Poster Number

9 **Aptamer library resampling**

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Aptamers are nucleic acid based binding molecules capable of specific, high affinity binding. Aptamers are isolated from a library of random ssDNA or RNA sequences using SELEX, a process involving successive rounds of selection for analyte binding and amplification. Due to insufficient library sequence space coverage and the stochastic nature of SELEX the probability of selecting the fittest aptamer is extremely low. You are however extremely likely to select family members of the fittest aptamer. Herein we describe 'Resample', a computer program coded in Visual Basic which takes an input of an aptamer family motif and outputs a library representing every aptamer permutation of the family motif. By taking sequences isolated using SELEX and using sequence alignment you can deduce with high probability the aptamer family motif of the highest affinity aptamer. This motif can then be used by 'Resample' to combinatorially generate an aptamer library containing many novel high affinity aptamers and most probably the highest affinity aptamer which exists. This library could then be synthesised in solution or onto the surface of a microarray and subsequent selections performed to isolate extremely high affinity aptamers. Increasing aptamer affinity in this way is extremely valuable for reducing the limit of detection of aptamer based diagnostic tests for disease as well as increasing efficacy of aptamer based therapeutics.

10 **Effects of lysogeny on the ecophysiological fitness of E. coli**

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Escherichia coli is a symbiont of warm-blooded animal. However, E. coli was found in external environment without fecal input, where it was faced a large number of environmental stresses that were absent in the animal host. It is well known that prophages (i.e. DNA of phages residing in the genome of bacterial cells) play a significant role in the genome diversification and niche expansion of pathogenic E. coli strains from one host species to another, but whether prophages can facilitate to E. coli niche expansion from the animal host to the external environment still remains unknown. In our study, a model system composed of an environment E. coli strain, and a pair of pre- and post-lysogenic facal E. coli strain was used to elucidate the effect of lysogeny on the ecophysiological fitness of E. coli. By analyzing the whole genome sequences of the three strains, it is confirmed that the pre- and post-lysogenic strains are isogenic, with a P2-like prophage from the environmental strain is acquired by the post-lysogenic strain. Sediment and seawater microcosm experiments show that the post-lysogenic fecal strain decay significant slower than the pre-lysogenic strain. The metabolic profiles of the pre- and post-lysogenic pair are also appeared to be different. By applying genetic engineering, the P2 prophage acquired by the post-lysogenic fecal strain is knocked out completely and the impact of the prophage deletion to the host survival is undergoing investigation.