

## MCMS Opportunity for Collaboration

### The Genomics Education Partnership is seeking new members....

The Genomics Education Partnership (GEP) is looking for faculty at primarily undergraduate institutions who teach genetics, molecular biology, etc and are interested in strengthening the work in genomics in these and other courses. The advent of genomic and other high-throughput technologies has changed the way we do research in biology, and hence is changing the way we teach. At Washington University, a new upper level lab course, Bio 4342, "Research Explorations in Genomics" allows students to participate in a collaborative genome sequencing project, each student taking responsibility for sequencing and annotating a segment of DNA. The purpose of the Genomics Education Partnership (GEP) is to make this opportunity available to students on other campuses.

The GEP at present is a consortium of over 30 colleges and universities. You can view the membership list and learn more about the GEP at our website, <http://gep.wustl.edu>. The GEP is funded by the Howard Hughes Medical Institute through a grant to Washington University. The grant supports an annual workshop for faculty who wish to join the GEP, workshops for TA's to work with these faculty, materials support for sequence improvement (with the wet bench work being carried out at the WU Genome Sequencing Center) and computer staff to help manage data and communications. We are now seeking additional faculty interested in joining the GEP through attendance at our **workshop June 8-13, 2008**, at Washington University.

### Four Levels of Participation

Interested faculty at primarily undergraduate institutions are invited to join with us to share teaching materials that 1) use genomics data in problem solving, 2) make use of WU capabilities to generate sequence data (single reads) for wet lab experiments, 3) allow students to participate in annotating sequence data, and 4) allow students to participate in sequence improvement. Students who participate in a collaborative project at levels 3 and 4 can be co-authors on a resulting manuscript, and some campuses might undertake level 2 projects with this goal in mind.

The GEP envisions supporting a number of collaborative projects on sequence improvement and annotation, with sequencing improvement being carried out in the spring semester each year. The raw sequencing data (taken from public data bases) will be posted on the GEP server in student-sized packages, along with instructional materials, training exercises, and computer tools to allow students to take ownership of a segment of DNA. Each student will then be able to call for additional "reads" (sequencing reactions) as needed to finish their segment to a high level of accuracy. The WU Genome Sequencing Center will carry out these sequencing reactions and post the additional data for the student to use. At Washington University, we have found that each student can finish one fosmid (40-50 kb) in the first half of the semester in a lab course meeting 8 hr/wk. (Note that the software we use in sequence improvement, Consed, is designed for unix-based computers, including Mac OS X). Participating in sequence enhancement is challenging, but very satisfying for students, as they contribute new knowledge to the public data bases used by scientists and students alike.

During the second half of the semester, the WU students annotate their fosmid sequence, using BLAST and other tools to identify genes, repetitious sequences, and other features. Students may also use Clustalw to create multiple alignments, doing various evolutionary comparisons, etc. You can choose to participate in annotation without participating in sequence improvement. Because annotation is entirely computer-based, and relies on tools and data bases available on the web, it is easy to incorporate annotation projects into a variety of teaching schedules.

We understand that not every curriculum can afford a full course dedicated to genome sequencing. Therefore, we are developing two less time consuming alternatives. We are preparing some ready-to-go data sets and worksheets so students can experience real problems in genome sequence enhancement and annotation within the context of a more

general advanced lab course, spending a few weeks rather than the whole semester on the project. For some campuses, this alternative may be the most expeditious way to join the project initially. As a second alternative, WU can also run sequencing samples of your favorite DNA, generated by your students at your campus, posting the results on the GEP server for them to analyze. Sample introductory student labs based on generating and using DNA sequence information are posted on the GEP web site, but this service can also be used for experiments of your own design.

