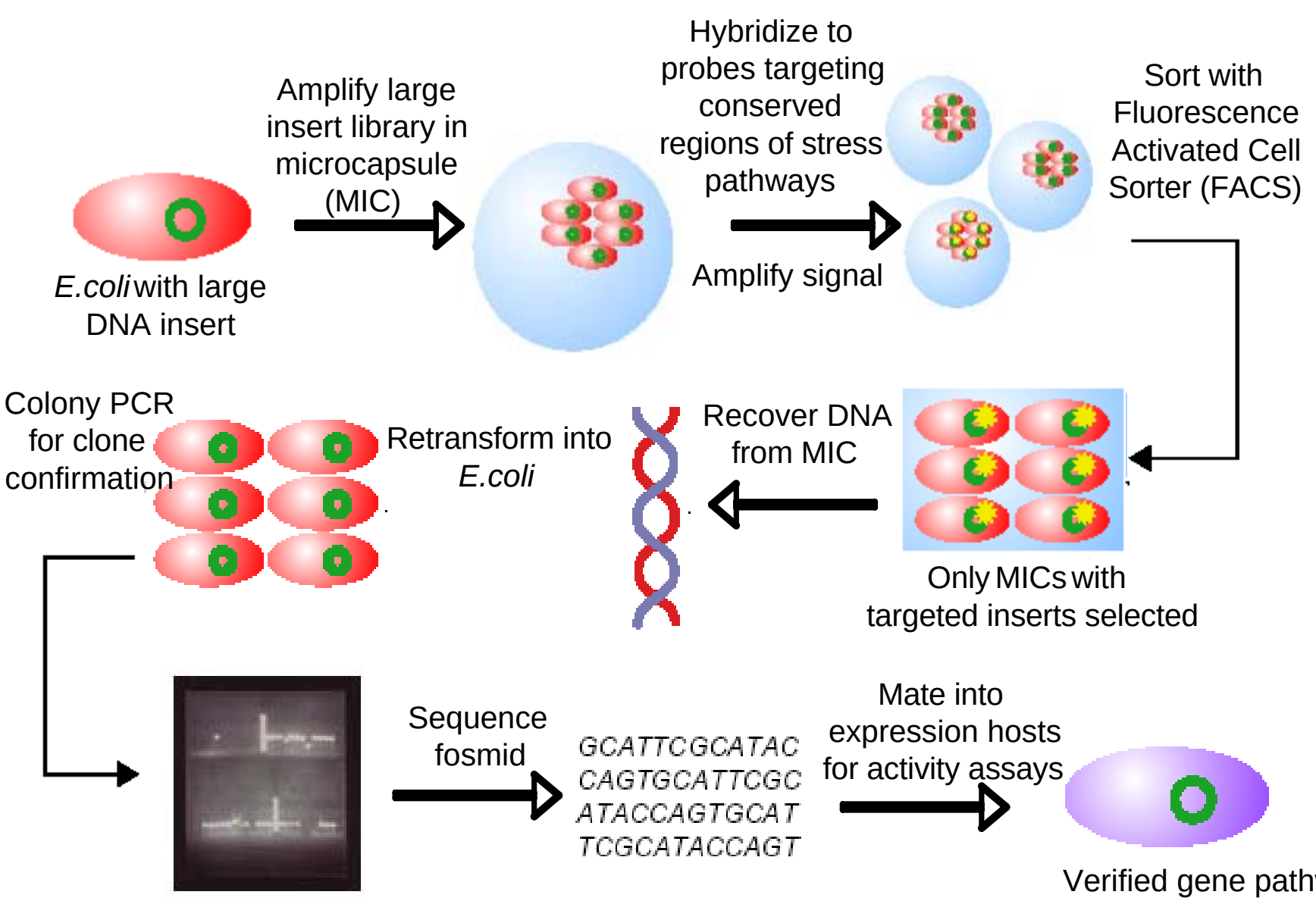
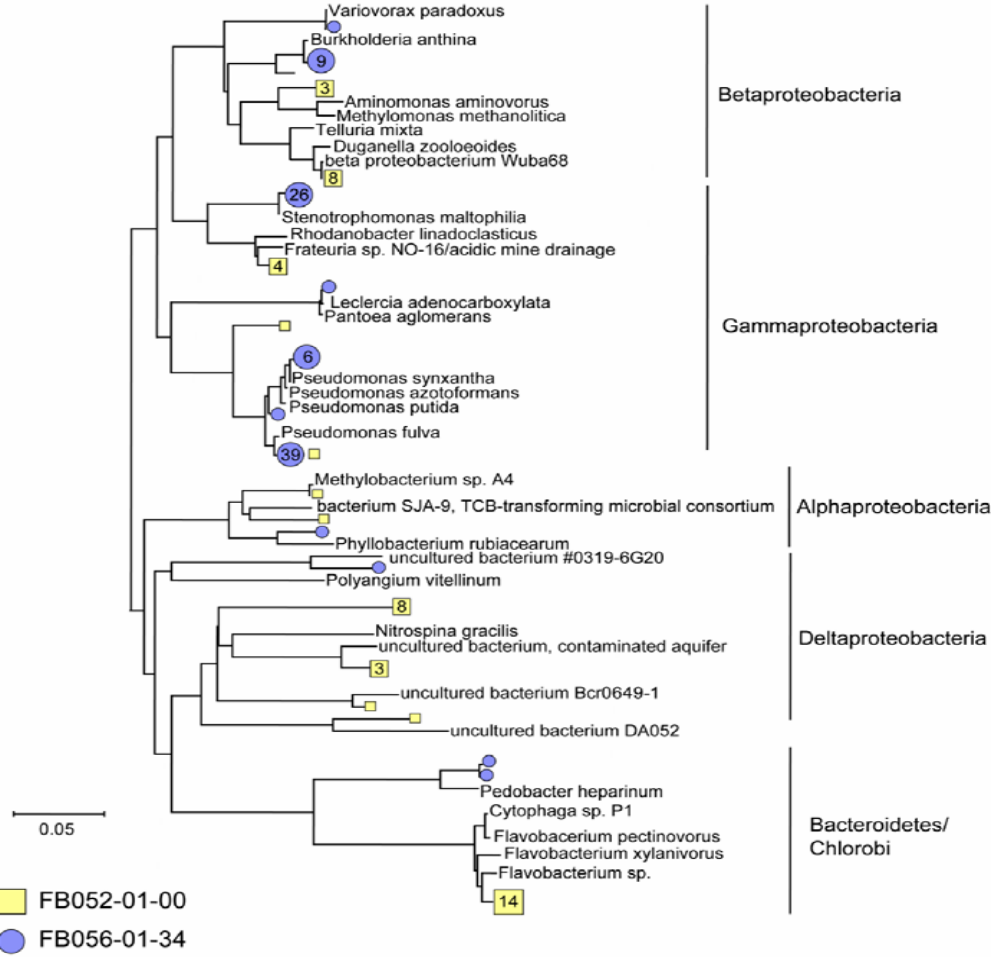
The environment is the context in which genomes evolved, function, and continue to evolve. It is the only context in which they can be fully understood.

