Scientific Research Project Management

ESPP2 Environmental Stress Pathway Project

DOE GENOMICS:GTL ACCELERATING DISCOVERY FOR ENERGY AND ENVIRONMENT

VIMSS Virtual Institute for Microbial Stress and Survival | Massachusetts Institute of Technology | Missouri | University of Washington | Montana State University | Southern | Oklahoma | Sandia National Laboratories | Oak Ridge National Laboratory | Berkeley | 75 | http://vimss.lbl.gov

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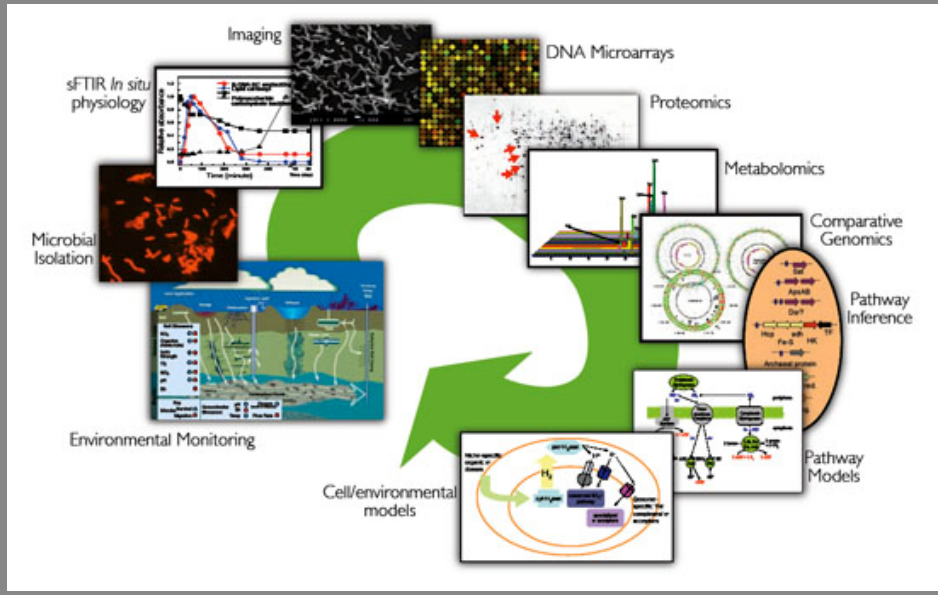
Physical Biosciences Division



Managing Projects and Resources for Effective Project Management

June 5-6, 2008 | Philadelphia, PA

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.

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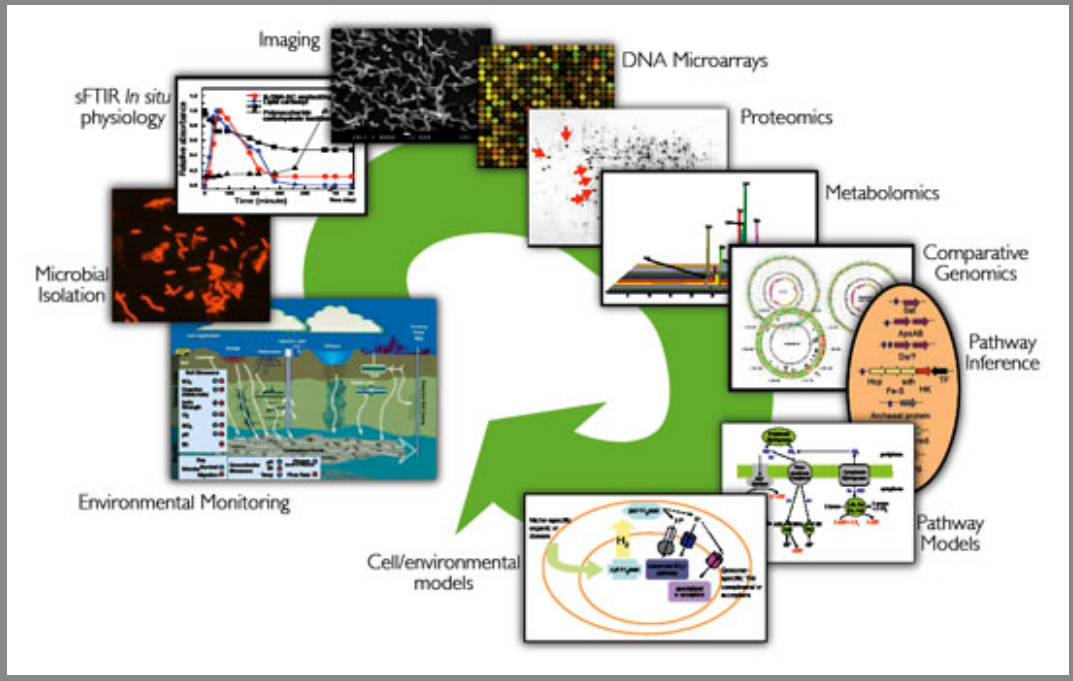
VIMSS Virtual Institute for Microbial Stress and Survival | Massachusetts Institute of Technology | Missouri | University of Washington | Montana State University | Oklahoma | Sandia National Laboratories | Oak Ridge National Laboratory | Berkeley | http://vimss.lbl.gov

- VIMSS is Switzerland
- Team Science Approach
- Communications
- Milestones & Budgets
- Dashboards



VIMSS:ESPP Then & Now

ESPP2 Environmental Stress Pathway Project

DOE GENOMICS:GTL ACCELERATING DISCOVERY FOR ENERGY AND ENVIRONMENT

JOINT BIOENERGY INSTITUTE

Clean, Green, Renewable Energy

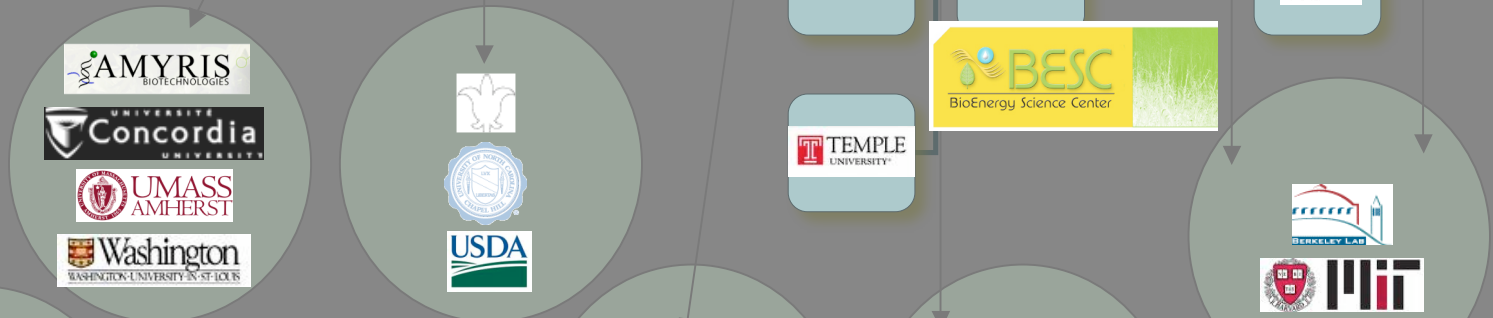
VIMSS — Adam P. Arkin, Terry C. Hazen

Energy Biosciences Institute

AEMC — Terry C. Hazen

FGIC — Jay Keasling, Aindrila Mukhopadhyay

CSBC — Adam P. Arkin, Paramvir Dehal



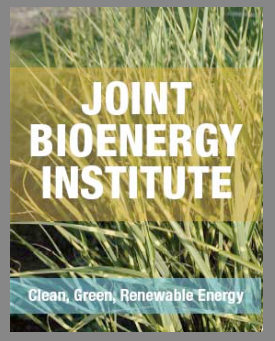
Leveraging Synergy or "VIMSS is Switzerland"

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.