### **Growing Experience with Undergraduate Genome Sequencing**

Our current project is to sequence the small (1.2 Mb) dot chromosome of various *Drosophila* species. The biological interest in this problem comes from the fact that the small dot chromosome appears to be heterochromatic in *D. melanogaster* (and several closely related species) but euchromatic in *D. virilis* (and possibly other species). Since most of the same genes are present on the dot in the different species, we are interested in looking at the overall sequence organization for parameters that might dictate the difference in chromatin packaging. Careful annotation of the genes by our students is creating a high-quality resource for a variety of studies. Our goal is to engage the students in publishable work, and the first published paper can be seen at <http://genomebiology.com/2006/7/2/R15>:

Slawson EE, Shaffer CD, Malone CD, Leung W, Kellmann E, Shevchek RB, Craig CA, Bloom SM, Bogenpohl J 2nd, Dee J, Morimoto ET, Myoung J, Nett AS, Ozsolak F, Tittiger ME, Zeug A, Pardue ML, Buhler J, Mardis ER, Elgin SC. Comparison of dot chromosome sequences from *D. melanogaster* and *D. virilis* reveals an enrichment of DNA transposon sequences in heterochromatic domains. *Genome Biol.* 2006; 7(2):R15.

We are currently developing plans to collaborate with scientists working on gut bacteria and on plants (corn).

The easiest way for you to learn more about the GEP is to browse the web site (still being built, but there is a lot already up) at <http://gep.wustl.edu>. The site includes curriculum materials we have used in our workshops, a video tour of the WU Genome Sequencing Center, examples of student work, and a section ("Workshops") that includes the draft schedule and logistics for the June workshop. A bulletin board and wiki have been started. (If you would like faculty access to these sections, let us know and we can provide a temporary name and password.) We have been very impressed with what the students have been able to accomplish, as shown by their final reports and our quality control checks. Our assessment indicated that our students gain a great deal of understanding of "how new knowledge is created in the field," and end the course with a real sense of accomplishment.

### **HHMI Support Covers Faculty and TA Training plus Wet Lab Costs**

The current four-year grant provides funds to bring college faculty from primarily undergraduate institutions to Washington University for a workshop that introduces current teaching materials, allows faculty to gain facility with the computer tools that we use, and allows for joint discussion, sharing, and planning. All travel and local costs are covered. Many of you will already be familiar with BLAST searches, which lie at the heart of the annotation, but will not be familiar with Consed, the program commonly used for sequence improvement - the process of identifying weak and missing data and calling the reads necessary to fill in the gaps. We also have funds that allow each faculty member to send a student to a TA workshop in August or January, and provide a \$1000 honorarium for that student to support their work with you as you implement new materials in genomics into your teaching. Note that the one item that will not be covered by present or proposed grants at WU will be your student computers; it is necessary to run the course in a setting where each student can use a computer with web access.

We hope that many of you will be interested in joining us in this new venture. Becoming a partner commits you to introducing new material in genomics into one or more of your courses, at any of the levels of participation described above (Level 1: working with

prepared genome sequence data and worksheets; Level 2, engaging students in a lab in which each student generates a sample for single-read sequencing and analysis, which we can run for you; Level 3, participating in a *de novo* annotation project; and Level 4, participating in a collaborative project finishing and annotating a genomic sequence). We ask the GEP TA's to generate short implementation and assessment reports, and ask that your students participate in a pre-course / post-course on-line survey. (Sample surveys can be viewed on the GEP web site). (Note that TA support from the grant is provided for the first year implementation only- be sure to recruit some bright juniors who can TA the following year!) Implementation can involve a large lab class, or in the first instance can be done with just a few students in a special topics course. At WU, Bio 4342 typically enrolls 12-14 juniors and seniors.

### **ACTION ITEM**

If you are interested in joining the GEP, now or in the future, please let me know! If you have a colleague whom you think would be interested, please forward this email. The June workshop will be divided into two segments, with annotation being the focus from Sunday evening through noon Wednesday, and sequence improvement ("finishing") being the focus from noon Wednesday to noon Friday. A draft agenda can be seen on the web site. Depending on your experience and interests, you can attend one segment without attending the other. I plan to have both WU Bio 4342 student alumni, and possibly some of our current faculty members in attendance to describe and discuss our collective experiences this year.

We will have space for 20 new members at the annotation workshop and up to 14 at the sequencing enhancement workshop. Let me know your interests, and any questions or concerns you might have. Email is best to start with, and I am happy to arrange times to chat by telephone. Registration is currently underway!

Regards, Sarah Elgin  
HHMI Professor and Viktor Hamburger Professor of Arts & Sciences (Biology)  
Washington University in St. Louis  
[selgin@biology.wustl.edu](mailto:selgin@biology.wustl.edu); Tel. 314-935-5348