High Throughput Technology for Enriching Low-Copy Number Pathways



Sequence Analysis

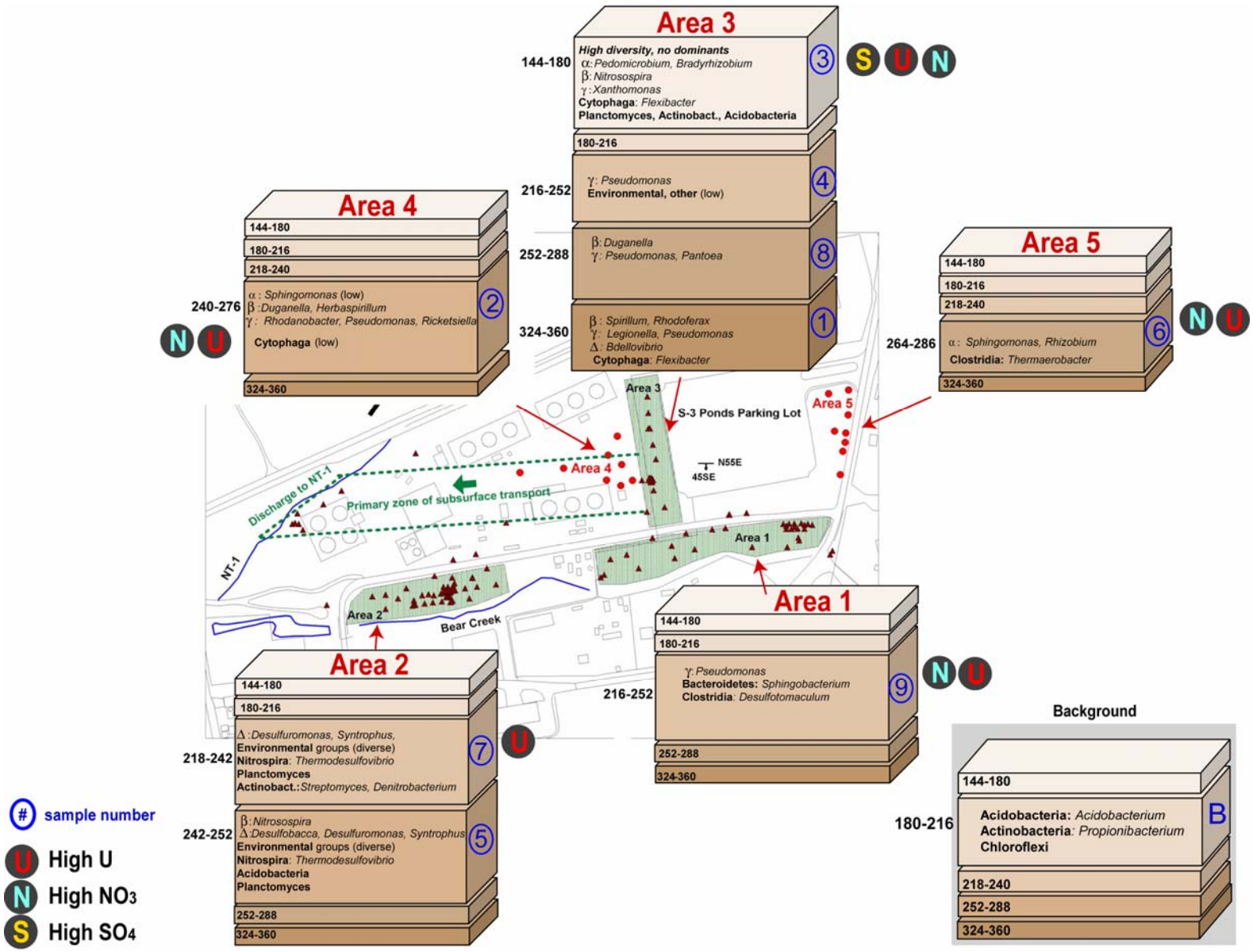


Sample of blast hits from clones in a library constructed from amplified gDNA from sample #FB052.

Evalue	Functional category based on blast hits
	Transporters and small molecule binding
1.00E-33	lead,cadmium,zinc and mercury transporting ATPase
4.00E-39	Permeases of the drug/metabolite transporter (DMT) superfamily
2.00E-15	ABC-type multidrug transport system, ATPase subunit
3.00E-18	extracellular solute-binding protein
5.00E-50	putative cation-diffusion-facilitator; metal tolerance, zinc, cadmium
8.00E-99	cobalt/cadmium/zinc transporter
	Toxicity response
5.00E-28	Radical activating enzymes
2.00E-33	Organic radical activating enzymes
	Intermediate central metabolism
2.00E-47	glucose-1-phosphate thymidylyltransferase
2.00E-33	Glycine/D-amino acid oxidases (deaminating)
5.00E-27	Glycosyltransferase
6.00E-67	NAD synthase
5.00E-15	acyl-CoA dehydrogenase
	DNA, RNA and protein synthesis
1.00E-15	DNA repair protein RAD51
2.00E-45	ATPases involved in chromosome partitioning
1.00E-34	DNA-directed RNA polymerase beta subunit/160 kD subunit

Diversity analysis of genomic DNA from soil samples #FB052 and #FB056 based on rRNA genes. The neighbor-joining phylogenetic tree was generated using genetic distances calculated with DNADIST in the PHYLIP package. Representative related database sequences were included for reference. Clusters of sequences with higher than 95% identity were represented by symbols indicating the number of those sequences.

