

Extensive genomic interactions between two *S. cerevisiae* transcription factors

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ABSTRACT

Copper and ion homeostasis are closely interconnected cellular processes in S. cerevisiae. Two transcription factors, Mac1 and Aft1, are molecular sensors that serve to activate their transcription programs after fluctuations in copper and iron availability respectively. Given their role in distinct but interconnected processes, we investigated whether they are functional collaborators by analyzing their binding patterns in copper and iron starvation conditions. The binding pattern of each one was also assessed in the absence of the other factor. Our results indicate that in normal conditions the two factors occupy a significant number of similar targets, with a lot of genes being unrelated to copper and ion homeostasis. The deletion of one factor, affects dramatically the binding pattern of the corresponding partner at both short and longrange levels. Short range changes mean that binding is shifted towards the 3' end of genes, while long-range ones suggest a global re-distribution of binding in a different, more extended set of genes. Interestingly, binding shifts are in most cases not accompanied by changes in expression levels. Our results may indicate cases of nonproductive binding or suggest other, unknown roles for the studied transcription factors.

12th Scientific FORTH Retreat, FORTH/ICE-HT, Patras, October 14-16 2019