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FY09 Final Report for LDRD Project: Understanding Viral Quasispecies Evolution through Computation and Experiment

C. Zhou

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Proposed Work from last year's proposal

In FY09 we will (1) complete the implementation, verification, calibration, and sensitivity and scalability analysis of the in-cell virus replication model; (2) complete our design of the cell culture (cell-to-cell infection) model; (3) continue the research, design, and development of our bioinformatics tools: the Web-based structure-alignment-based sequence variability tool and the functional annotation of the genome database; (4) collaborate with the University of California at San Francisco on areas of common interest; and (5) submit journal articles that describe the in-cell model with simulations and the bioinformatics approaches to evaluation of genome variability and fitness.

Enter accomplishments below:

In FY09 we (1) completed the implementation and verification of an in-cell virus replication stochastic simulation modal. The calibration and sensitivity/scalability of this model is underway as we continue to analyze data received from our UCSF collaborator; (2) completed the design, implementation and verification of a cell-to-cell infection model (ahead of schedule); (3) we continued the R&D of bioinformatics tools and completed a new algorithm for sequence variability analysis; (4) we continued a collaboration with UCSF researchers in exploring polio genetics and evolution; and (5) we have 2 journal articles in preparation (one describing the sequence variability algorithm and the other a study of virual quasispecies theory); we expect to submit these for review in early FY10.