Determining the effect of a Gene Recruitment Sequence on Gene Localization

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The genome is spatially organized within the nucleus so that individual chromosomes are not randomly positioned, but instead adopt preferred conformations. Furthermore, the position of specific genes can be influenced by their expression. Although the nuclear periphery is traditionally associated with repression and heterochromatin, several genes are targeted to the periphery upon induction. This is dependent on interaction with the nuclear pore complex (NPC) and may help facilitate the rapid export of mRNA transcripts from the nucleus. A short *cis*-acting DNA element discovered in the promoter of the *INO1* gene acts as a DNA zip code that is sufficient to target the gene to the nuclear periphery. A perfect match of this 8 base pair gene recruitment sequence (GRS I) can be found in the promoters of many other genes that are upregulated by stress conditions, including the gene *TSA2*. Like *INO1*, *TSA2* is targeted to the nuclear periphery upon transcriptional activation. This led to the question of whether the GRS I targets genes to the nuclear periphery in general, or if it sends genes to a specific NPC or subset of NPCs. By tagging these two genes with a LacO or TetO array and coexpressing LacI-RFP and TetR-GFP, the location of the genes was visualized by confocal microscopy as a red and green dot and the distance between them was measured. *INO1* and *TSA2* conditionally colocalized upon activation in a GRS I-dependent manner. This suggests that the GRS I is a specific targeting sequence that may help coordinate the regulation of genes that are activated under stress conditions.