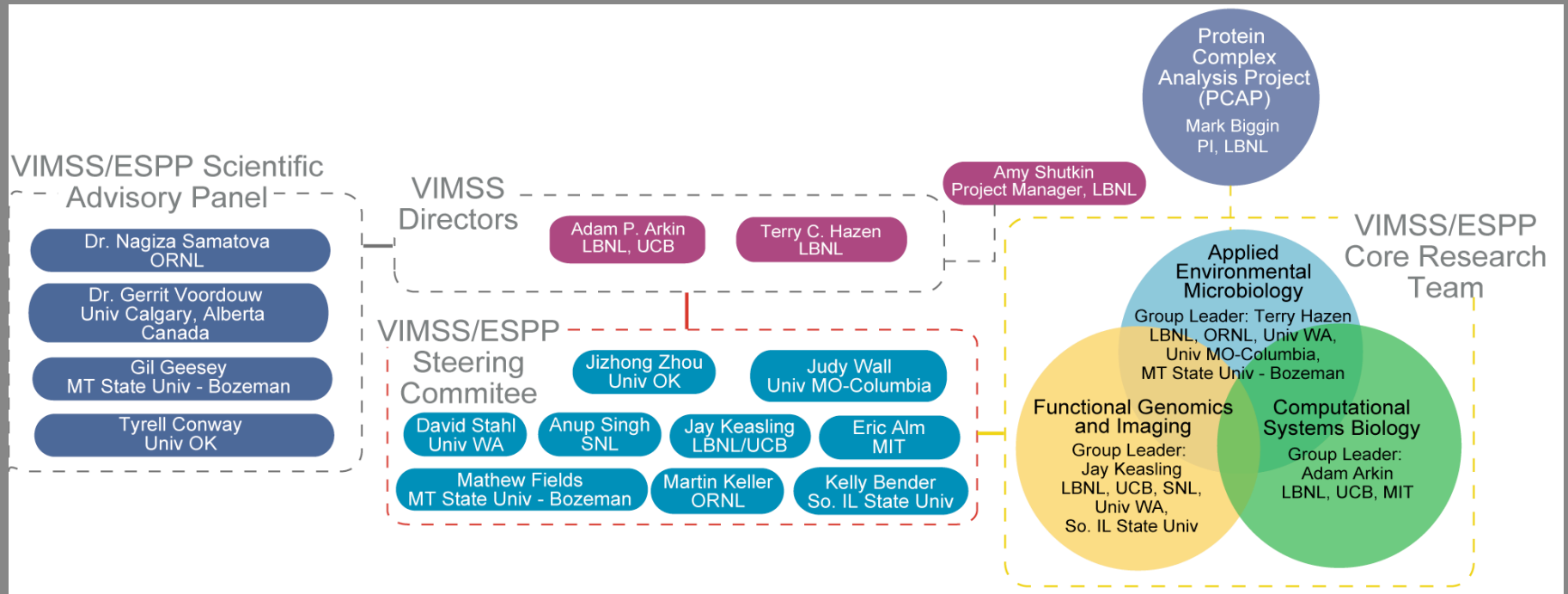
Herding Cats

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



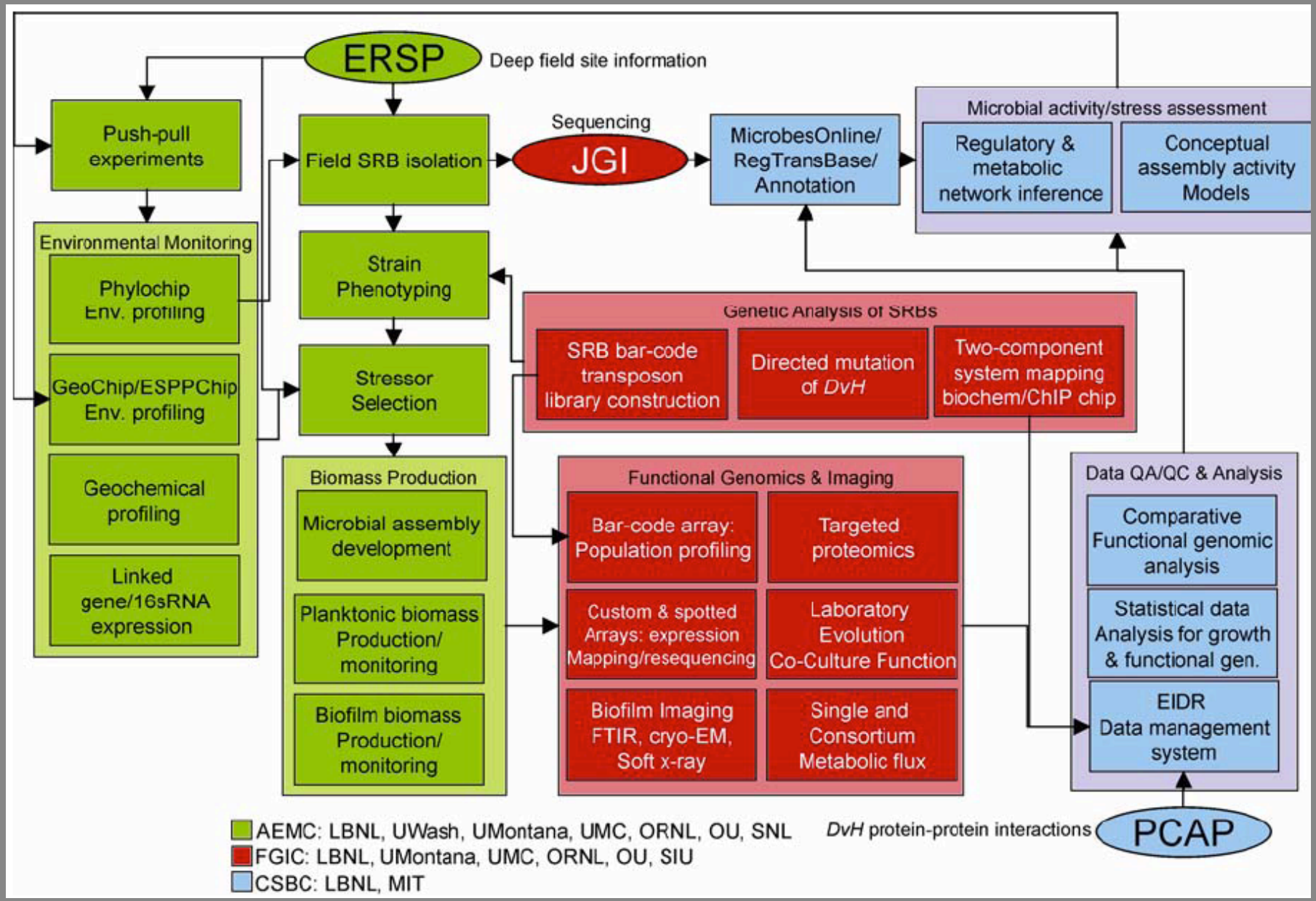
Steering Committee responsible for ensuring effective and efficient scientific operations. Meet monthly for 1-2 hour video or tele-conference to review resource allocations, budget performance, milestones and timelines, and to assess progress on each task. Convenes annually at: DOE Genomics:GTL Grantees'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

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

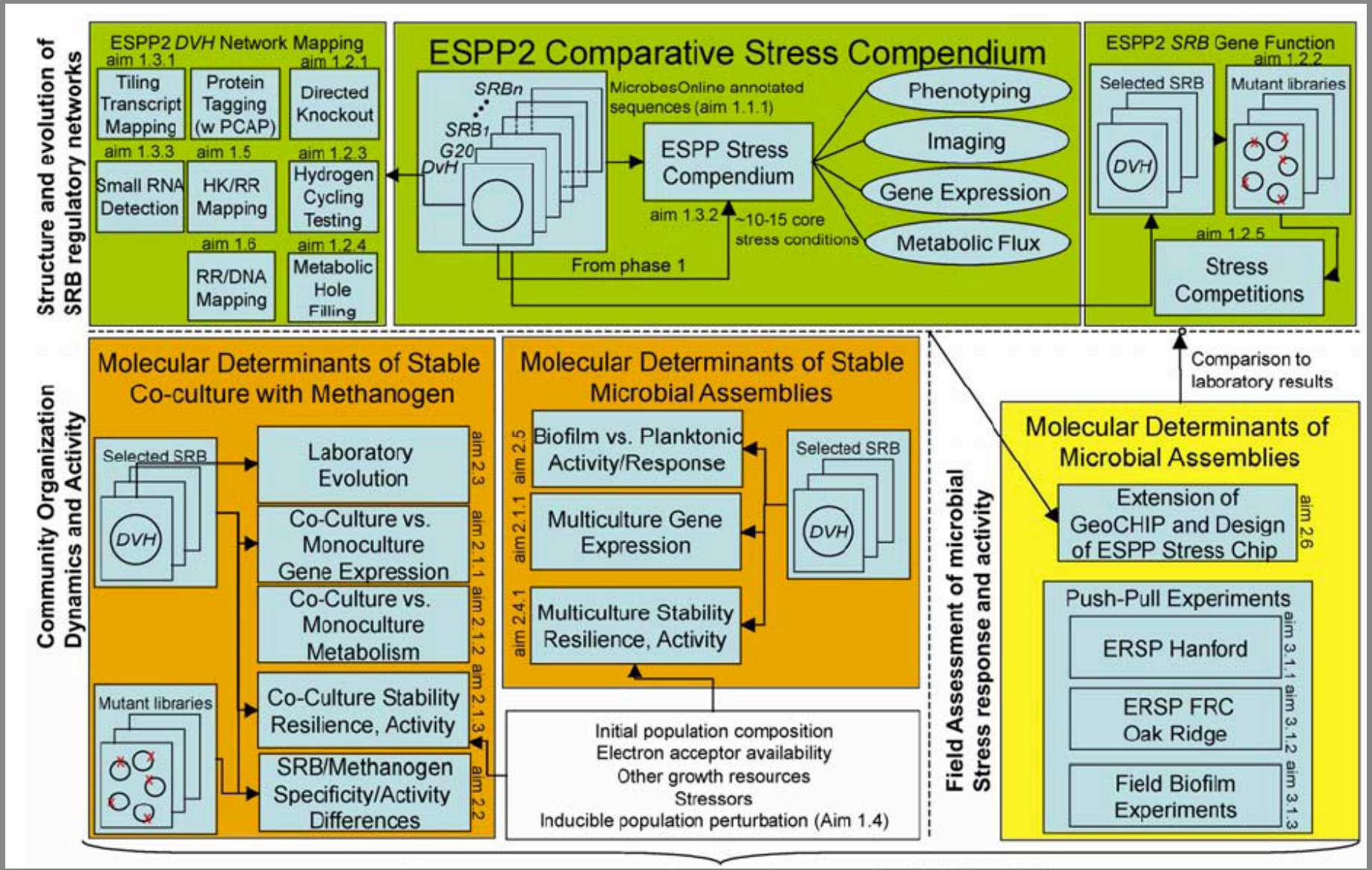
Scientific Advisory Panel annual 1 day review ensures that project's technical development is aligned with related DOE efforts working with the targeted organisms. With project team leaders and DOE assigned Federal Program Manager; discussions include exchange of data and information, the state of the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

