Gene Transcription in Yeast:
From single molecules to separated phases

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cover art: Umberto Aiello
Evolutionarily conserved kinases and phosphatases regulate RNA polymerase II (RNAPII) transcript synthesis by modifying the phosphorylation status of the carboxyl-terminal domain (CTD) of the largest subunit, Rpb1. Proper levels of Rpb1-CTD phosphorylation are required for RNA co-transcriptional processing and transcription coordination with other nuclear processes, such as chromatin remodeling and histone modification. Whether other RNAPII subunits are phosphorylated and if this influences their role in gene expression is still an unanswered question. Much less is known about RNAPI and RNAPIII phosphorylation, whose subunits do not contain functional CTDs. We have compiled all the phospho-sites identified to date for S. cerevisiae RNAPs in different phospho-proteomic studies. Several RNAPI and RNAPIII subunits are susceptible to phosphorylation. Some of these phosphorylation sites are distributed within subunits common to all three RNAPs whereas others are only shared between RNAPI and RNAPIII. This suggests that the activities of all RNAPs might be modulated by phosphorylation and raises the idea that this could coordinate the activities of the three RNAPs. In addition, we have studied the particular case of Rpb4, which together with Rpb7 forms the RNAPII stalk domain, with important functions in gene expression regulation. Rpb4 is indeed phosphorylated in vivo and our preliminary data suggest that Rpb4 phosphorylation levels could play a role in the regulation of transcription.
Studying new RNAPII phosphorylation sites

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