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Recent Work

Title
Scientific Research Project Management

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Physical Biosciences Division

Managing Projects and Resources for Effective Project Management
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ACKNOWLEDGEMENT

ESPP2 is part of the Virtual Institute for Microbial Stress and Survival supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics Program:GTL through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.
• VIMSS is Switzerland
• Team Science Approach
• Communications
• Milestones & Budgets
• Dashboards
Leveraging Synergy or “VIMSS is Switzerland”

BP announced in 2006 that it would invest $500 million over the next ten years to establish the Energy Biosciences Institute (EBI).

- **EBI** is a partnership between BP, UC Berkeley, LBNL and the University of Illinois. EBI’s multidisciplinary research teams, including teams lead by **Adam Arkin** and **Terry Hazen**; explore total-system solutions to global energy problems that include the sustainable production of cellulosic biofuels, enhanced biological carbon sequestration, bioprocessing of fossil fuels, biologically-enhanced petroleum recovery, and the social and economic impacts of transitioning to sustainable energy.

U. S. DOE announced in 2007 it will invest up to $375 million in three new Bioenergy Research Centers to accelerate basic research in the development of cellulosic ethanol and other biofuels.

- **BESC** led by **Martin Keller** at DOE Oak Ridge National Laboratory in Oak Ridge, Tennessee. BESC will focus on the resistance of plant fiber to breakdown into sugars and is studying potential energy crops.
- **JBEI** led by **Jay Keasling** at DOE Lawrence Berkeley National Laboratory. JBEI will concentrate on “model” crops and is exploring microbial-based synthesis of fuels beyond ethanol.
Herding Cats
Best Practices and Code of Conduct

To guide our project team members’ encounters, to create synergy while advancing the professionalism and effectiveness of the virtual research team environment, and to help protect our project members from harm, the VIMSS:ESPP Project Manager and Principle Investigators, have adopted Best Practices and Code of Conduct in the following areas:

• Ethics and Confidentiality
• Research and Publications Information Exchange
• Mutual Respect
• Preparation and Completion
• Understanding and Action
Team Science Approach

Steering Committee responsible for ensuring effective and efficient scientific operations. Meet monthly for 1-2 hour video or tele-conference to review resource allocations, budget performance, milestones and timelines, and to assess progress on each task. Convenes annually at: DOE Genomics:GTL Grantees’ Workshop, annual 2-day retreat and ASM working dinner meeting.

Scientific Advisory Panel annual 1 day review ensures that project’s technical development is aligned with related DOE efforts working with the targeted organisms. With project team leaders and DOE assigned Federal Program Manager; discussions include exchange of data and information, the state of the work and possible changes in technical approach or biological focus.

Project Manager facilitates communications, maintains the publications databases and provides co-PIs monthly financial summaries including graphical representation of budget vs. spend plan. Daily to weekly correspondence, calls and meetings with Directors.

VIMSS/ESPP Team Members meet annually at 2-day strategic planning retreat.
Team Science Approach

- **ERSP**
  - Deep field site information
  - Sequencing
  - MicrobesOnline/RegTransBase/Annotation
  - Microbial activity/stress assessment
  - Regulatory & metabolic network inference
  - Conceptual assembly activity Models

- **Push-pull experiments**
- **Field SRB isolation**
- **Stressor Selection**
- **SRB bar-code transposon library construction**
- **Directed mutation of DvH**
- **Two-component system mapping biochem/ChIP chip**

- **Genetic Analysis of SRBs**
  - SRB bar-code transposon library construction
  - Directed mutation of DvH
  - Two-component system mapping biochem/ChIP chip

- **Functional Genomics & Imaging**
  - Bar-code array: Population profiling
  - Targeted proteomics
  - Custom & spotted Arrays: expression mapping/resequencing
  - Laboratory Evolution Co-Culture Function
  - Biofilm Imaging FTIR, cryo-EM, Soft x-ray
  - Single and Consortium Metabolic flux

