

ATTACHMENT 1
GRANT OUTCOME PLAN (#1660)

Outcome 1: CAMERA tools and use-case scenarios developed to understand biodiversity and evolution of metagenomes from environmental samples and their associated metadata. Expected Date: 11/15/10					Reporting¹	
<i>Output</i>		<i>Activities</i>	<i>Expected Completion Date</i>	<i>Monitor</i> ✓	<i>% Complete</i>	<i>Actual Date</i>
1	Characterize metagenomic microbial biodiversity and biogeography from CAMERA data.	1.1 Guidelines and weightings for using different gene families in metagenomic based diversity assays (Eisen).	11/10	✓		
		1.1a. Generate alignments and trees for targeted set of 50-100 gene families; Deliver trees to projects 1b, 1c, 1d, 2a, and 2b; Generate scores for targeted set of 50-100 gene families; Test utility of scores using simulated and real metagenomic data sets.	12/08	✓		
		1.1b. Generate alignment, trees, and scores for expanded set of ~500 families; Test utility of these scores using simulated and real metagenomic data sets.	12/09	✓		
		1.1c. Integrate scores with development of diversity assays.	11/10	✓		
		1.1d. Create and update database of scores for different genes and integrate database into CAMERA.	11/10	✓		

¹ These columns of information to be supplied by UCD as part of the scheduled reporting required by Grant Agreement (GALA).

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1	Characterize metagenomic microbial biodiversity and biogeography from CAMERA data.	1.2 Searching for novel phylogenetic types in metagenomic data (Eisen)	11/10	✓		
		1.2a. Develop an automated system for novel branches using rRNA sequences in metagenomic data.	12/08	✓		
		1.2b Integrate methods into CAMERA.	12/09	✓		
		1.2c. Develop an automated system for searching for novel branches for protein coding genes.	12/09	✓		
		1.2d. Identify novel branches for each gene family; Identify other genes linked to genes identified as novel; Develop a Unifrac-like system for indentifying the amount of novelty in metagenomic data for a particular gene family; Compare the novelty of phylogenetic marker gene families versus functionally important families; Compare analysis of gene family novelty with metagenomic sample metadata to determine if any types of environments are enriched for novelty.	11/10	✓		
		1.2e. Integrate methods into CAMERA.	11/10	✓		

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1	Characterize metagenomic microbial biodiversity and biogeography from CAMERA data.	1.3 Metagenomic analysis of community phylogenetic structure (Green).	11/10	✓		
		1.3a. Metagenomic community phylogenetic analysis of rRNA genes.	12/08	✓		
		1.3b. Metagenomic community phylogenetic analysis of all 50 gene families identified in 1a.	11/10	✓		
		1.3c. Assess utility of gene families from community phylogenetic perspective.	11/10	✓		
		1.3d. Integrate methods into CAMERA tools.	11/10	✓		
		1.4 Estimating biodiversity from metagenomic samples (Green).	11/10	✓		
		1.4a. Assess the fidelity of currently used species (or phylotype richness estimators).	12/08	✓		
		1.4b. Develop and evaluate novel biodiversity estimators geared toward metagenomics.	11/10	✓		
		1.4c. Apply diversity estimators to publicly available data.	11/10	✓		
		1.4d. Apply diversity estimators to publicly available data.	11/10	✓		

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2	Identify evolutionary dynamics of microbes in nature as illustrated in CAMERA data.	2.1 Molecular evolution of gene families (Pollard).	11/10	✓		
		2.1a. Develop and evaluate molecular evolutionary methods for metagenomics.	12/08	✓		
		2.1b. Focused assessment of global evolutionary patterns and trends.	12/09	✓		
		2.1c. Detailed investigation of particular cases of very rapid genome evolution.	11/10	✓		
		2.1d. Integrate methods into CAMERA tools.	11/10	✓		
		2.2 Population genomics (Eisen).	11/10	✓		
		2.2a. Develop FST like measures of genomic variation within communities versus between communities.	12/08	✓		
		2.2b. Develop methods to quantify insertion-deletions, recombination, and rearrangement by comparison to reference genomes.	12/09	✓		
		2.2c. Develop the genomic x spatial species concept for microbes.	12/09	✓		
		2.2d. Develop phylogenetic sliding window approach for determining if multiple populations are present in a single bin.	12/09	✓		

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		2.2e. Estimate effective population (Ne) sizes for different microbes and design of methods to detect community-level bottlenecks that may make communities vulnerable as seen in endangered species.	11/10	✓		
		2.2f. Correlation analysis on general patterns of “evolvability” such as mutation rates, population size, and recombination patterns with community characteristics.	11/10	✓		

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3	Develop statistical methods to correlate metagenomic sequence data with environmental metadata.	3.1 Metagenomic analysis of community phylogenetic structure (Green).	11/10	✓		
		3.1a. Survey metagenomic data to determine scope of data types.	12/08	✓		

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		3.1b. Methods for model selection in metagenomics.	12/09	✓		
		3.1c. Develop and evaluate methods for correlation analysis of metagenomic data.	12/09	✓		
		3.1d. Apply correlation analysis to publicly available data.	11/10	✓		
		3.1e. Integrate methods into CAMERA tools.	11/10	✓		