Team Science Approach



Team Science Approach



e-Science

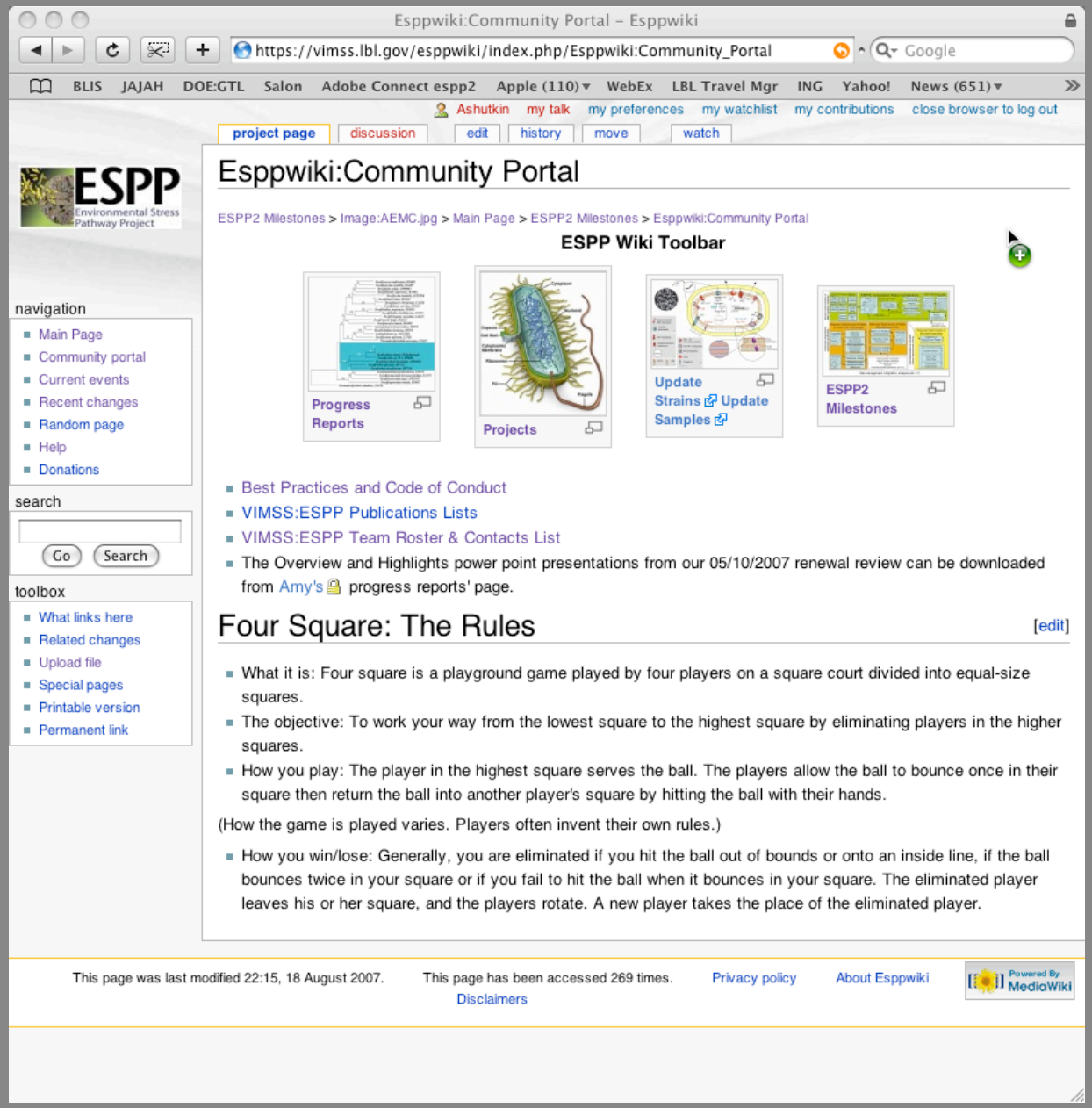
"The term "e-Science" denotes the systematic development of research methods that exploit advanced computational thinking."

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.

wiki communications



wi·ki |wikē|

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 wiki 'quick quick.'***

wiki communications

Aim 3.

Field experiments.

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

```
MF
Quite a bit of detail was omitted from the final (I and others
FRC and Hanford work.  For the FRC, I could list 4 papers and
for the field work as well as a basis for mixed culture establ
```

3.2 Biofilm experiments. See above. Only one paragraph. Not conv

```
MF
Detail was omitted from the final.  Published work by others o
the FRC and at t
```

Experimental Planning

Experiment Table

no. Description Proposer

1

Rebuttal

Arkin Review **Proposal Summary Commen**

```
Rapid Deduction of Stress Response Pathways i

Prinoipal Investigator: Arkin (Hazen), Adam (
Organization Name: University of California,
```

Evaluation of Progress

Papers under construction

Matthew

1. Cr(VI) toxicity in DvH (interanl 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
2. Walker, C.B., Yang, Z.K., He, Z., Stolyar, S., Jacobsen, J., Ringbauer, Jr, J.A., Wall, J.D., Zhou, J., Arkin, A.P. and Stahl, D.A. Energy conservation by Desulfovibrio vulgaris in syntrophic growth with a hydrogenotrophic methanogen.
3. Walker et al., DP4 genome
4. Walker et al., Gene expression in Methanococcus maripaludis growing in syntrophic association

Terry

- Jacobsen, J. S., D. C. Joyner, S. E. Borglin, T. C. Hazen, A. P. Arkin, and E. W. Bethel. In Prep. Visualization of Growth Curve Data from Phenotype Microarray Experiments
- Holman, H.-Y. N., Z. Lin, T. C. Hazen, M. C. Martin, and W. R. McKinney. Submitted. How an obligate anaerobe, Desulfovibrio vulgaris, survives in atmospheric oxygen – real-time molecular measurements. Science. Note: Resubmitted. LBNL-54957.
- Hazen, T. C., and B. Faybishenko. In Prep. Contaminants on DOE lands. Rewriting based on DOE review just received in
- Hazen, T. C., B. Faybishenko,……. In Prep. In situ bioreduction of chromium at Hanford 100H.
- Brodie, E., D. Joyner, B. Faybishenko, T. C. Hazen……In Prep. Treatability of Hanford sediments with HRC for Cr.

Adam

1. TF History paper submitted
2. FastHMM/FastBlast Paper in preparation
3. LSE analysis paper in construction
4. Clade specific marker paper in construction
5. Aiding Eric's on Comparative compendium paper in preparation
6. Aiding on Yinji's comparative Shewanella paper.
7. Aiding on Biofilm proteomics and microarray analysis

Team Comments

- Adam A.'s Comments
- Terry's Comments
- Joy's Comments
- Dave Stahl's Comments
- Kelly's Comments
- Kimberly's Comments
- Bill's Comments

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

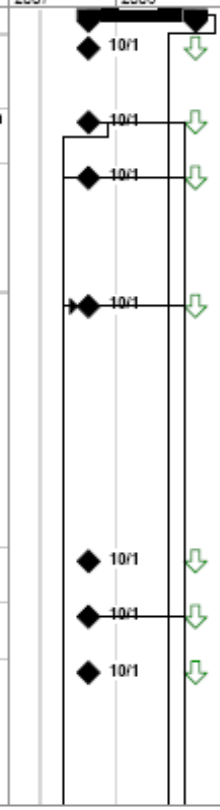
- •Extension of MicrobesOnline for 16SRNA, GeoCHIP/ESPPChip, Phenotype, metagenomic data.
- •Complete computational analysis of DvH and G20 and methanogen metabolism.
- •Establish flux model analysis methods for mono- and multicultures.
- •Developing tiling array and bar-code array design and analysis 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

VIMSS/ESPP2 Annual Milestones by Core Groups

ID	WBS	Task Name	Predecessors	Resource Names
1	1	**AEMC Year One**		Terry Hazen
2	1.1	Obtain previously isolated SRB, prepare DNA for sequencing submit to JGI		Terry Hazen
3	1.2	Begin isolation of SRB from ORNL/FRC and Hanford Sites		Matthew Fields,Martin Keller
4	1.3	Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species		David Stahl
5	1.4	Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation and steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.	4SS	Terry Hazen,David Stahl
6	1.5	Initial tests of multi-culture conditions.		David Stahl,Martin Keller,Joe Zhou
7	1.6	Initiation of co-culture evolution experiments.		Kristina Hillesland
8	1.7	Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co-culture.		Judy Wall,Adam Deutschbauer



