GLOBAL CHANGES IN CHROMOSOME CONFORMATION IN BUDDING YEAST IN DIFFERENT PHYSIOLOGICAL CONDITIONS

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A long-standing problem in eukaryotic cell biology is to understand how the genetic information is organized and folded to fit into the interphase nucleus. The organization of the genome is non-random and was shown to be important for the correct genome function. For example, the nuclear envelope plays a critical role in gene regulation and interactions between genes and the nuclear periphery can lead to gene repression. However, several genes, including the *GAL* gene locus in budding yeast, are recruited to the nuclear periphery upon activation. We have asked how the association of the single gene locus with the nuclear envelope influences the surrounding chromosome architecture. Using modeling and light microscopy assays we follow the movement of an entire chromosome in yeast demonstrating that peripheral recruitment of the *GAL* locus upon carbon source change is not an isolated event but part of a large scale rearrangement that shifts many chromosomal regions closer to the nuclear envelope. This process is likely due to the presence of independent anchoring points along the chromosome and depends on the activity of histone modifying enzymes.