Building Collaborative Student Research Consortiums Focused on Science Community Needs: The *Ciliate Genomics* Model

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Project Overview

More college educators today are integrating original research opportunities into their classrooms. However, the sustainability, dissemination, and adoption of these efforts is often challenged by the time required for their implementation, especially for faculty attempting to maintain a productive research program.

The **Ciliate Genomics Consortium** is a collaborative learning community of faculty and students across multiple institutions who share a common goal of annotating the *Tetrahymena* genome, while advancing faculty research agendas.

Undergraduates engage research on gene/protein function as part of their courses in cell biology, molecular biology, biochemistry, or introductory biology, guided by modules designed to explore a range of characteristics. Student-generated results and research reports are immediately disseminated through a website/ database that is linked to the official organism genome database for easy access and use by the broader scientific community. In this way, students make valued contributions directly to an ongoing, larger research effort.

What makes this class-based research sustainable for faculty?

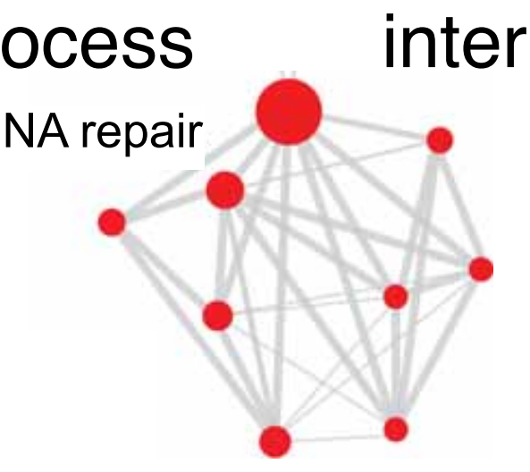
- It fulfills community needs for genome annotation that will persist for many years.
- It advances a faculty member's research through work on relevant genes.
- It is the basis for multi-institutional collaborative research networks of faculty and students who share technological expertise and resources.
- It involves a variety of research activities for integration into a variety of courses at different levels.

How It Works – The Model

1. Faculty select gene sets to investigate with their students - supports their research goals or community needs

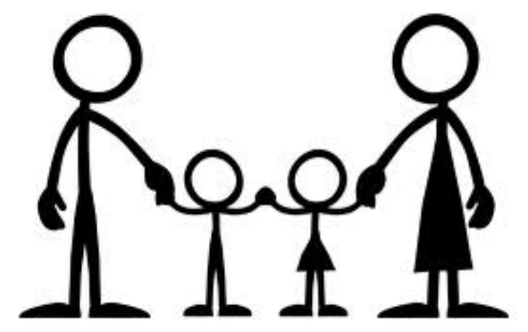
Genes related by:

biol. process

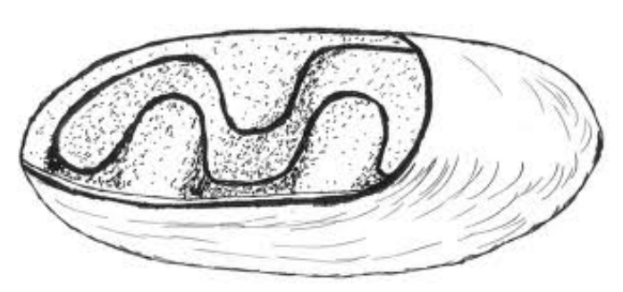


interactions

family



organelle compartment

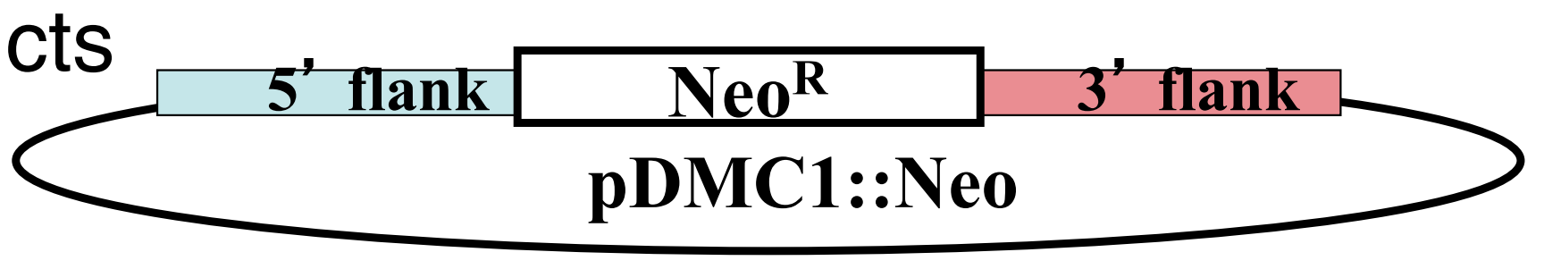


2. Class investigates gene/protein structure or function, learn basic molecular and cell biology techniques

MODULES

(1-9 lab sessions, 4hrs each)