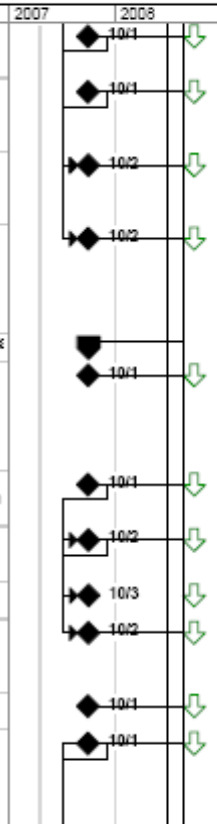
Project: Year 5 Milestones
Date: Tue 4/17/07

Task
Progress
Milestone
Summary
Rolled Up Task
Rolled Up Milestone
Rolled Up Progress
Split

Page 1

VIMSS/ESPP2 Annual Milestones by Core Groups

ID	WBS	Task Name	Predecessors	Resource Names
9	1.8	Complete membrane profiling of D. vulgaris in mono culture.		Terry Hazen
10	1.9	Complete membrane profiling M. mariplaudis in mono culture.		Terry Hazen
11	1.10	Complete membrane profiling of D. vulgaris / M. mariplaudis in syntrophic culture.	9,10	David Stahl
12	1.11	Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry.	3	Terry Hazen,Martin Keller,Matthew Fields,Joe Zhou
13	2	**FGIC Year One**		Jay Keasling,Aindrila
14	2.1	Create and sequence-verify saturating tagged transposon library of D. vulgaris and D. alaskensis G20.		Judy Wall
15	2.2	Prioritize HK/RR pair characterization with Computational Core		Aindrila Mukhopadhyay,Adam Deutschbauer
16	2.3	Initial HK/RR mapping by biochemical assay.	15	Aindrila Mukhopadhyay
17	2.4	Taq and purify HK/RR base pairs.	16	Aindrila Mukhopadhyay
18	2.5	Initial proof of concept RR DNA mapping using ChIP chip.	15	Adam Deutschbauer
19	2.6	Optimize barcode array design.		Adam Deutschbauer
20	2.7	Optimize tiling array for transcription start-stop mapping, small RNA detection and ChIP-chip in SRB for G20 and DvH.		Adam Deutschbauer,Kelly Bender



Project: Year 5 Milestones
Date: Tue 4/17/07

Task
Progress
Milestone
Summary
Rolled Up Task
Rolled Up Milestone
Rolled Up Progress
Split

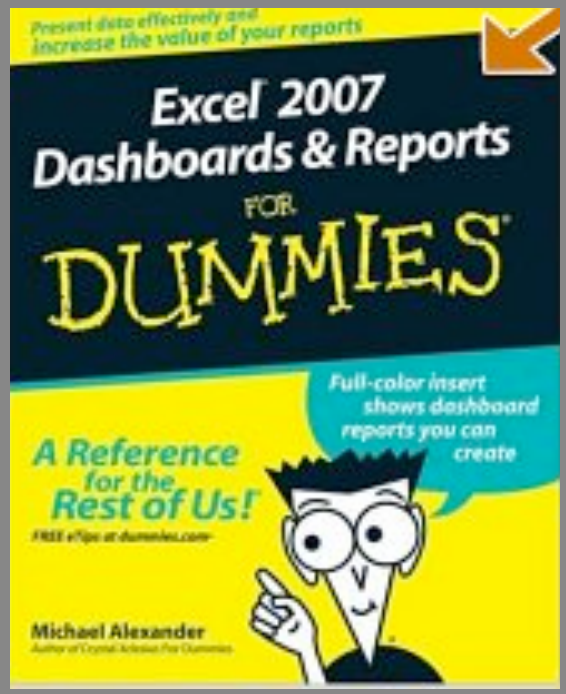
Page 2

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:

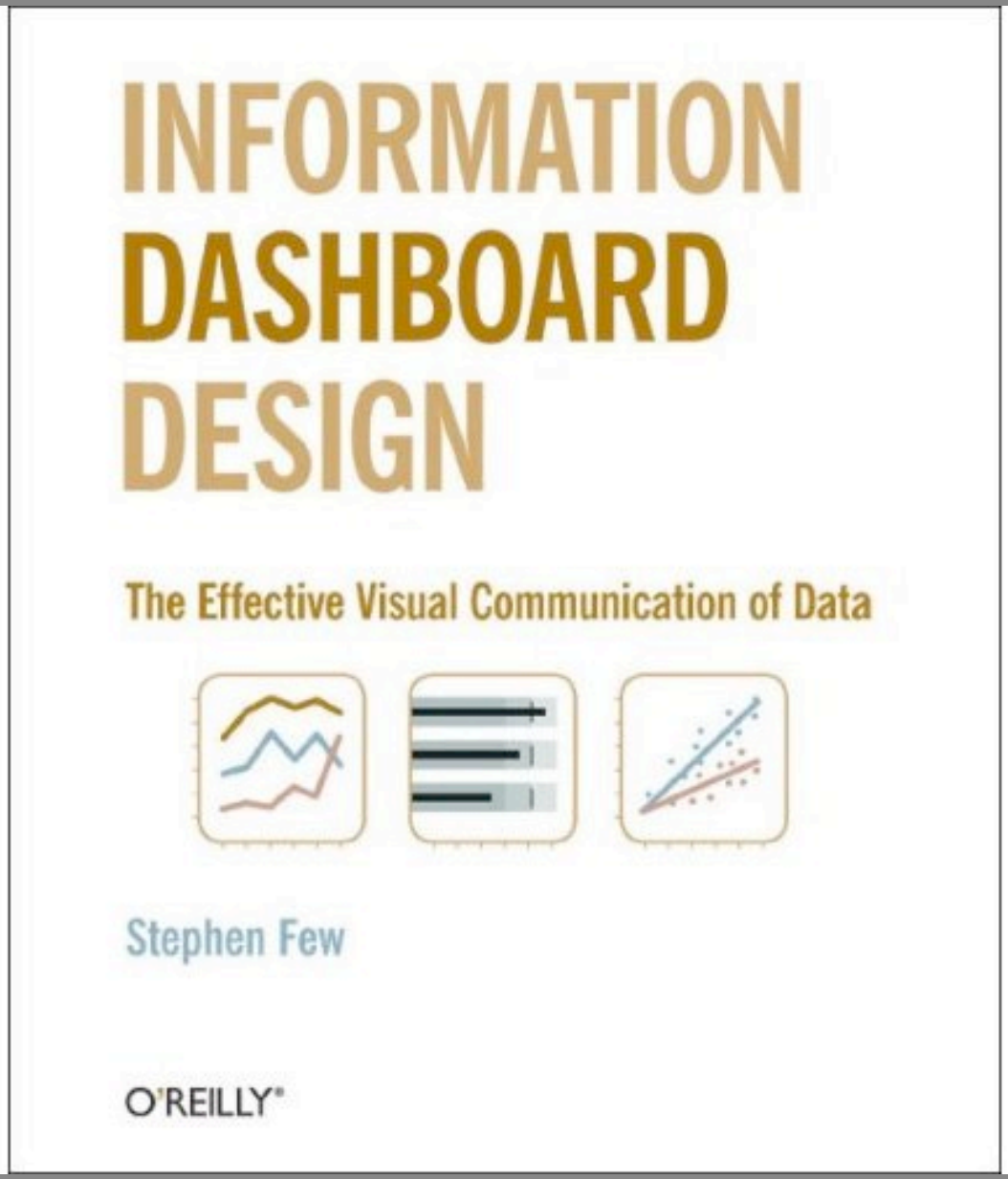
- ✓ Graphically focus attention on key trends, comparisons and exceptions
- ✓ Display only relevant data
- ✓ Inherently contain predefined conclusions



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

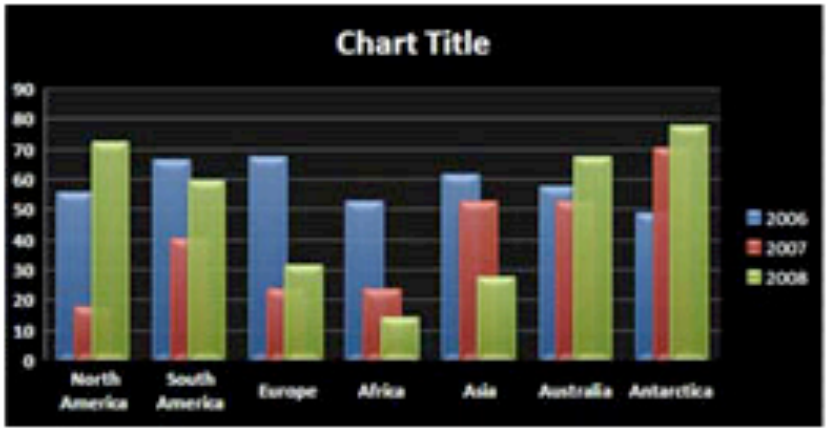
Visually featuring content & other items more than they deserve

