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**Project title: Evaluation of DNA damage repair capacity in sterlet embryos using qPCR and western blotting**.

Fish live in a wide range of marine and freshwater ecosystems and come in direct contact with several genotoxicants at each stage of development. Externally fertilizing fish release embryos directly into water which might be contaminated with DNA damaging agents, making them vulnerable to genotoxicity. Genome maintenance is crucial during embryogenesis. Replication of damaged DNA may impair normal development, survivability and can have far-reaching consequences at population level. In response to the challenges faced by DNA, fish embryos are equipped with developmental stage-specific DNA repair machinery. DNA repair pathways involve numerous genes and proteins which sense the damage, communicate information through signal transducers to effectors, which mediate the physiological response of the cell to mitigate the damage. Five major DNA repair pathways described in fish —base excision repair (BER), nucleotide excision repair (NER), mismatch repair (MMR), homologous recombination (HR), and nonhomologous end joining (NHEJ).

Sturgeons are categorized as one of the most threatened group of species with almost two-thirds population being critically endangered (<http://www.iucnredlist.org>). Water pollution is one of the reasons contributing to their declining number. Assessment of DNA damage repair capacity is essential to understand the extent of genotoxic threats faced by sterlet embryos at different stages of development.

In this study, we will analyse the DNA repair capacity of sterlet embryos at different stage of development using qPCR and western blotting. We will check the change in expression of some of the DNA repair genes and proteins in response to genotoxic stress on the samples collected during spawning season. During spawing season, we will expose sterlet embryos to a model genotoxicant Methyl methane sulfonate (MMS) during blastulation, gastrulation and neurulation. Subsequently, control and treated embryos will be collected at 1dpf (days of post fertilisation), 2dpf, 3dpf and 8dpf. MMS has been reported to induce DNA damage via alkylation. The candidate genes to be studied may include, *ogg1, apex1, xrcc1, polb, msh2, ercc1, xpc, mgmt,* and *ddb2* etc. Also, we aim to study the change in expression of DNA repair proteins; XRCC1, APEX1, MGMT, and DDB2 etc.

Thus, with the help of above mentioned techniques we will assess the DNA repair capacity of sterlet embryos at different stage of development. Results of the study can be envisioned for evaluating toxicity of different contaminants having potential to cause DNA damage in fish embryos.