



**University of
Zurich** ^{UZH}

Department of Evolutionary Biology
and Environmental Studies

BEEES (Behavior, Ecology, Environment and Evolution Seminar)

How one becomes another: exploring the role of exaptation on the evolution of gene regulation

Speaker:	Cauã Westmann IEU, UZH
Date/Time:	Thursday, 2024-05-02 12:38 to 13:00
Place:	Y03-G-95/UZH Irchel Winterthurerstr. 190; 8057 Zürich on site and on line
Access:	only intern
Host:	Andreas Wagner

Abstract:

Exaptation, the co-option of existing traits for new functions, is a central process in Darwinian evolution. However the molecular changes leading to specific exaptations remain unclear. Here, we investigated the potential of bacterial transcription factor binding sites (TFBSs) to evolve exaptively, examining three global transcription factors (TFs) from *Escherichia coli*: CRP, Fis, and IHF. Using a massively parallel reporter assay, we mapped three combinatorially complete adaptive landscapes, encompassing all intermediate sequences between three pairs of strong binding sites for each TF. Our results revealed that these landscapes are smooth and navigable, with a monotonic relationship between mutations and their impact on gene regulation. Starting from a strong TFBS for one of our TFs, Darwinian evolution can thus create a strong binding site for another TF through a small number of individually adaptive mutations. Notably, most intermediate genotypes are prone to transcriptional crosstalk – gene regulation mediated by both TFs. Because our landscapes are smooth, Darwinian evolution can also easily create binding sites that show such crosstalk whenever it is adaptive. Our study presents the first in vivo evidence that new TFBSs can evolve exaptively through multiple small and adaptive mutational steps. They also highlight the importance of regulatory crosstalk for the diversification of bacterial gene regulation.

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