Failing to link contents & other items that are related

Visually suggesting links between unrelated content

Enforcing a rigid symmetrical grid

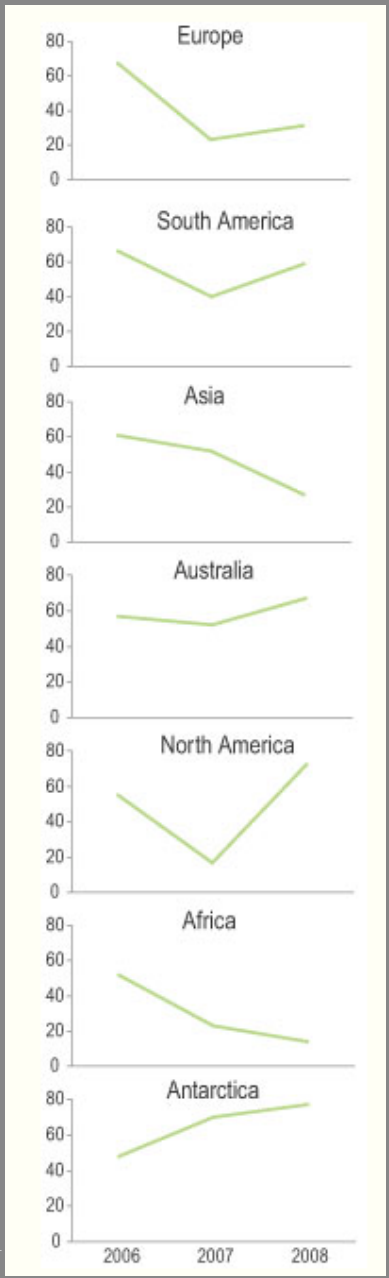
Dashboards - bad examples



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.

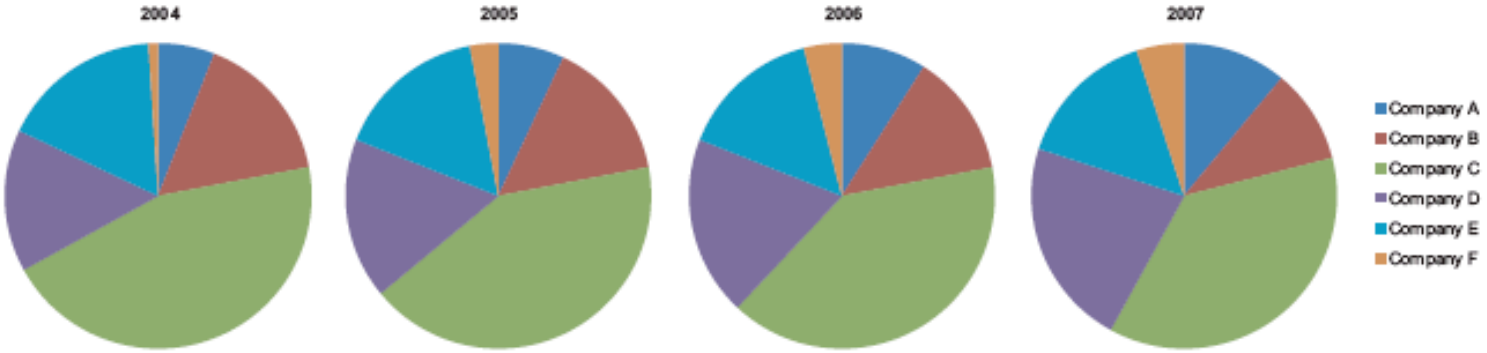
This new design is clean and clear—free of the visual distractions in the first two examples. Anyone viewing the graph would be able to examine the data, focusing perhaps on the large declines that are projected to occur in Europe and Africa, instead of the pretty, shiny bars.

Reduce the non-data ink

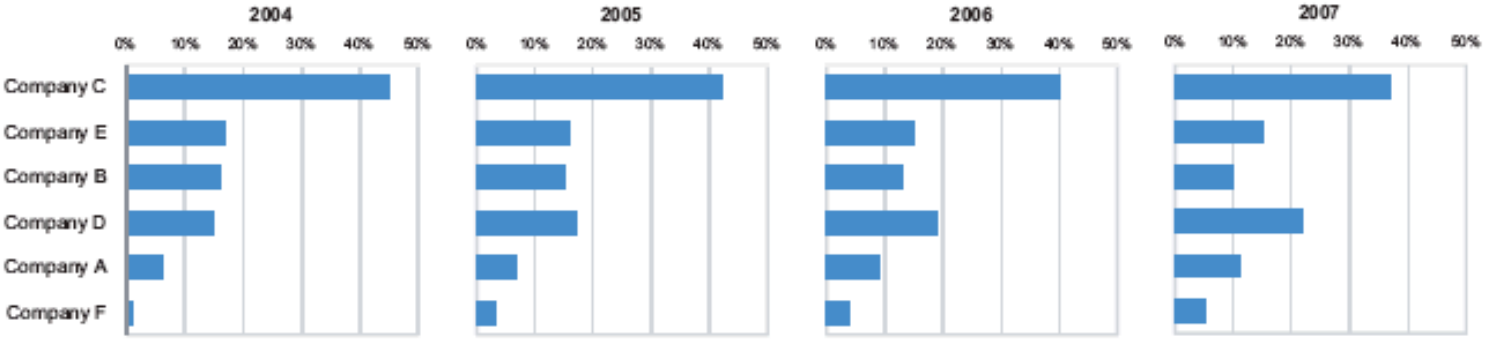
Enhance the data ink

Dashboards - evil pies

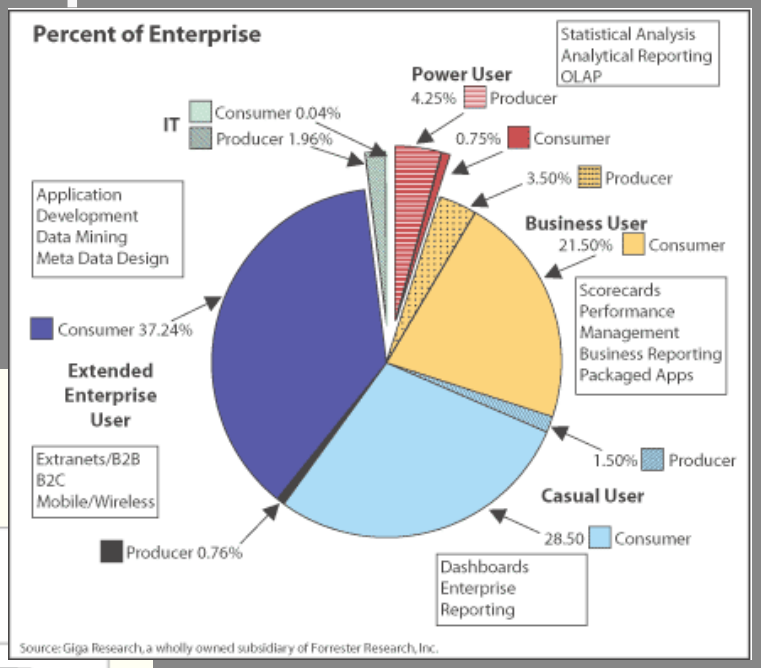
Let's examine another ineffective use of pie charts. Edward Tufte once said that "the only worse design than a pie chart is several of them, for then the viewer is asked to compare quantities located in spatial disarray both within and between pies" (Edward Tufte, *The Visual Display of Quantitative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



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:



Dashboards - evil pies

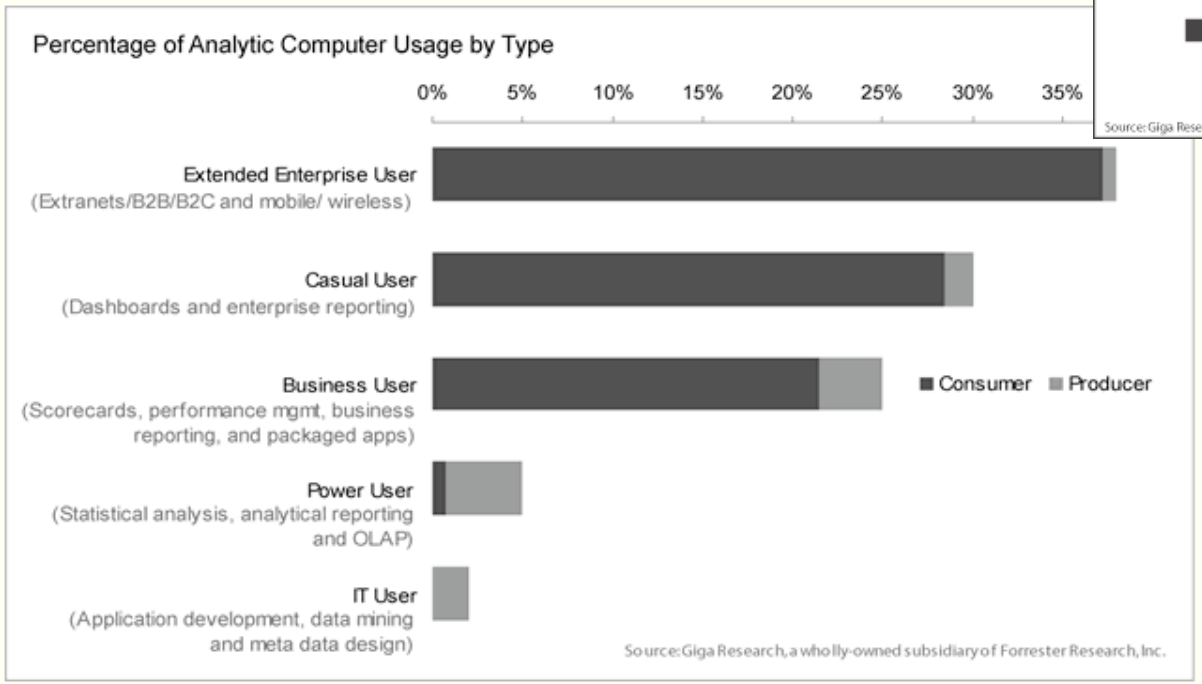


My Analysis

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

A Solution

Here's the same data displayed simply and clearly:



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?