- **Biomass Production**
  - Microbial assembly development
  - Planktonic biomass Production/monitoring
  - Biofilm biomass Production/monitoring

- **Environmental Monitoring**
  - Phylochip Env. profiling
  - GeoChip/ESPPChip Env. profiling
  - Geochemical profiling
  - Linked gene/16sRNA expression

- **Data QA/QC & Analysis**
  - Comparative Functional genomic analysis
  - Statistical data Analysis for growth & functional gen.
  - EIDR Data management system

**Legend:**
- **AEMC:** LBNL, UWash, UMontana, UMC, ORNL, OU, SNL
- **FGIC:** LBNL, UMontana, UMC, ORNL, OU, SIU
- **CSBC:** LBNL, MIT
- **DvH** protein-protein interactions
- **PCAP**
“The term “e-Science” denotes the systematic development of research methods that exploit advanced computational thinking.”
*Professor Malcolm Atkinson, Research Councils UK e-Science Envoy*

Such methods enable new research by giving researchers access to resources held on widely-dispersed computers as though they were on their own desktops. The resources can include:

- data collections,
- very large-scale computing resources,
- scientific instruments and
- high performance visualization.
noun

a Website that allows collaborative editing of its content and structure by its users.

ORIGIN: coined by programmer Ward Cunningham (1949), from Hawaiian *wiki* ‘quick quick.’
Aim 3.

Field experiments.

3.1 Push-pull experiments at Hanford and Oak Ridge. Technically, the team seems to be adequate to the goals and have sufficient resources that I could see.

Papers under construction

Matthew

1. Cr(VI) toxicity in DvH (internal review)
2. Cr(VI) transcriptomics (in prep)
3. Community analysis during biostimulation (in prep)
4. MR-1 PAS mutant (submitted)
5. Biofilm transcriptomics proteomics (in prep)
6. DvH PAS mutant (in prep)

Dave

1. Stolyar, S., Wall, J., Stahl, D. The physiological role of the Ech hydrogenase in D. vulgaris Hildenborough
3. Walker et al., DP4 genome
4. Walker et al., Gene expression in Methanooccus maripaludis growing in syntrophic association

Terry

- Hazen, T. C., B. Faybishenko… In Prep. In situ bioextraction of chromium at Hanford 100H.

Adam

1. TF History paper submitted
3. LSE analysis paper in construction
4. Close specific marker paper in construction
5. Aiding Erin's on Comparative compendium paper in preparation
6. Aiding on Yinji’s comparative Shewanella paper.
7. Aiding on Biofilm proteomics and microarray analysis
Milestones: Year One 09/30/2008

AEMC
- Obtain previously isolated SRB (especially for DOE contaminated sites), prepare DNA for sequencing submit to JGI.
- Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species.
- Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation & steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.
- Initial tests of multiculture conditions.
- Initiation of co-culture evolution experiments.
- Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co-culture.
- Complete membrane profiling of *D. vulgaris* and *M. maripaludis* in mono culture and together in syntrophic culture.
- Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry and Hanford and Oak Ridge, including initial testing of in well sediment/attachment simulation systems.
- Design larger scale attached stress experiments for comparison with planktonic experiments (transcriptomics).
- Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.

FGIC
- Create and sequence-verify saturating tagged transposon library of *D. vulgaris* and *D. alaskensis* G20.
- Prioritize HK/RR pair characterization with Computational Core.
- Tag and purify HK/RR pairs.
- Initial HK/RR mapping by biochemical assay.
- Initial proof of concept RR/DNA mapping using ChIP-chip.
- Optimize barcode array design.
- Optimize tiling array for transcription start-stop mapping, small RNA detection and ChIP-chip in SRB for G20 and DvH.
- Optimize multiplex gene expression design for G20.
- Complete stress response transcriptomics for G20.
- Initial survey of possible small RNA regulators.
- Complete design and testing of ESPPChip microarray.