- Test gene structure models (*RT-PCR, sequencing, DNA preparations*)
- Gene expression analysis with different treatments (*RT-PCR or qPCR*)
- Protein localization by GFP-tagging (*cloning and expression techniques*)
- Protein-protein interactions by co-immunoprecipitation (*protein techniques*)
- Engineer gene knockout constructs
- Gene knockout analyses (*test for cellular phenotypes*)



- Bioinformatics-based predictions (*computational techniques to analyze protein functional domains*)

The Model *(cont.)*

3. Students generate data

I. Gene structure and expression modules – examples of student data

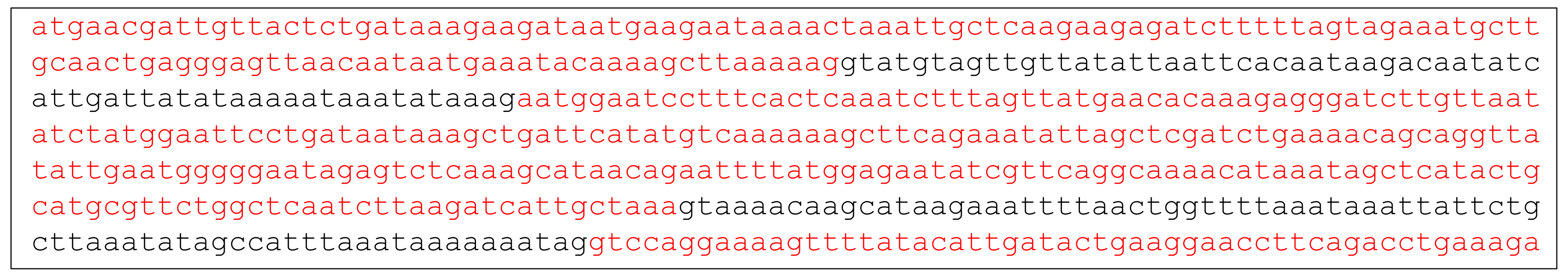


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Fig 1. **Intron identfication.** Introns (black) were identified by cloning and sequencing cDNA.

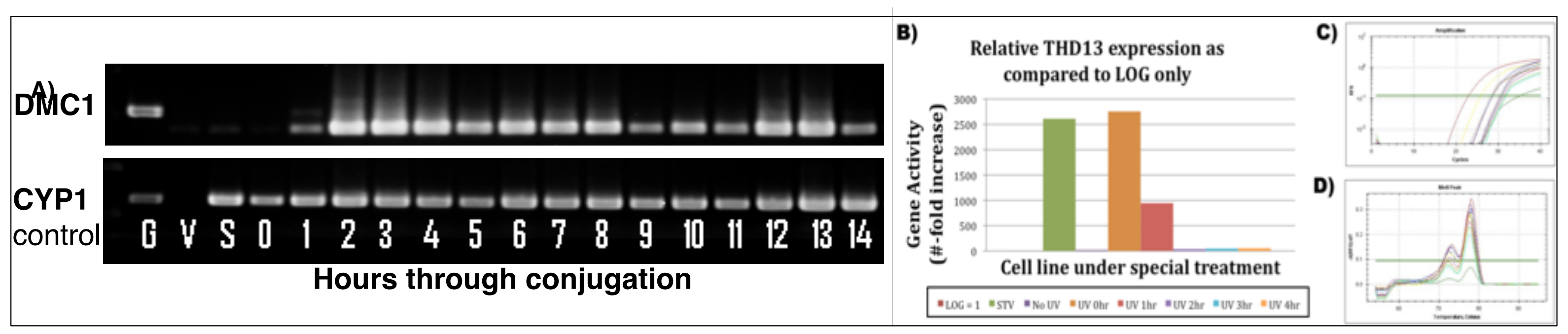


Fig 2. **Expression analysis.** *Tetrahymena* genes were analyzed by conventional (A) and (B,C,and D) real-time qrtPCR.