Reduce the non-data ink

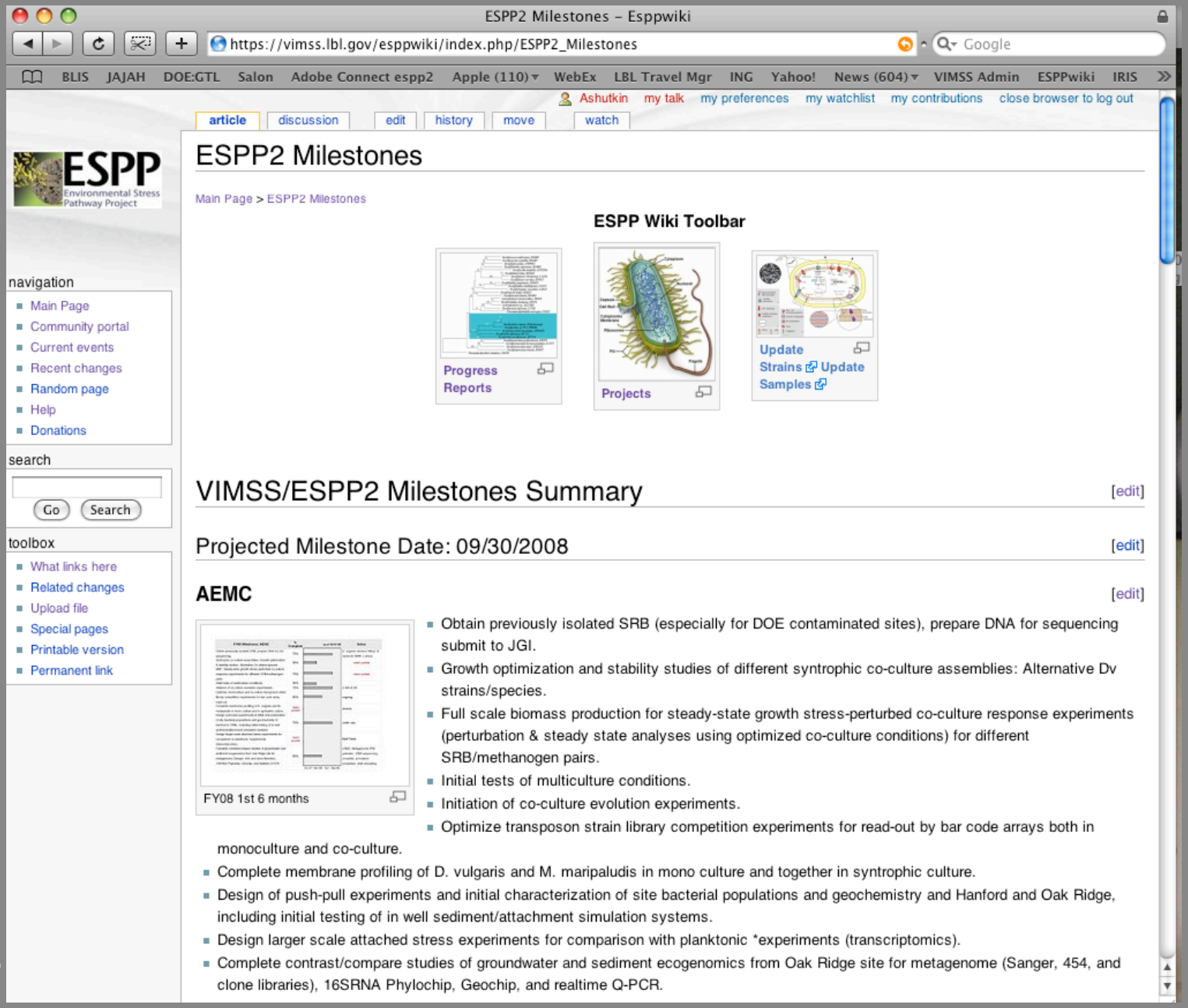
Enhance the data ink

Dashboard Milestone Reports

FY08 Milestones: AEMC	% Complete	as of 04/01/08	Notes
Obtain previously isolated SRB, prepare DNA for JGI sequencing.	70%		*D. vulgaris Hanford HBLS, D. hanfordii HMW + others*
Syntrophic co-culture assemblies: Growth optimization & stability studies: Alternative Dv strains/species.	30%		*need update*
BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%		*need update*
Initial tests of multiculture conditions.	30%		
Initiation of co-culture evolution experiments.	70%		*U WA & OK*
Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.	50%		*ongoing*
Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and in syntrophic culture.	*need update*		*Aindrila*
Design push-pull experiments & initial characterization of site bacterial populations and geochemistry @ Hanford & ORNL, including initial testing of in well sediment/attachment simulation systems.	70%		*under way*
Design larger scale attached stress experiments for comparison w/ planktonic *experiments (transcriptomics).	*need update*		*Matt Fields*
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.	50%		*CSBC: Metagenome FRC grdwater - DNA sequencing complete, annotation completed, draft circulating.*
		Oct 07- Mar 08 Apr - Sep 08	

Key Performance Indicators (KPI) ~
essential tasks draw attention to problem areas

Dashboard Milestone Reports



ESPP wiki

Dashboard Milestone Reports

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Syntrophic co-culture assemblies: Growth optimization & stability studies: Alternative Dv strains/species.	30%		*need update*
BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%		*need update*
Initial tests of multiculture conditions.	30%		
Initiation of co-culture evolution experiments.	70%		*U WA & OK*
Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.	50%		*ongoing*
Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and in syntrophic culture.	*need update*		*Aindrila*
Design push-pull experiments & initial characterization of site bacterial populations and geochemistry @ Hanford & ORNL, including initial testing of in well sediment/attachment simulation systems.	70%		*under way*
Design larger scale attached stress experiments for comparison w/ planktonic *experiments (transcriptomics).	*need update*		*Matt Fields*
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.	50%		*CSBC: Metagenome FRC grdwater - DNA sequencing complete, annotation completed, draft circulating.*
		Oct 07- Mar 08 Apr - Sep 08	

Size of this preview: 776 × 600 pixels

Full resolution (2200 × 1700 pixel, file size: 276 KB, MIME type: image/jpeg)
ESPP2 Milestones > Image:AEMC.jpg > Main Page > ESPP2 Milestones > Image:AEMC.jpg

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Cost Estimation & Budget Oversight

	Rate Type	FY07	FY08	FY09	FY10	FY11	FY12 (est)	5 Year Totals
	Escalation Rates							
Original Project Budget Assumptions	LBNL Labor							
	LBNL Supplies & Other Expenses (OMB)							
	Total Labor	$3,77						
	Total Supplies & Other Expenses (OMB)	$4,26						
	Totals	$8,04						
Renewal Budget Assumptions	LBNL Labor							
	Equipment, Supplies & Other Expenses, LBNL (OMB)							
	LBNL Total							
	Total Direct Costs, LBNL							
	Total Indirect Costs, LBNL							
	Total Direct Costs less Other Inst. Indirect Costs, LBNL							
	SNL							
	ORNL							
	ESPP2 Total							
	% original projection							

DOE F 4620.1 (04-93) All Other Editions Are Obsolete

U.S. Department of Energy
Budget Page
(See reverse for Instructions)