CSBC
- Extension of MicrobesOnline for 16SRNA, GeoCHIP/ESPPChip, Phenotype, metagenomic data.
- Complete computational analysis of DvH and G20 and methanogen metabolism.
- Establish flux model analysis methods for mono- and multicultures.
- Developing tiling array and bar-code array design and analysis techniques.
- Complete annotation of Dv Miyazaki, Ds 27774, and one Dv Hanford isolate.
- Complete initial reannotation of DvH.
- Begin design of conceptual model of stress, ED, TEA responses for Hanford Cr and Oak Ridge U contaminated sites.
Work Breakdown Structure by Milestones

Schedule Development & Execution

### VIMS/ESP2 Annual Milestones by Core Groups

<table>
<thead>
<tr>
<th>ID</th>
<th>WBS</th>
<th>Task Name</th>
<th>Predecessors</th>
<th>Resource Names</th>
<th>2007</th>
<th>2008</th>
<th>2009</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>AEMC Year One</td>
<td></td>
<td>Terry Hazen</td>
<td></td>
<td></td>
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<tr>
<td>2</td>
<td>1.1</td>
<td>Obtain previously isolated SRB, prepare DNA for sequencing submit to JGI</td>
<td></td>
<td>Terry Hazen</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>1.2</td>
<td>Begin isolation of SRB from ORNL/FRC and Hampton Sites</td>
<td>Matthew Phillips, Martin Keller</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>1.3</td>
<td>Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species</td>
<td>David Stahl</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>1.4</td>
<td>Full scale biomass production for lab-scale growth experiments; co-culture experiments (perturbation and steady state analysis) using optimized co-culture conditions</td>
<td>Terry Hazen, David Stahl</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>1.5</td>
<td>Initial tests of multi-culture conditions</td>
<td>David Stahl, Martin Keller, Joe Zhou</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>1.6</td>
<td>Initiation of co-culture experiments</td>
<td>Kristina Hilslander</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>1.7</td>
<td>Optimize transposon strain library competition experiments for readout by bar code arrays both in monoculture and co-culture</td>
<td>Judy Wall, Adam Deutschbauer</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>9</td>
<td>1.8</td>
<td>Complete membrane profiling of D. vulgaris in monoculture</td>
<td>Terry Hazen</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>1.9</td>
<td>Complete membrane profiling of M. maripaludis in monoculture</td>
<td>Terry Hazen</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>11</td>
<td>1.10</td>
<td>Complete membrane profiling of D. vulgaris / M. maripaludis in syntrophic culture</td>
<td>David Stahl</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>1.11</td>
<td>Design of push-pull experiments and initial characterization of free bacterial populations and geochemistry</td>
<td>Terry Hazen, Martin Keller, Matthew Phillips, Joe Zhou</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>2</td>
<td>FGIC Year One</td>
<td>Jay Keesling, Alan Druff</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>14</td>
<td>2.1</td>
<td>Create and sequence-verify saturating tagged transposon library of D. vulgaris and D. alaskensis G20</td>
<td>Judy Wall</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>2.2</td>
<td>Prioritize HK/RR pair characterization with Computational Core</td>
<td>Andria Muthupadhyay, Adam Deutschbauer</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>2.3</td>
<td>Initial HK/RR mapping by functional assay</td>
<td>Andria Muthupadhyay</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>2.4</td>
<td>Tag and purify HK/RR base pairs</td>
<td>Andria Muthupadhyay</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>2.5</td>
<td>Initial proof of concept RR DNA mapping using CIP-chip</td>
<td>Adam Deutschbauer</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>2.6</td>
<td>Optimize barcode array design</td>
<td>Adam Deutschbauer</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>20</td>
<td>2.7</td>
<td>Optimize tiling arrays for transcription start-site mapping, small RNA detection, and CIP-chip in SRB for G20 and D/H</td>
<td>Adam Deutschbauer, Kelly Bender</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
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</table>

Project: Year 5 Milestones

<table>
<thead>
<tr>
<th>Task</th>
<th>Progress</th>
<th>Rolled Up Task</th>
<th>Project: Year 5 Milestones</th>
<th>Date: Tue 4/17/07</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milestone</td>
<td></td>
<td>Rolled Up Milestone</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Summary</td>
<td></td>
<td>Rolled Up Progress</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Dashboards - defined

“A dashboard is a visual interface that provides at-a-glance views into key measures relevant to a particular objective or business process.”