II. Protein localization module – examples of student data

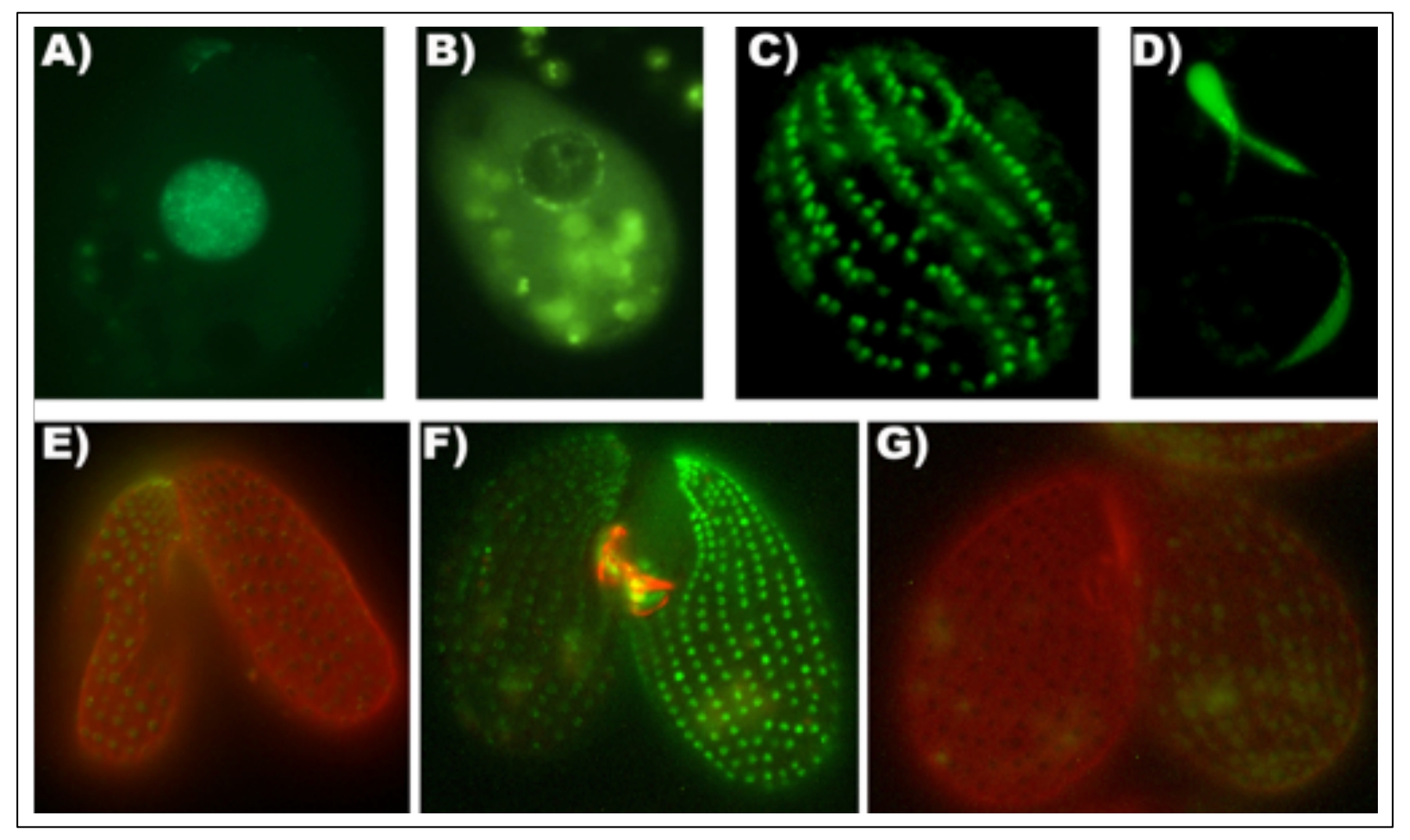
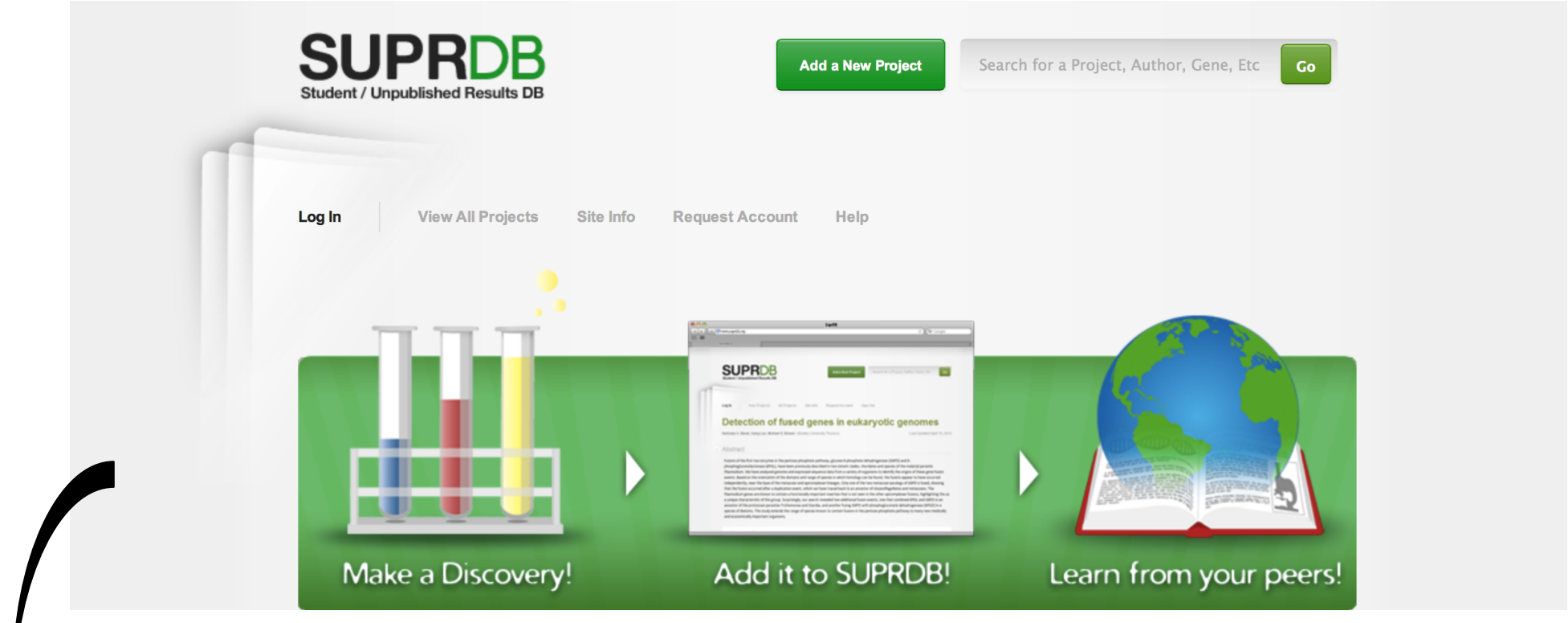