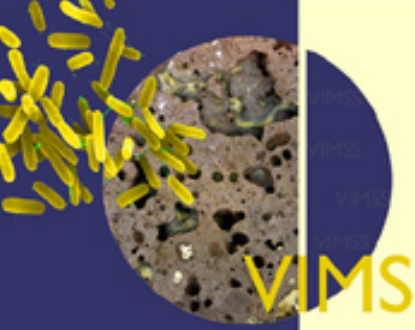
Samples From the NABIR FRC Site



COG Analysis

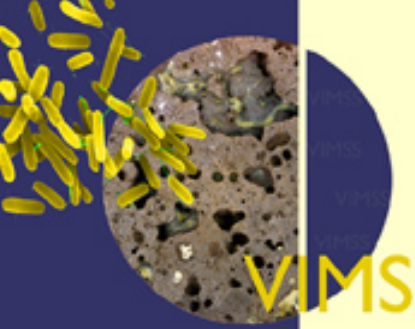
Table 4. Cog analysis

Function classification	Area 3, Deep		Area 3, Shallow		Area 2	
	No. of sequences	%	No. of sequences	%	No. of sequences	%
Amino acid transport and metabolism	64	4.0558	47	4.1337	75	4.6325
Carbohydrate transport and metabolism	187	11.8504	184	16.1829	232	14.3298
Cell cycle control, cell division, chromosome partitioning	16	1.0139	11	0.9675	21	1.2971
Cell motility	4	0.2535	4	0.3518	7	0.4324
Cell wall/membrane/envelope biogenesis	117	7.4144	88	7.7397	122	7.5355
Coenzyme transport and metabolism	68	4.3093	23	2.0229	31	1.9148
Defense mechanisms	42	2.6616	28	2.4626	43	2.656
DNA replication, recombination and repair	85	5.3866	61	5.365	84	5.1884
Energy production and conversion	216	13.6882	162	14.248	246	15.1946
Function unknown	117	7.4144	47	4.1337	67	4.1384
General function prediction only	119	7.5412	100	8.7951	130	8.0296
Inorganic ion transport and metabolism	88	5.5767	57	5.0132	44	2.7177
Intracellular trafficking, secretion, and vesicular transport	12	0.7605	12	1.0554	15	0.9265
Lipid transport and metabolism	36	2.2814	12	1.0554	22	1.3589
Nucleotide transport and metabolism	30	1.9011	21	1.847	47	2.903
Posttranslational modification, protein turnover, chaperones	190	12.0406	146	12.8408	196	12.1062
RNA processing and modification	1	0.0634		0	3	0.1853
Secondary metabolites biosynthesis, transport and catabolism	26	1.6477	21	1.847	13	0.803
Signal transduction mechanisms	80	5.0697	31	2.7265	91	5.6208
Transcription	37	2.3447	30	2.6385	47	2.903
Translation, ribosomal structure and biogenesis	43	2.725	52	4.5734	83	5.1266
Total	1578		1137		1619	



Ecogenomics

- Ecogenomics could be very useful in elucidating the functioning of microbial communities:
  - types of metabolic capabilities that are present would provide clues on how to culture microbes (e.g., by identifying degradative pathways, etc.)
  - find possible dependencies between different species (e.g., It may show that one species requires a metabolic product of another as an energy/carbon source or growth factor), which could also explain why some organisms cannot be cultured
  - elucidate the energy sources
  - mechanisms by which nutrients are cycled among microbes



Linkage Ecogenomics/Biogeochemistry

- How do we measure disturbance or stability of ecosystems?
- Can we integrate organismal/functional arrays for physical/chemical environmental process measurements in situ?
- We need to understand how the environment responds to microbial community composition and activity. This will aid us in gaining predictive capabilities from these response patterns for bioremediation, biofuels, and climate change.
- We also need to develop comprehensive ecological databases that can supply us with information about the ecological context of molecular, physiological, and genetic data

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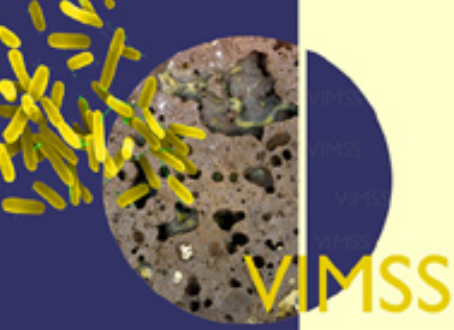

Ecogenomics Paradigm Change?

- Sequence environments based upon dominance of one important biogeochemical pathway, rather then individual organisms or all community interconnections, e.g. sulfate reduction, denitrification
- Use Expert Panel to pick target environments or microbes for the DOE relevant pathway of interest

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