Key Attributes:
✓ Graphically focus attention on key trends, comparisons and exceptions
✓ Display only relevant data
✓ Inherently contain predefined conclusions

Note: Collecting user requirements is KEY

from ‘Excel 2007 Dashboards & Reports for Dummies’ by Michael Alexander
Information Dashboard Design:
The Effective Visual Communication of Data

About the Author

Stephen Few has worked for over 20 years as an IT innovator, consultant, and teacher. Today, as Principal of the consultancy Perceptual Edge, Stephen focuses on data visualization for analyzing and communicating quantitative business information. He teaches in the MBA program at UC Berkeley. You can learn more about Stephen’s work and access an entire library of articles at www.perceptualedge.com.
Dashboards - bad examples

Common Problems:

- Positioning content in places that don’t fit its importance
- Positioning content in places that fail to support its use
- Including items that serve no useful purpose
- Sizing content larger than it deserves
- Separating content excessively
- Visually featuring content & other items more than they deserve
- Failing to link contents & other items that are related
- Visually suggesting links between unrelated content
- Enforcing a rigid symmetrical grid
Dashboards - bad examples

Here are a few of this graph’s problems:

- There are several distracting (and detracting) visual effects: the reflection of light, transparency, and 3-D effects on the bars (and squares in the legend) add no value.

- The bars have been overlayed on one another, which partially obscures the first two sets and gives them different visual salience. Because the bars for the year 2008 appear in the forefront of each cluster, their greater importance is implied, which was probably not intended. While I can’t be sure, the graph’s original post date of 2005, suggests that these values are projections, albeit unbelievably volatile ones. Without knowing more about the data, I can’t say for sure, but the 2006 projections are probably the surest and most relevant, yet they are partly obscured by the other two years.

- Although the gridlines in this graph are thin and light, because these values are projections, we probably don’t need to know precise values. As such, the gridlines are not necessary.

- The bar colors are more intense than they should be. The use of high-intensity colors should be reserved for making important data salient. Regular data should be shown using less intense colors. After all, when you display all of your data to stand out, nothing does.

- The continents have not been ordered in a logical way. At the very least they could have been alphabetized, but, as we'll see below, there's almost always a better way to order your data.

- Although bar graphs are great for showing and comparing the magnitudes of different variables, they are inferior to lines for showing how the values change through time. Because the pattern of change through time is likely more important than the actual magnitudes of the individual values, a line graph would have worked better.
Dashboards - solutions

Line graphs make it especially easy to see the patterns of change and to focus on trends. To avoid the clutter of seven lines on a single graph, I used “small multiples,” a series of seven small graphs, which vary by region, but otherwise look and work the same. Small multiples may be arranged vertically (shown above), horizontally, or in a matrix. Because this information is a projection (and so the exact magnitudes are probably not as important), I have made the assumption that the graphs should be arranged to make it easiest to compare the patterns of change for the various regions, which is why I aligned the years by arranging the graphs vertically. If the magnitudes of the lines were more important, then a horizontal layout would have been preferable, for easier magnitude comparisons. Notice that the horizontal label (showing the years) is only shown on the very bottom of the graph. This is all that’s necessary to show which part of each line belongs to which year. Duplicating these labels for each graph would have resulted in redundancy and clutter.

I have reordered the continents based on the 2006 values, with the highest at the top and the lowest at the bottom. I based the sequence on the 2006 value because, as these values are projections, the first year is likely to be most reliable and of greatest interest to decision-makers.