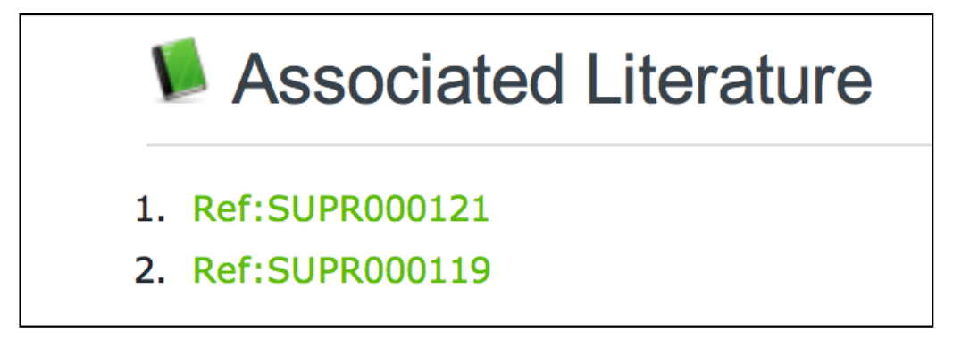
Fig 3. **Localization of GFP and RFP tagged proteins by fluorescence microscopy.** A) GFP-HHP1 localized to chromatin bodies B) GFP-THD14 localized to nucleoli and C) mitochondria. D) GFP-DMC1 in meiotic nuclei. E) KDA3-YFP + TCBP-CFP, F) KDA3-YFP + TetrinA-CFP, and G) KDC2-YFP and TCBP-CFP all in conjugating *Tetrahymena.*

4. Students publish findings on a web database (SUPRdb)



SUPRDB (suprdb.org) is freely available for publication of any student-generated data or research report. It may also be specifically tailored for use by specific model organism communities, if desired. Links can be made from SUPRDB pages to any model organism database.

