Alternative chromatin structures of the 35S rRNA Genes in Saccharomyces cerevisiae provide a molecular basis for the selective recruitment of RNA polymerases I and II

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In all eukaryotes, a specialized enzyme, RNA polymerase I (Pol I), is dedicated to transcribe the 35S rRNA gene from a multicopy gene cluster, the ribosomal DNA (rDNA). In certain Saccharomyces cerevisiae mutants, 35S rRNA genes can be transcribed by RNA polymerase II (Pol II). In these mutants, rDNA silencing of Pol II transcription is impaired. It has been speculated that upstream activating factor (UAF), which binds to a specific DNA element within the Pol I promoter, plays a crucial role in forming chromatin structures responsible for polymerase specificity and silencing at the rDNA locus. We therefore performed an in-depth analysis of chromatin structure and composition in different mutant backgrounds. We demonstrate that chromatin architecture of the entire Pol I-transcribed region is substantially altered in the absence of UAF, allowing RNA polymerases II and III to access DNA elements flanking a Pol promoter-proximal Reb1 binding site. Furthermore, lack of UAF leads to the loss of Sir2 from rDNA, correlating with impaired Pol II silencing. This analysis of rDNA chromatin provides a molecular basis, explaining many phenotypes observed in previous genetic analyses.
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