This new design is clean and clear—free of the visual distractions in the first two examples. Anyone viewing the graph would be able to examine the data, focusing perhaps on the large declines that are projected to occur in Europe and Africa, instead of the pretty, shiny bars.

Reduce the non-data ink
Enhance the data ink
Dashboards - evil pies

Let’s examine another ineffective use of pie charts. Edward Tufte once said that “the only worse design than a pie chart is several of them, for then the viewer is asked to compare quantities located in spatial disarray both within and between pies” (Edward Tufte, *The Visual Display of Quantitative Information*, Graphics Press, 1983, p. 178.) I share Tufte’s opinion that this is an ineffective way to compare multiple part-to-whole relationships.

![Pie charts for different years showing company data](image)

Try to follow the changes of these various companies and how they compare to one another through time. It is nearly impossible. Notice how easily you can do it, however, using the following display:

![Bar charts for different years showing company data](image)
Dashboards - evil pies

My Analysis

The data is great but the display is a jumbled mess.

A Solution

Here's the same data displayed simply and clearly:

### Percentage of Analytic Computer Usage by Type

<table>
<thead>
<tr>
<th>Type</th>
<th>Percent of Enterprise</th>
</tr>
</thead>
<tbody>
<tr>
<td>IT</td>
<td>Consumer 0.06%</td>
</tr>
<tr>
<td>Application Development</td>
<td>Producer 1.96%</td>
</tr>
<tr>
<td>Data Mining</td>
<td></td>
</tr>
<tr>
<td>Metadata Design</td>
<td></td>
</tr>
<tr>
<td>Power User</td>
<td>Consumer 0.79%</td>
</tr>
<tr>
<td>Business User</td>
<td>Producer 21.50%</td>
</tr>
<tr>
<td>Consumer 37.24%</td>
<td></td>
</tr>
<tr>
<td>Extended Enterprise User</td>
<td>Consumer 37.24%</td>
</tr>
<tr>
<td>(Extranets/B2B/B2C and mobile/wireless)</td>
<td>Producer 0.79%</td>
</tr>
<tr>
<td>Casual User</td>
<td>Producer 4.25%</td>
</tr>
<tr>
<td>(Dashboards and enterprise reporting)</td>
<td></td>
</tr>
<tr>
<td>Business User</td>
<td></td>
</tr>
<tr>
<td>(Scorecards, performance mgmt, business reporting, and packaged apps)</td>
<td>Producer 1.96%</td>
</tr>
<tr>
<td>Power User</td>
<td></td>
</tr>
<tr>
<td>(Statistical analysis, analytical reporting and OLAP)</td>
<td></td>
</tr>
<tr>
<td>IT User</td>
<td></td>
</tr>
<tr>
<td>(Application development, data mining and meta data design)</td>
<td></td>
</tr>
</tbody>
</table>

Source: Giga Research, a wholly-owned subsidiary of Forrester Research, Inc.

Reduce the non-data ink
Enhance the data ink

I could have used colors but, frankly, this graph doesn't need them. Limiting it to black and white allows you to photocopy this useful information and pass it on without any loss of quality. Can you imagine what the original pie chart would look like if you photocopied it in black and white?
## FY08 Milestones: AEMC

