

RNA-Seq for *Danio rerio*, exposed to pulp and paper wastewaters

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Motivation and Aim: The wood processing industry (mainly pulp and paper complexes) occupy third place in the amount of waste water produced [1]. The waste water of the wood processing industry is contaminated with both organic and non-organic compounds (lignins, tannins, chlorine derivatives etc.) [2] typically passed mechanical, physical, chemical as well as microbiological treatment to remove or decrease the abundance of these compounds. However, imperfect treatment regularly leads to the leakage of contaminants, which may have a significant impact on the environment, especially on neighboring water systems. The associated risks particularly for fish include the growth of harmful bacteria decreasing dissolved oxygen levels and leading to fish anoxia, low visibility because of low water transparency, a reduction in the abundance of feedstock (invertebrates) and hence fish population densities, the accumulation of trace and toxic elements in fish, which could be transferred to human, physiological changes [3, 4], as well as evolutionary responses particularly in immune and metabolic pathways. The goal of the project is to characterize the transcriptome response of zebrafish to the contamination from the wood processing wastewaters.

Methods and Algorithms: Fishes are exposed to wastewaters with variable concentrations. For acute experiment fishes are exposed for 96 hours to detect acute toxicological effect on fishes mortality, and limiting concentration of the wastewaters. For chronic toxicological effect, fishes are exposed to wastewaters with concentrations less than acute concentration for 30 days. By the end of exposure, survived fishes are prepared for RNA-Sequencing.

Results and Conclusion: in process.

References

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