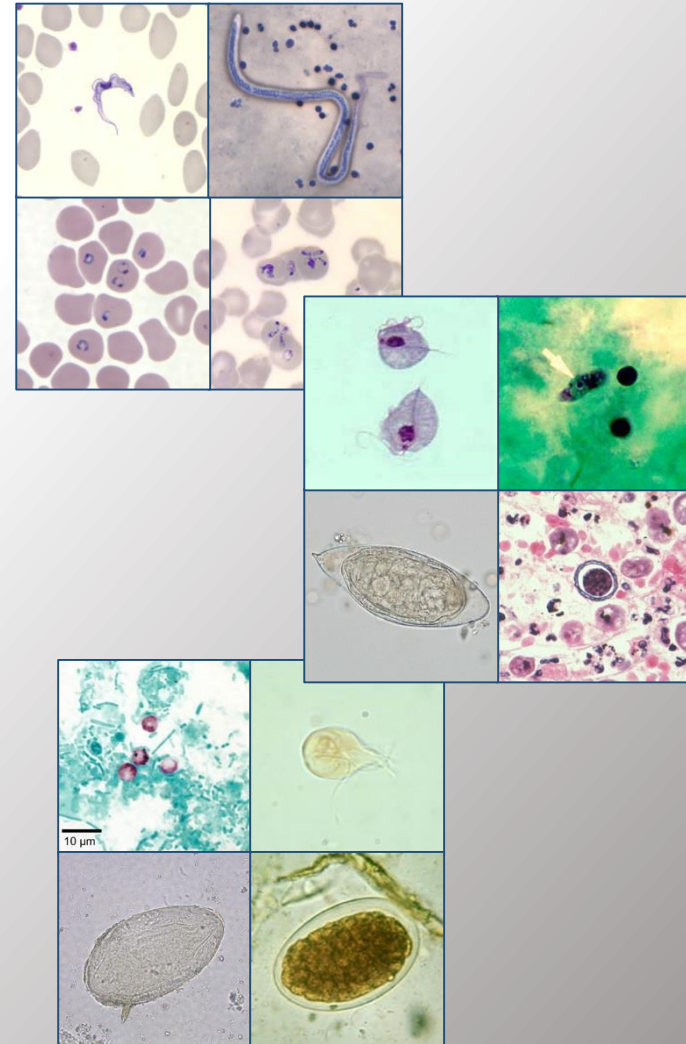
**Research goal:** Identify novel targets in the *Plasmodium* host-pathogen interaction from a system biology approach.

**How?** Perform transgenic experiments targeting genes of interest in the *Plasmodium knowlesi* genome.

**Samples/Model System:** Non human primate models.

**The challenge:** Applying a systems biology approach to understand expression variation through the various *Plasmodium* lifecycles.

**Workshop goals:** To become more familiar with EuPath/PlasmoDB to assist in future proteomics and genomics research.





# Identification of the candidate genes for TSWV resistance in peanut

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**Research goal:** To develop a high density genetic map and fine map the QTL for tomato spotted wilt virus (TSWV) resistance

**How?** By SNP identification using the whole genome re-sequencing (WGS) of the parents (10x to 12x) and the RIL population individuals (3x to 5x)

**The samples:** Leaf samples of the parental genotypes and the RIL population

**The challenge:** To identify the recombination break points and define the recombination bins to be used as markers for marker trait association

**Workshop goals:** To learn how EuPathDB can assist in analyzing my results and informing my research