<table>
<thead>
<tr>
<th>Task</th>
<th>% Complete</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Obtain previously isolated SRB, prepare DNA for JGI sequencing.</td>
<td>70%</td>
<td>D. vulgaris Hanford HBLS, D. hanfordii HMW + others</td>
</tr>
<tr>
<td>Syntrophic co-culture assemblies: Growth optimization &amp; stability studies: Alternative Dv strains/species. BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.</td>
<td>30%</td>
<td>need update</td>
</tr>
<tr>
<td>Initial tests of multiculture conditions.</td>
<td>30%</td>
<td>need update</td>
</tr>
<tr>
<td>Initiation of co-culture evolution experiments.</td>
<td>70%</td>
<td>U WA &amp; OK</td>
</tr>
<tr>
<td>Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.</td>
<td>50%</td>
<td>ongoing</td>
</tr>
<tr>
<td>Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and in syntrophic culture. Design push-pull experiments &amp; initial characterization of site bacterial populations and geochemistry @ Hanford &amp; ORNL, including initial testing of in well sediment/attachment simulation systems. Design larger scale attached stress experiments for comparison w/ planktonic *experiments (transcriptomics). Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16S RNA Phylochip, Geochip, and realtime Q-PCR.</td>
<td>70%</td>
<td>need update</td>
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<tr>
<td></td>
<td></td>
<td>need update</td>
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<tr>
<td></td>
<td></td>
<td>need update</td>
</tr>
<tr>
<td></td>
<td></td>
<td>need update</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CSBC: Metagenome FRC grdtwater - DNA sequencing complete, annotation completed, draft circulating.</td>
</tr>
</tbody>
</table>

Oct 07 - Mar 08  Apr - Sep 08

### Key Performance Indicators (KPI) ~

essential tasks draw attention to problem areas
Dashboard Milestone Reports

ESPP2 Milestones

Main Page > ESPP2 Milestones

ESPP Wiki Toolbar

VIMSS/ESPP2 Milestones Summary

Projected Milestone Date: 09/30/2008

AEMC

- Obtain previously isolated SRB (especially for DOE contaminated sites), prepare DNA for sequencing submit to JGI.
- Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species.
- Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation & steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.
- Initial tests of multiculture conditions.
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- Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co-culture.
- Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and together in syntrophic culture.
- Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry and Hanford and Oak Ridge, including initial testing of in well sediment/attachment simulation systems.
- Design larger scale attached stress experiments for comparison with planktonic ‘experiments (transcriptomics).
- Complete contrast/comparative studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.

FY08 1st 6 months
## Dashboard Milestone Reports

<table>
<thead>
<tr>
<th>FY08 Milestones: AEMC</th>
<th>% Complete</th>
<th>as of 04/01/08</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Obtain previously isolated SRE, prepare DNA for JGI sequencing.</td>
<td>70%</td>
<td></td>
<td>D. vulgare Hanford HGYS, D. hancockii HGWS + others</td>
</tr>
<tr>
<td>Syntrophic co-culture assemblies: Growth optimization</td>
<td>30%</td>
<td></td>
<td>need update</td>
</tr>
<tr>
<td>&amp; Stability studies: Alternative Dy strains/species</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BMP: steady-state growth stress-perturbed co-culture response experiments for different SRE/methanogen pairs</td>
<td>70%</td>
<td></td>
<td>need update</td>
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<tr>
<td>Initial tests of multiculture conditions.</td>
<td>30%</td>
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<td>U WA &amp; OK</td>
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<td>Initiation of co-culture evolution experiments.</td>
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<td>ongoing</td>
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<tr>
<td>Optimize monoculture and co-culture transposon strain library complement experiments for bar code array read-out.</td>
<td>50%</td>
<td></td>
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<tr>
<td>Complete membrane profiling of D. vulgare and M. maripaludis in mono-culture and in syntrophic culture</td>
<td>need update</td>
<td></td>
<td>Amanita</td>
</tr>
<tr>
<td>Design push-pull experiments &amp; initial characterization of eubacterial populations and geochemistry @ Hanford &amp; CNRL, including initial testing of in well sediment/attachment simulation systems.</td>
<td>need update</td>
<td></td>
<td>under way</td>
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<tr>
<td>Design larger scale attached stress experiments for comparison with planktonic &quot;experiments&quot; (transcriptomics).</td>
<td>70%</td>
<td></td>
<td>Matt Fields</td>
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<td>Complete contrast/comparative studies of groundwater and sediment ecoinformatics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries). 16SRNA Phylochip, Geochip, and realtime Q-PCR.</td>
<td>50%</td>
<td></td>
<td>CSSIC: Metagenome FRC graminet - DNA sequencing complete, annotation completed, draft circulating.</td>
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</table>