ORGANIZATION: Ernest O. Lawrence Berkeley National Laboratory

PRINCIPAL INVESTIGATOR/PROJECT DIRECTOR: Arkin, Adam

Overall Project Budget

A. SENIOR PERSONNEL: PI/PD, Co-PI's, Faculty and Other Senior Associates (List each separately with title; A.6. show number in brackets)	DOE Funded Person-mos. CAL	ACAD	SUMR
1. Arkin, Adam	15.00		
2. Keasling, Jay	6.00		
3. Hazen, Terry	6.00		
4. Dubchak, Inna	18.00		
5.			
6. (6) OTHERS (LIST INDIVIDUALLY ON BUDGET EXPLANATION PAGE)	231.00		
7. (11) TOTAL SENIOR PERSONNEL (1-6)	336.00		
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)			
1. (6) POST DOCTORAL ASSOCIATES	108.00		
2. (25) OTHER PROFESSIONAL (TECHNICIAN, PROGRAMMER, ETC.)	699.00		
3. (2) GRADUATE STUDENTS	54.60		
4. (0) UNDERGRADUATE STUDENTS	0.00		
5. (2) SECRETARIAL - CLERICAL	30.00		
6. (0) OTHER	0.00		
TOTAL SALARIES AND WAGES (A+B)			
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)			
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A+B+C)			
D. PERMANENT EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM.)			
TOTAL PERMANENT EQUIPMENT			
E. TRAVEL 1. DOMESTIC (INCL. CANADA AND U.S. POSSESSIONS)			
2. FOREIGN			
TOTAL TRAVEL			
F. TRAINEE/PARTICIPANT COSTS			
1. STIPENDS (Itemize levels, types + totals on budget justification page)			
2. TUITION & FEES			
3. TRAINEE TRAVEL			
4. OTHER (fully explain on justification page)			
TOTAL PARTICIPANTS (0) TOTAL COST			
G. OTHER DIRECT COSTS			
1. MATERIALS AND SUPPLIES			
2. PUBLICATION COSTS/DOCUMENTATION/DISSEMINATION			
3. CONSULTANT SERVICES			
4. COMPUTER (ADPE) SERVICES			
5. SUBCONTRACTS			
6. OTHER			
TOTAL OTHER DIRECT COSTS			
H. TOTAL DIRECT COSTS (A THROUGH G)			
I. INDIRECT COSTS (SPECIFY RATE AND BASE) *Please see the indirect calculation sheets*			
TOTAL INDIRECT COSTS			
J. TOTAL DIRECT AND INDIRECT COSTS (H+I)			
K. AMOUNT OF ANY REQUIRED COST SHARING FROM NON-FEDERAL SOURCES			
L. TOTAL COST OF PROJECT (J+K)			

LBNL Forward Pricing Rates
Effective October 1, 2006
Revision 5

Rate Type

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

Institutional Rates

General and Administrative
- G&A (Off Site) Rate - OFF
- Site Support (Fabrication) Rate - FAB
  - Gretina
  - Animal Care
- General Rate - GR1

LDRD Rate
- LDRD Operating and Equipment
- (LDRD rate is based on proposed structure, which is currently being reviewed by DOE)

IGPP Rate
- IGPP

Procurement Burdens (Base: Cost of procured materials & services)
- PO's $1-$500,000
- PO's Over $500,000 (per PO) $
- R&D subcontract's $1-$300,000
- R&D subcontract's over $300,000 $
- Intra-University Transfers (IUTs) $1-$200,000
- Intra-University Transfers (IUTs) over $200,000
- Genomics Procurements (PO's $1-$500,000)
- Molecular Foundry (PO's $1-$500,000)
- Project Management (PO's $1-$500,000)

Travel (Base: Travel Costs)
- Travel Rate

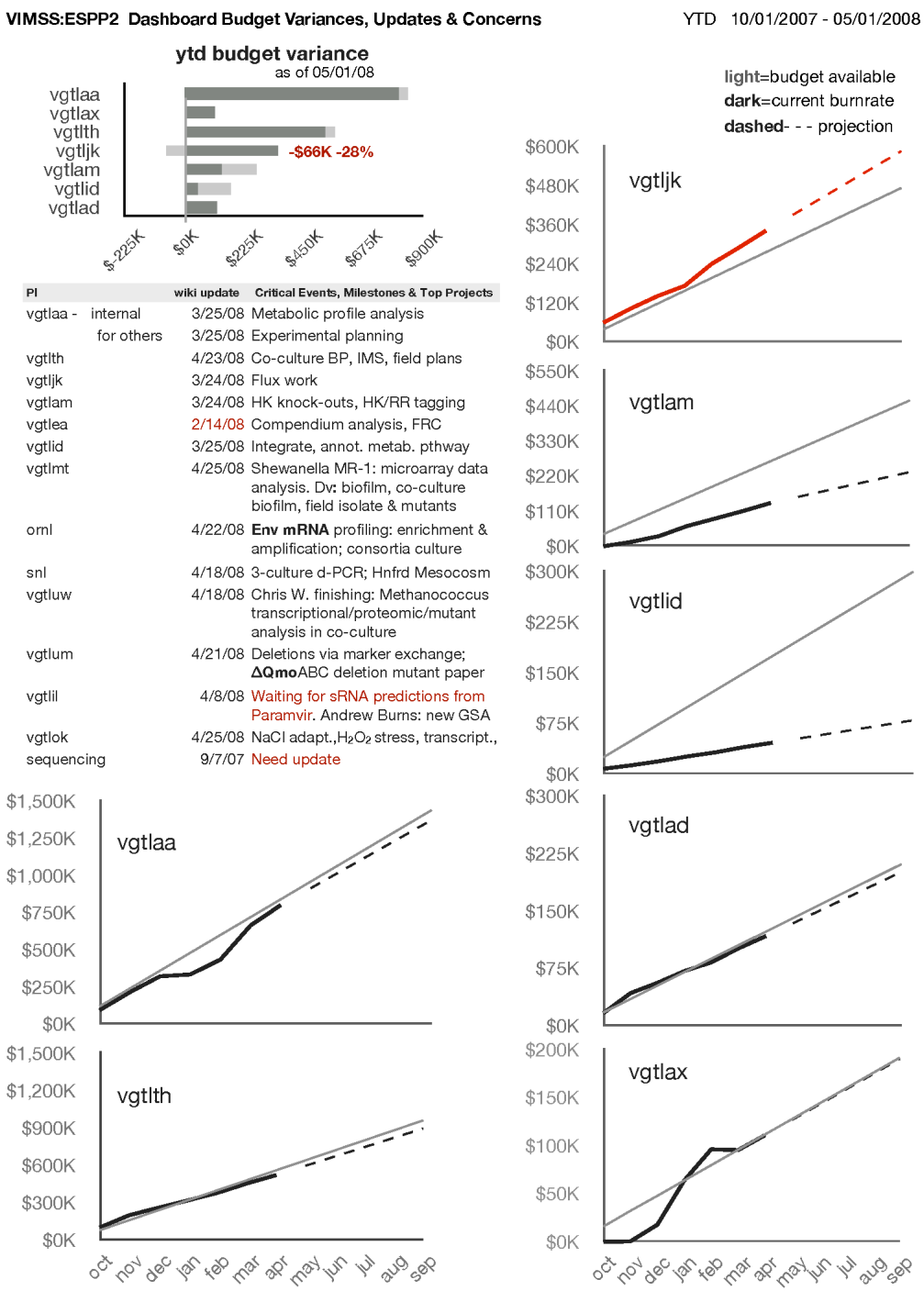
Payroll Burden (Base: Delivered effort cost only)
- **Career&Term Employees**
- Post Docs, Visiting Post Docs, Limited Employees, and Visting Researchers
- GSRAs
- Students/Rehired Retirees/Employees working variable time
- Summer Faculty

Fringe Benefits Only (Base: FTE gross pay only)
- **Career&Term Employees**
- Post Docs, Visiting Post Docs, Limited Employees, and Visting Researchers
- GSRAs
- Students/Rehired Retirees/Employees working variable time
- Summer Faculty

Dashboard Integrated Milestone & Budget Reports

"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*



Dashboard Integrated Milestone Report

Publications in Preparation:

