

Plant Tracer: An App to quantify Plant Movement

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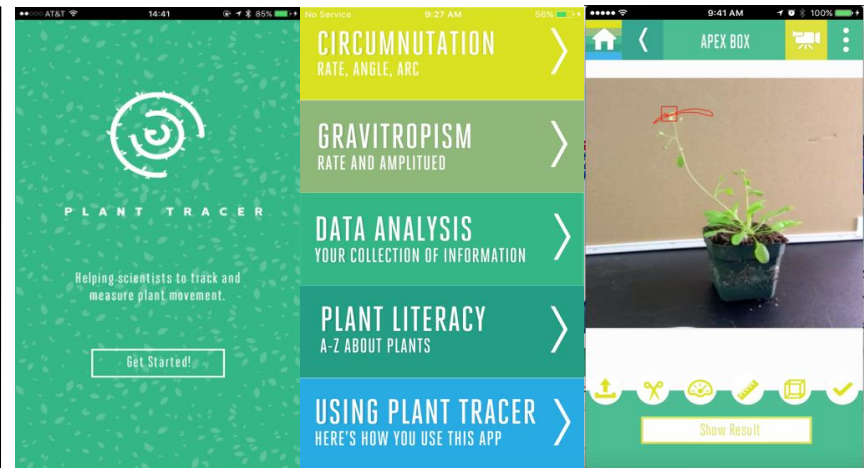
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- Plants are constantly on the move with shoots and roots searching for light, water, nutrients and interacting with their neighbors. The molecular underpinnings of this dynamism is poorly understood.
- We are developing, *Plant Tracer*, an App that enables students and researchers to quantify plant movement using their smart phone or tablets.

- We are using *Plant Tracer* to detect mutants in *Arabidopsis thaliana* (pictured above) that are impaired in Circumnutation (periodic swaying) and gravitropism (movement against gravity) to identify the genes that control these processes.
- We are distributing *Plant Tracer* to our partner universities in a crowd sourced effort to both expand this mutant screen and interest students in plant biology as a way of alleviating the widespread problem of "*Plant Blindness*".

Disentangling the molecular basis of adaptation to hypoxia in an African cichlid fish

PI: Dr. Erika Crispo

Student:
Pamela Suman

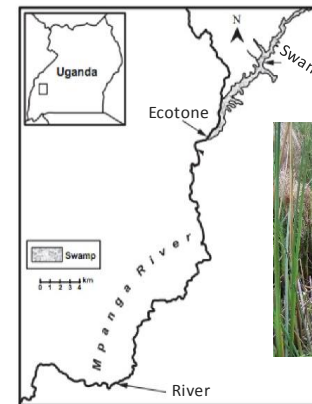
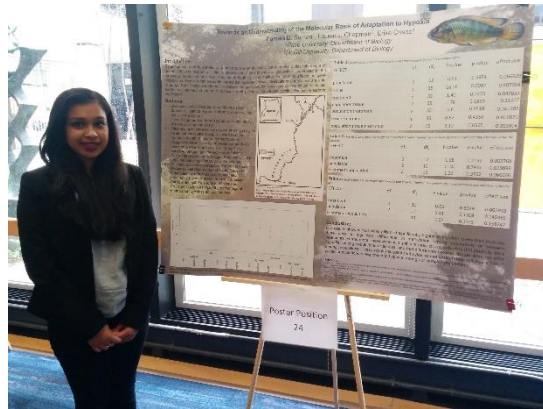


Fig. 1 Map of study sites within the Mpanga River drainage in Uganda. Water flows in the north-south direction. Inset on the map of Uganda depicts the location of the Mpanga River drainage.



Goals:

- Identify genes that are differentially expressed among populations and between oxygen treatments in the lab.
- Use next-generation sequencing to identify methylated cytosines in the genome.
- Find associations between cytosine methylation and gene expression.
- Determine whether these patterns are inherited (evolution) or acquired (phenotypic plasticity).

Evolution can lead to adaptation to the environment, but phenotypic plasticity may also be an adaptive response. Little is known about how phenotypic plasticity is controlled at the molecular level; one way may be through cytosine methylation (5mC) and its effects on gene expression. We test whether hypoxia influences plastic or evolutionary changes in 5mC in a widespread African cichlid, *Pseudocrenilabrus multicolor victoriae*.

Using genetics to inform oyster restoration science

PI: Dr. Erika Crispo

Students:

Chelsi Napoli

Suruj Devi Singh

Andrea Gabriele



Goals:

- Use genetic markers to understand how populations are connected by 'gene flow', or movement of genes via interbreeding among populations
- Determine which functional genes are impacted by the environment, identifying 'stress response' genes that can be used as indicators of stress.

In order to understand the dynamics of a population, it is fruitful to study its genes. Where did the individuals in the population come from? What part of the DNA is functionally important in one population versus another? Addressing these questions is important to fully understand how we can best restore oysters in the Hudson River estuary.

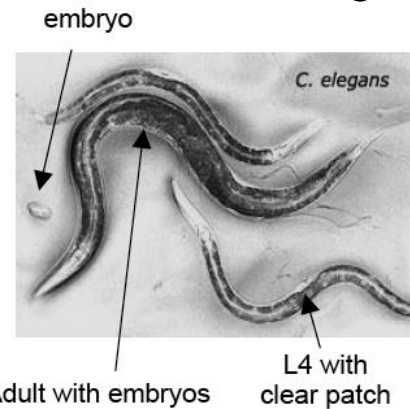
Unraveling the Molecular Basis of Sperm-Egg Fusion and Development

- Participants

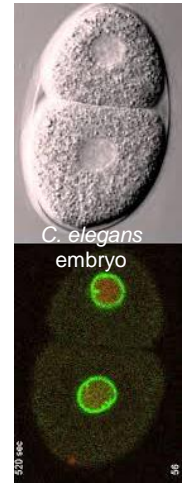
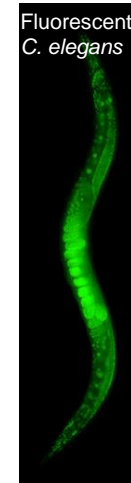
Matthew R. Marcello, Ph.D.

- Yeva Shamailova • Arlena Hui
- Sabah Khurshid • Agata Durda
- Rita Devyatkina • Amber Jacob
- Danielle Cooley

Caenorhabditis elegans



Adult with embryos L4 with clear patch



- Overall Goal/Purpose

- Discover the molecular basis of sperm-egg fusion and early embryo development
- We use the nematode *Caenorhabditis elegans* as a model for reproduction

- Specific Research Aims

- Analyze the gene mutations from infertile patients
- Identify novel genes necessary for fertilization
- Characterize the proteins needed for sperm-egg fusion