Size of this preview: 776 x 530 pixels

Full resolution (2200 x 1700 pixel, file size: 276 KB, MIME type: image/jpeg)

ESPP2 Milestones > Image AEMC.jpg > Main Page > ESPP2 Milestones > Image AEMC.jpg

File history

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- (del) 30.09, 7 April 2008 . Aush, A (Talk | contribs) . 2020+1700 (262,122 bytes)
- Upload a new version of this file
- Edit this file using an external application

24
Cost Estimation & Budget Oversight

### Escalation Rates

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<th>Rate Type</th>
<th>FY07</th>
<th>FY08</th>
<th>FY09</th>
<th>FY10</th>
<th>FY11</th>
<th>FY12 (est.)</th>
<th>5 Year Totals</th>
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<td>LBNL Labor</td>
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<td>LBNL Supplies &amp; Other Expenses (OMB)</td>
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<td>Total Direct Costs, LBNL</td>
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<td>Total Indirect Costs, LBNL</td>
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<tr>
<td>ORNL</td>
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### Renewal Budget Assumptions

- **LBNL**
  - Labor
  - Supplies & Other Expenses
  - Equipment, Supplies & Other Expenses (OMB)
  - Total Direct Costs, LBNL
  - Total Indirect Costs, LBNL
  - Total Direct Costs less Other Inst. Indirect Costs, LBNL

- **SNL**
- **ORNL**
- **ESP2**

### Original Project Budget Assumptions

- **LBNL**
- **SNL**
- **ORNL**

### Rate Type

- **Escalation Rates**
- **Trends**

### Other Information

- **LBNL Forward Pricing Rates**
- **Effective October 1, 2006**
- **Revision 5**

#### Institutional Rates

- **General and Administrative**
  - G&A (Eff/Ext) Rate: OFF
  - Site Support (Fabrication) Rate: FAB
- **Operating**
  - Animal Care
  - General Rate: GR1

#### KIP Rate

- **Labor**
- **Supplies & Other Expenses (OMB)**
- **Construction Projects (OECM)**

#### Payroll Burden (Base: Delivered effort cost only)

- **Career & Term Employees**
- Post Docs, Visiting Post Docs, Limited Employees, and Visiting Researchers
- GSRA
- Students/Retired Employees working variable time
- Summer Faculty

### Fringe Benefits Only (Base: FTE gross pay only)

- **Career & Term Employees**
- Post Docs, Visiting Post Docs, Limited Employees, and Visiting Researchers
- GSRA
- Students/Retired Employees working variable time
- Summer Faculty

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<tr>
<th>Rate Type</th>
<th>FY07</th>
<th>FY08</th>
<th>FY09</th>
<th>FY10</th>
<th>FY11</th>
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<td>J. (100.60%)</td>
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<td>O. (103.34%)</td>
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<td>X. (103.34%)</td>
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<td>Y. (100.60%)</td>
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<td>Z. (100.43%)</td>
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</tbody>
</table>
“How then do we make it easy for people to compare related sets of values when they are associated with different units of measure? …

The … most obvious is to place them in separate graphs, positioned close to one another so that the patterns in each can be compared to one another, but magnitude comparisons will be discouraged.” Stephen Few
## FY08 Milestones: AEMC

<table>
<thead>
<tr>
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<th>Notes</th>
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<tbody>
<tr>
<td>70%</td>
<td>D. vulgaris HfS/L, D. halophila HMW others (need update)</td>
</tr>
<tr>
<td>30%</td>
<td>D. vulgaris HfS/L, D. halophila HMW others (need update)</td>
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<tr>
<td>70%</td>
<td>OPAL, U WR &amp; OK (ongoing)</td>
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<tr>
<td>N/A</td>
<td>Protonics not funded (under way)</td>
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<td>70%</td>
<td>Matt Fields - under way</td>
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## FY08 Milestones: FGIC