1. Arkin, Adam P. and Alm, Eric. Bioinformatics for metabolic engineering.
2. Borglin, Sharon, Joyner, Dominique and Jacobsen, Janet. Defined media for DvH.
3. Chakrobarty, Romy. PCS.
4. Chakrobarty, Romy. Hanford Microbiology.
5. Chhabra, Swapnil and Zane, Grant. Endogenous complex.
6. Clark, M.E., Redding, A., He, Z., Mukhopadhyay, A., Keasling, J., Zhou, J. and Fields, M.W. Characterization of *D. vulgaris* biofilms via transcriptomic and proteomic analyses.
7. DeSantis, T., Huber, Hugenholtz, P., Andersen, G. Bellerophon: chimera screening web tool for massive 16S rRNA clone libraries
8. Eddy,J.L., Clark, M.E., Ringbauer, J., Wall*, J.D. and Fields* M.W. A Sensory Box-Histidine Kinase in *Desulfovibrio vulgaris* Hildenborough Involved in Sensing Hydrogen Sulfide.
9. Fields, M.W., Klonowska, A., He, Z., Hazen, T.C., Thieman, S.B., Alm, E.J., Arkin, A.P., Wall, J.D. and Zhou, J. Global Transcriptomic Analysis of Chromium(VI) Exposure of *Desulfovibrio vulgaris* Hildenborough Under Sulfate-Reducing Conditions.
10. Gao. mRNA amplification.
11. Gao. Osmotic stress in So.
12. He, John. Nitrate stress.
13. He, John. Acetone.
14. He, Zhili. Designing Oligos.
15. He, Zhili, He, Qiang, Alm, Eric J., Wall, Judy D., Fields, Matthew W., Hazen, Terry C., Arkin, Adam P. and Zhou, Jizhong. Exploration of Salt Adaptation Mechanisms in *Desulfovibrio vulgaris* Hildenborough. *AEM, JB, or Microbiology*
16. Hemme, Chris. FRC metagenome.
17. Holman, H.-Y.N., Borglin S., Hazen, T.C., and E. Wozei. Dynamics of membrane structure and composition observed in *Desulfovibrios* during adaptation to nitrate stress, *J. Bacteriol.*
18. Holman, H.-Y. Lin, N., Z., Hazen, T. C., Martin, M. C. and McKinney, W. R. How an obligate anaerobe, *Desulfovibrio vulgaris*, survives in atmospheric oxygen – real-time molecular measurements. Science
19. Holman, Hoi-Ying. Comparing O2 adaptation in DvH, So, Caulobacter.
20. Joyner, Dominique and Borglin, Sharon. PM techniques.
21. Massol. DvH and explosives.
22. Price, M.N., Dehal, P.S., and Arkin, A.P. Protein sequence analysis for millions of genes: FastBLAST and FastHMM
23. Sapra, R., Gaucher, S.P., Hazen, T.C. and Singh, A.K. Identification of Proteins that are post-translationally modified in DvH during oxygen stress
24. Sapra, Rajat. Identification of Proteins that are post-translationally modified in DvH during peroxide stress
25. Tang, Y.J., Dehal, P.S., Meadows, A., Chu, J., Martin, H.G., Arkin, A.P., and Keasling, J.D. Metabolic flux analysis of evolutionary , genetic and environmental robustness, and flexibility in central carbon metabolism of *Shewanella oneidensis* MR-1
26. Van Nostrand, J. D., et al. Changes in the Functional Microbial Community during Starvation and Reoxidation Periods in a Groundwater Recirculation System
27. Walker, C.B., Yang, Z.K., He, Z., Stolyar, S.S., Jacobsen, J., Ringbauer, Jr, J.A., Wall, J.D., Zhou, J., Arkin, A.P. and Stahl, D.A. Energy conservation by *Desulfovibrio vulgaris* in syntrophic growth with a hydrogenotrophic methanogen. *PNAS*
28. Walker, C.B., Stolyar, S.S. and Stahl, D.A. Genome plasticity of *Desulfovibrio vulgaris* species. *Appl. Environ. Microbiol.*
29. Wall, Judy and Yen, Bill. Low pH pipeline.
30. Wall, Judy. G20 genome.
31. Wall, Judy. Cytochrome C3 Deletion Mutant Comparison.
32. Zane, G.M., Yen, H.-C. and Wall, J.D. Effect of a qmoABC deletion and subsequent complementation on sulfate-reduction in Desulfovibrio vulgaris Hildenborough
33. Zhou, Aifen. H_2O_2 Proteomics
34. Zhou, Aifen, et al. The Dynamics and Genetic Bases of Adaptation to Salt Stress in *Desulfovibrio vugaris*/ Hildenborough

FY08 Milestones: FGIC	% Complete	as of 04/23/08	Notes
Metabolomics			
Utilize 13C/12C labeling to obtain metabolic response to previously studied stresses in D. vulgaris	80%		*E. coli: Francesco completing study for publication. Application in D. vulgaris tbd*
Methionine Biosynthesis Pathway in D. vulgaris: targeted study	50%		*Peter & Ed*
Using tagged proteins in D. vulgaris Flux Analysis: proof of concept	50%		*Method published, 100% complete. Dv collaboration ESPP w/ JBEI.*
Complete CEMS profile for DvH metabolites (ESPP-1 Milestone) Method published. Study ongoing.	50%		*Study only addressed 1 set of metabolites via positive ion mode on the CE & number of metabolites IDed limited by standards on hand*

FY08 Milestones: FGIC	% Complete	as of 04/23/08	Notes
Create and sequence-verify saturating tagged transposon libraries for:			
Shewanella oneidensis	50%		*Adam D.*
D. desulfuricans G20	10%		*Adam D.*
Prioritize HK/RR pair characterization w/ CSBC.	30%		*Aindrila*
Tag and purify HK/RR pairs.	70%		*RR - 90%, HK - 50%*
Initial HK/RR mapping by biochemical assay.	50%		*Post-doc to begin 05/12. All HK knock-outs: 12/64 genes completed, 2-3 checked. Paper in process.*
Initial proof of concept RR/DNA mapping using ChIP-chip.	50%		*Ready to go - waiting on Nimblegen chips (Adam D. & Paramvir)*
Optimize barcode array design.	100%		*Commercial Affemetrix TAG4*
Optimize tiling array for transcription start-stop mapping,	10%		*Small RNA detection & ChIP-chip in SRB for G20 & DvH will be recast into year 2 milestones.*
G20: Optimize multiplex gene expression design	5%		*Small volume RNA isolation protocol confirmed.*
G20: Complete stress response transcriptomics	5%		*Adam D.*
Initial survey of possible small RNA regulators.	30%		*Waiting for predictions of sRNAs from Paramvir*
Complete ESPPChip microarray design & testing.	*tbd*		*Redundant? Combine w/ Chip-chip development?*
Gene expression compendium	5%		*G20: 1st 12 conditions*
		Oct 07- Mar 08 Apr - Sep 08	

FY08 Milestones: AEMC	% Complete	as of 04/23/08	Notes
Obtain previously isolated SRB, prepare DNA for JGI sequencing.	70%		*D. vulgaris Hanford HBLS, D. hanfordii HMW + others*
Syntrophic co-culture assemblies: Growth optimization & stability studies: Alternative Dv strains/species.	30%		*need update*
BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%		*need update*
Initial tests of multiculture conditions.	30%		*ORNL*
Initiation of co-culture evolution experiments.	70%		*U WA & OK*
Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.	50%		*ongoing*
Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and in syntrophic culture.	*N/A*		*Proteomics not funded*
Design Hanford & ORNL push-pull experiments & initial charac. of site bacterial populations and geochemistry.	70%		*under way*
Design larger scale attached stress experiments for comparison w/ planktonic experiments (transcriptomics).			*Matt Fields - under way*
Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome.	50%		*CSBC: Metagenome FRC grdwater - DNA sequencing complete, annotation completed, draft circulating.*

FY08 Milestones: CSBC	% Complete	as of 04/01/08	Notes
Extension of MicrobesOnline for:			
16SRNA	50%		
GeoCHIP/ESPPChip	**0%**		*working w/ ORNL to incorporate Selexa data*
Phenotype	50%		*usefulness will depend on human (undergrads) annotation*
Metagenomic data	25%		
Complete computational analysis of DvH & G20 + methanogen metabolism.	50%		*Waiting on data.*
Establish flux model analysis methods for mono- and multicultures.	50%		*High potential value & high interest*
Developing tiling array and bar-code array design and analysis techniques.	90%		*Analysis techniques will continue to evolve & improve*
Complete annotation of Dv Miyazaki, Ds 27774, and one Dv Hanford isolate.	50%		*Waiting for these + other sequences before expression array & analysis*
Complete initial reannotation of DvH.	50%		*Critical Task: Additional data to include? Tiling array?*
Begin design of conceptual model of stress, ED, TEA responses for Hanford Cr and Oak Ridge U contaminated sites.	**0%**		*Critical Task: Participating in experimental design - conceptual model depends on data to be collected*
		Oct 07- Mar 08 Apr - Sep 08	

Acknowledgements

ESPP2 Environmental Stress Pathway Project

DOE GENOMICS:GTL ACCELERATING DISCOVERY FOR ENERGY AND ENVIRONMENT

VIMSS Virtual Institute for Microbial Stress and Survival | Massachusetts Institute of Technology | Missouri | University of Washington | Montana State University | Southern Illinois University | Oklahoma | Sandia National Laboratories | Oak Ridge National Laboratory | Berkeley | http://vimss.lbl.gov

Adam P. Arkin and Terry C. Hazen, Directors

Applied Environmental Microbiology Core:

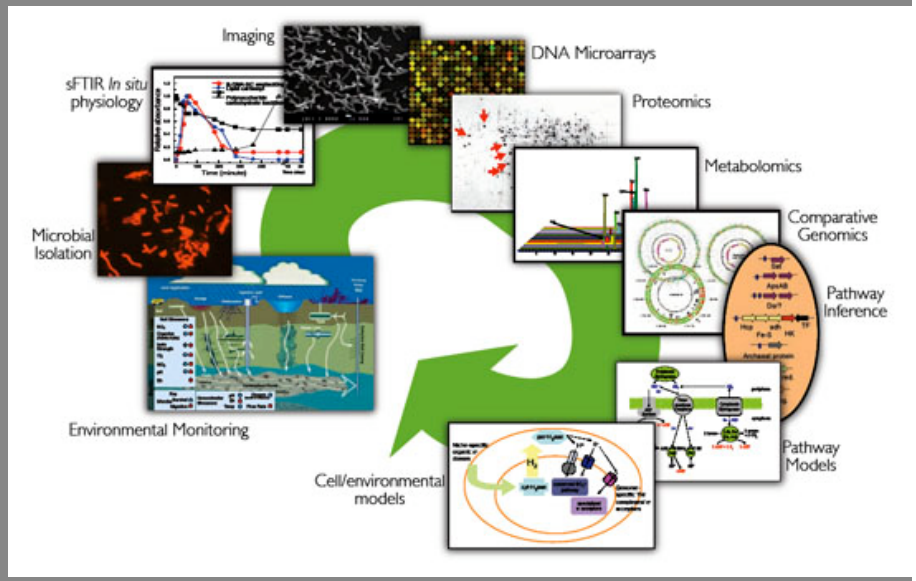
- **LBNL**, Terry C. Hazen
- **University of Washington**, David Stahl
- **Montana State University**, Matthew Fields

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



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