INTERACTION BETWEEN NUCLEOME AND PLASTOME: HEAT SHOCK RESPONSE REGULATION IN PLASTIDS OF PLANTS

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Motivation and Aim: Understanding interactions between nuclear and plastid genomes is important. Here we consider one example: a suggested mechanism of the heat shock response in chloroplasts. The mechanism well explains known experimental data for chloroplasts.
Methods and Algorithms: To study a competition of RNA polymerases of different types in plastids we developed a model based on a sophisticated system of interacting stochastic and deterministic processes. It is implemented in two versions: a program for multiprocessor clusters (tested with the 1024 parallel CPU on MBC-100K supercomputer of the Joint Supercomputer Center RAS) and a standalone PC program with real-time computing progress graphic monitor. Both programs are available at http://lab6.iitp.ru/rivals/, along with detailed algorithm descriptions and usage examples.
Results: Let's consider an example. *Hordeum vulgare* contains two copies of the following set of genes: *trnI*–*rpl*23–*rpl*2–(*trnH*)–*rps*19. One set competes with neighboring gene *psbA*: P1-*trnI-rpl23-rpl2*-(*trnH*-P2)-*rps19*-(*psbA*-P3), and the other set adjoins the next operon on the same strand: P1-*trnI-rpl23-rpl2*-(*trnH*-P2)-*rps19-rpl22-rps3-rpl16-rpl14-rps8-infA-rpl36-rps11-rpoA*. The transcription level ratios were measured experimentally for these sets at the temperatures of 21°C and 40°C [1].
Conclusion: Our model predictions conform within experimental error with the *in vitro* measurements for values of the promoter binding efficiency P1=1.4, P2=0.7, P3=0.3s^{-1}, and the RNA polymerase elongation rates R_{21}=9.2 and R_{40}=36.8bp/s at lower and higher temperatures, respectively, which also agrees with independent observations [2]. Thus, the modeled competition of RNA polymerases can explain the heat shock response mechanism at least in isolated chloroplasts. Noteworthy, our quantitative predictions are in good agreement with the sigma subunit knockout experiments in other loci, where we also predict the elongation termination sites verified with the multiple alignment and biological data. Such is locus P1–*psbB*–*psbT*–(*psbN*–P2)–*psbH*–*petB*–*petD*–(*rpoA*–*rps*11–P3–*rpl*36–*trnI*–N) in *Arabidopsis thaliana,* where the sites are conserved 44bp palindromes (presumably DNA cross-hairpins), e.g. TTAACGTAATCAGCCTCCAAATATTTGGA GGCTGATTACGTTAA, downstream the *psbT* gene.
References:
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