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<tbody>
<tr>
<td>50%</td>
<td>CSIC: Metaprotome PRC (greater) - DNA sequencing complete, annotation complete, draft circulating.</td>
</tr>
</tbody>
</table>

## FY08 Milestones: Metabolomics
- Metabolomics: Utilize 13C/12C labeling to obtain metabolic response to previously studied stresses in D. vulgaris.
- Methionine Biosynthesis Pathway in D. vulgaris: targeted study.
- Complete CEMS profile for DHV metabolites (ESP21 Milestone) Method published. Study ongoing.

## FY08 Milestones: FGIC
- Create and sequence-verify saturating tagged transposon libraries for:
  - Shewanella oneidensis
  - D. desulfuricans G20
  - Prioritize HR/RR pair characterization w/ CSBC.
  - Tag and purify HR/RR pairs.
- Initial HK/RR mapping by biochemical assay.
- Initial proof of concept RR/EDA mapping using CHIP-chip.
- Optimize barcode array design.
- Optimize tiling array for transcription start-stop mapping.
- G20: Optimize multiplex gene expression design.
- G20: Complete stress response transcriptomics.
- Initial survey of possible small RNA regulators.
- Complete ESP21 microarray design & testing.
- Gen expression compendium.

<table>
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<tr>
<td>30%</td>
<td>AmyDE</td>
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<tr>
<td>70%</td>
<td>Initial HK/RR mapping by biochemical assay.</td>
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<tr>
<td>50%</td>
<td>Initial proof of concept RR/EDA mapping using CHIP-chip.</td>
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<tr>
<td>50%</td>
<td>Optimize barcode array design.</td>
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<tr>
<td>100%</td>
<td>Optimize tiling array for transcription start-stop mapping.</td>
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<tr>
<td>10%</td>
<td>G20: Optimize multiplex gene expression design.</td>
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<td>5%</td>
<td>G20: Complete stress response transcriptomics.</td>
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<tr>
<td>30%</td>
<td>Initial survey of possible small RNA regulators.</td>
</tr>
<tr>
<td>5%</td>
<td>Complete ESP21 microarray design &amp; testing.</td>
</tr>
</tbody>
</table>

## FY08 Milestones: CSBC
- Extension of MicrobesOnline for: 16S RNA.
  - GeoCHIP/ESP21Chip: 9% working w/ ORNL to incorporate Seleka data. Usefulness will depend on human (undergrad) annotation.
- Virtuoso:
  - Phenotype: 50% Waiting on data.
  - Metagenomic data: 50% High potential value & high interest.
  - Developing tiling array and core/constitutive design.
  - Complete annotation of D. Mivialis, D. 2777A, and D. Halophila isolate: 50% Waiting for these + other sequences before expression array & analysis techniques.
  - Complete reannotation of D. Halophila isolate: 50% Critical Task: Additional data to include? Tiling array?
- Critical Task: Participating in experimental design - conceptual model depends on data to be collected.
Acknowledgements

Adam P. Arkin and Terry C. Hazen, Directors

Applied Environmental Microbiology Core:
• LBNL, Terry C. Hazen
• University of Washington, David Stahl
• Montana State University, Matthew Fields

Functional Genomics and Imaging Core:
• LBNL, Jay Keasling and Aindrila Mukhopadhyay
• University of Missouri-Columbia, Judy Wall
• Southern Illinois University, Kelly Bender
• Sandia National Laboratory, Anup Singh
• Oak Ridge National Laboratory, Martin Keller
• University of Oklahoma, Jizhong (Joe) Zhou

Computational and Systems Biology Core:
• LBNL: Adam P. Arkin, Inna Dubchak, Paramvir Dehal
• MIT: Eric Alm

ACKNOWLEDGEMENT

ESPP2 is part of the Virtual Institute for Microbial Stress and Survival supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics Program:GTL through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.