Abstract Submitted
for the MAR06 Meeting of
The American Physical Society

Discovering the recognition code bacteria use to sense their environment by tracking co-evolutionary patternsBacteria typically posses tens of distinct signaling pathways that allow the organism to translate diverse environmental conditions into action ROBERT WHITE, The Scripps Research Institute (TSRI), TERRY HWA, The Center for Theoretical Biological Physics (UCSD), JIM HOCH, TSRI — Bacteria typically posses tens of distinct signaling pathways that allow the organism to translate diverse environmental conditions into action. A common signaling mechanism is a bucket brigade of phosphate triggered by the auto-phosphorylation of "sensor kinase" (SK) then passed to a protein called a "response regulator" (RR). The phosphorylation state of the RR regulates its function, thereby completing the signaling pathway. In one organism—but in pathways responsible for sensing diverse signals—the domains at which the transfer of the phosphate group occurs show surprising homology to each other. What keeps the organism from getting its signals crossed? We present a detailed bioinformatic study of over 1500 cognate SK/RR pairs that reveals patterns that can be used to predict the presence of evolved crosstalk and shed light on the paralogous divergence of these essential messengers.

Robert White
The Scripps Research Institute

Date submitted: 07 Dec 2005

Electronic form version 1.4