5. Links to official Tetrahymena Genome Database Wiki are made



Associated Literature

1. Ref:SUPR000121
2. Ref:SUPR000119

Links are easily made due to Wiki format of TGD. Links to gene data pages on SUPRDB are listed under "Associated Literature", thus student investigations are used to reference functional annotations.

6. Data passed to another consortium faculty member - further exploration using different modules.

BACK TO STEP 1

Outcomes

I. GROWTH OF THE CONSORTIUM AND COMMUNITY BENEFIT

- 21 faculty, 21 institutions (state and private universities, liberal arts colleges)
- 18 courses, taught multiple times; intro bio, cell bio, mol bio, biochemistry
- Involved 600+ undergraduates in class-based research
- ***~340 genes investigated; new annotations to genome database***

II. FACULTY SCHOLARSHIP BENEFITS

- 8 peer-reviewed publications; 28 undergraduate authors
- Multiple faculty research collaborations: ***sharing of technical expertise and resources; summer student lab exchanges***

III. PUBLIC RESOURCES

- A web-publishing resource for student results (SUPRdb.org)
- Manual of modules with support materials (*http://tet.jsd.claremont.edu*)

IV. STUDENT RESEARCH ENGAGEMENT

- 24% (av) increase in students pursuing post-grad research (job or school) in year after CGC involvement (Fig. 4)
- Opportunity to web-publish to the research community increased motivation to engage research (assessed by tracking time-on-task; Table 1)

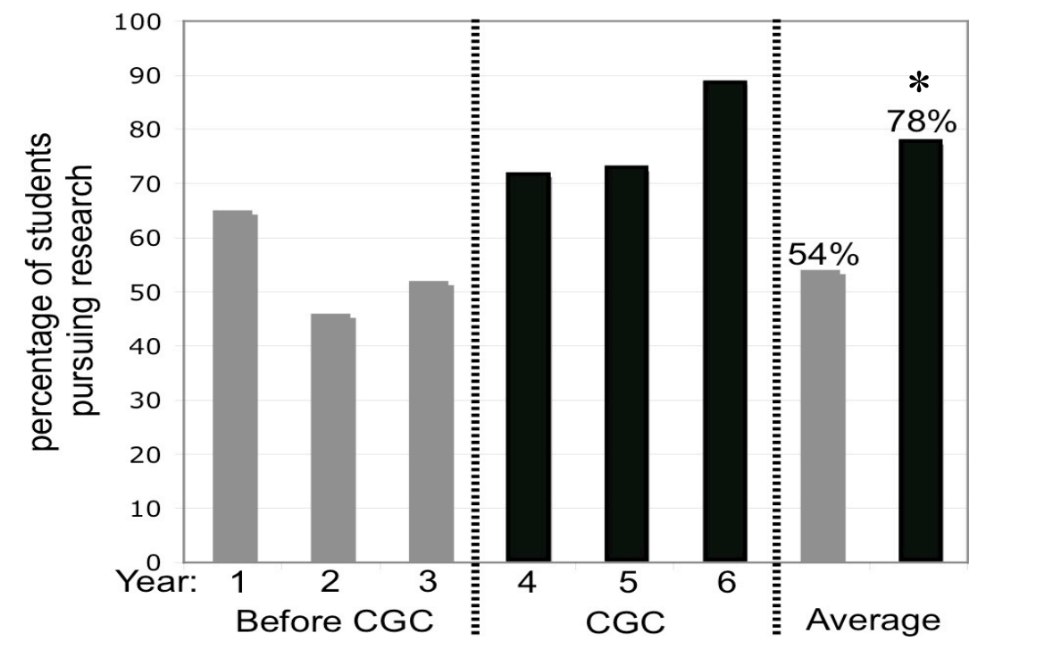


Fig 4. Percentage of students from Bio170L (Molecular Biology) who self-reported pursuing research the year after the course (n=18 for each course; *sig. difference, $p<0.001$, Student's T-Test to compare the means.)

