Cellular Programs

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Assignment 3

Handed out: 13.05.25

Due: 20.05.2025 10.00 am

Submit your solutions by e-mail with a single PDF attachment

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Label your pdf solution as MATRICULATIONNR_YOURNAME.pdf.

Every student should submit his/her own solution. Plagiarism of solutions will be penalized. Indicate whether you used AI tools. Label your assignment sheet with your name and matriculation number. Don't exceed specified page lengths by more than 0.25 pages.

All problems refer to paper #6: Hiroto Fukushima et al. EMBO Rep., 25, 3300–3323 (2025).

Problem 1:

Fig. 1B shows that H3K9me3 levels are strongly reduced during progression from 1-cell to 16-cell stage of medaka embryos. The authors tested whether this is due to active or passive demethylation. Although they showed that it is due to passive demethylation, let us consider here the hypothesis that there exists active demethylation.
a) If the reduction of H3K9me3 levels would be indeed caused by active demethylation, why does one expect that extending the cell cycle results in greater reduction of H3K9me3 levels?
b) Could one test the active-demethylation hypothesis also by overexpression/siRNA-silencing of certain genes? Which genes should be tested? What results would you expect for H3K9me3 levels when you overexpress/siRNA-silence these genes? (0.25 page).

Problem 2:

ZGA stands for zygotic genome activation. The authors injected the RNA polymerase II inhibitor α-amanitin into medaka embryos so that transcription of mRNAs from the genome was effectively blocked. Still, Fig. 2B shows that number and morphology of embryos are comparable until late blastula stage (ca. 4000 cells) between non-inhibited conditions and the α-amanitin-treated case. How is this possible? Is transcription not needed in early development? How can cell division occur? How many cell division cycles do you expect (on average, assuming that all cells divide equally fast) until late-blastula stage? (0.25 page)

Problem 3:
The authors claim that Figs. 4A-C show that before MBT, Setdb1 was mainly localized in the cytoplasm, whereas after MBT Setdb1 was localized in both nuclei and cytoplasm. Explain **based on Figs. 4A and 4B only** how the authors arrived at this conclusion. (0.25 page)