Table 1. Database publishing increased student motivation to engage research tasks. Two courses assessed. 'Control' group, n=49; 'Experimental' group, n=95

Motivation measure	Control (- publ)	Exprmntl (+ publ)	Difference
% students working outside class time[a] (+/- SD)	35 (+/- 6)	83 (+/- 9)	+ 48%**
# hours outside of class, per student, per week[a] (+/- SD)	0.5 (+/- 0.1)	2.2 (+/- 0.46)	+ 440%**
% students working beyond end of course[a] (+/- SD)	2 (+/- 1)	61 (+/- 15)	+59%**
% students pursuing more research within 1 yr[b] (+/- SD)	54 (+/- 7)	67 (+/- 6)	+13%*

[a] Time and student # on-task measurements

[b] Student self-reporting

*$p<0.05$; **$p<0.001$ with Student's T-Test

V. OTHER STUDENT GAINS

CURE surveys (Lopatto et al., 2008) show student gains in multiple areas (Fig. 5).

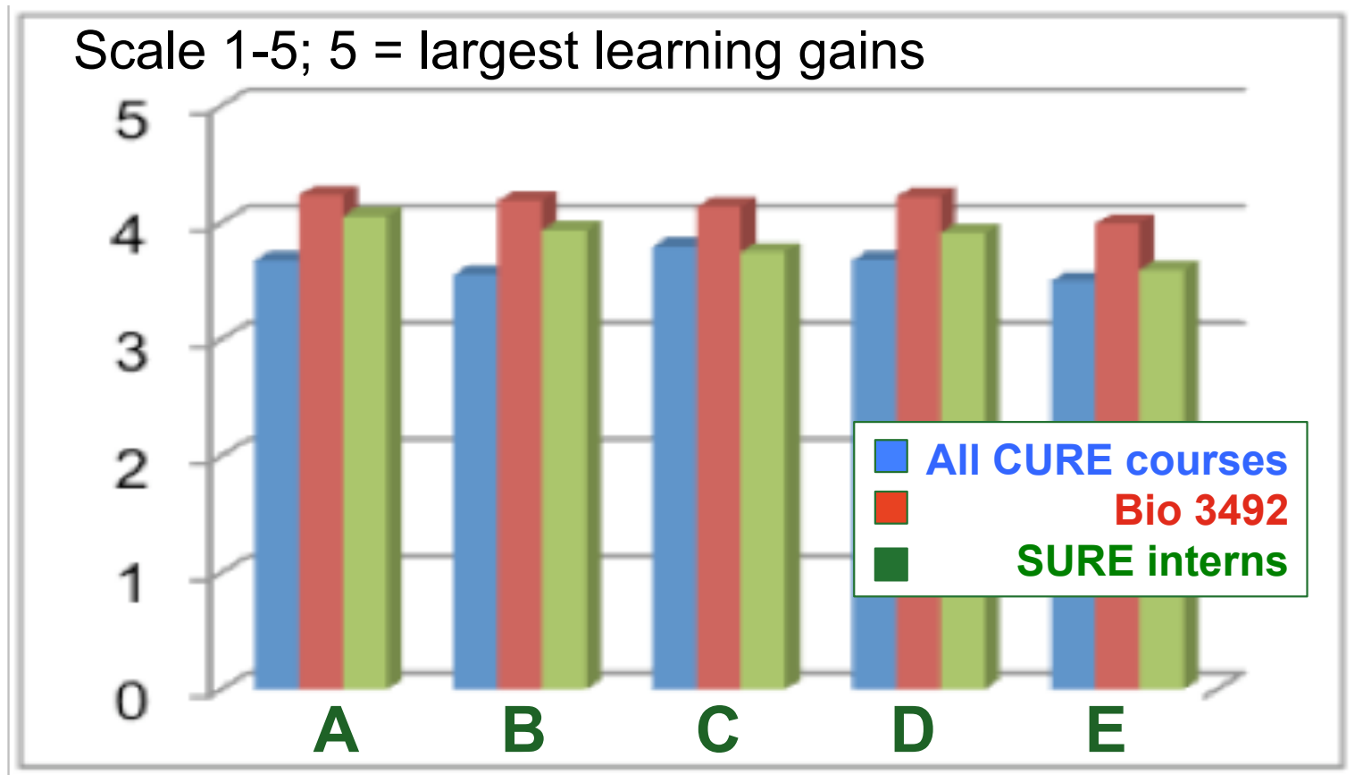


Fig 5. **Cure survey results.** Four years of data was collected from Bio 3492 at Washington University (n=37). Comparison shown is against the average CURE course (blue) and students in summer research internships (SURE).

A) Understanding the research process
B) Readiness for more demanding research
C) Ability to analyze data
D) Understanding how scientists approach problems
E) Understanding how scientists think

Acknowledgements

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