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Subculture of fin explants: a powerful optimization of fin cell production for cryobanking purposes

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HYPOXIA AND BRANCHIAL BASKET DEVELOPMENT: KEEPING PACE WITH A LIMITING RESOURCE

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Symposium: Climate Change

Presentation Type: Oral

Abstract: The mouthbrooding cichlid *Pseudocrenilabrus multicolor* exhibits developmental plasticity in gill size that may contribute to its persistence across a wide range of habitats. An important question is whether this plasticity is reversible during ontogeny. If the plastic response to high dissolved oxygen (DO) in early life is to produce small gills, but this is not reversible, there is a risk of encountering low DO later in life without adequate compensatory mechanisms. In a rearing experiment, *P. multicolor* broods were split into four groups. Group 1 was raised initially under low DO, followed by a switch to high DO after 4 months. Group 2 was raised under high DO and switched to low DO. As controls, two groups were reared under either low- or high DO. Results showed that gill development tracked the temporal shift in DO. Such developmental flexibility may be important for persistence in changing and/or novel DO environments.

IN SILICO IDENTIFICATION OF DAPHNIA PULEX MIRNAS

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Symposium: Fish in a Toxic World

Presentation Type: Poster

Abstract: *Daphnia pulex* has long served as an important model organism. With its parthenogenetic life cycle and several well-studied environmental stressor related phenotypes, *D. pulex* offers various benefits for aquatic toxicological research. MicroRNAs (miRNAs) are 21-25 nucleotide small non-coding RNAs that are key regulators of gene expression. In the last few years, there is increasing evidence of miRNAs and their target genes being affected by toxicants and environmental influences, suggesting an important role of miRNAs in toxicology. However, compared with other model animals that have hundreds of miRNAs reported, there are only 45 miRNAs reported to miRBase for *Daphnia pulex*, not to mention the absence of several deeply conserved miRNA families (like the let-7 family). As miRNAs are highly conserved between sister groups and with the sequence of the *D. pulex* genome, we are trying to use computational methods to annotate miRNAs in the *D. pulex* genome.

SUBCULTURE OF FIN EXPLANTS: A POWERFUL OPTIMIZATION OF FIN CELL PRODUCTION FOR CRYOBANKING PURPOSES

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Symposium: Fish Cell Cultures

Presentation Type: Poster

Abstract: Incorporation of diploid somatic fin cells in cryobank compensates for fish egg and embryo inability to cryopreservation. The obtention of large quantity of cells derived from primary culture of fin explants is therefore of considerable importance, notably in the case of threatened species where only small fin pieces can be collected. In this study developed on goldfish, we explored whether the re-plating of fin explants would allow a second round of cell production. We demonstrated that explant re-plating indeed gave a new cell population, with better proliferation properties than cells from the first explant plating. Cells from explant re-plating had the same immunochemical epithelial pattern as cells from the first explant plating. A more specific characterization of the re-plating culture using molecular markers (transcripts level and expression pattern over culture time) will be presented. Such cell production after explant re-plating counteracts the overall poor sub-culture ability of fin cells.

THE ROLES OF IROQUOIS GENES IN ZEBRAFISH RETINAL AND CARDIAC DEVELOPMENT

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Symposium: Zebra Fish

Presentation Type: Oral

Abstract: The Iroquois homeobox genes play important roles in zebrafish retinogenesis and heart development. The zebrafish Iroquois homolog *irx1a* is expressed during retinogenesis and knockdown of *irx1a* results in a retinal phenotype strikingly similar to those of sonic hedgehog (*shh*) mutants. Analysis of *shh*-GFP transgene expression in *irx1a* knockdown retinas revealed that *irx1a* is required for the propagation of *shh* expression through the retina. Transplantation experiments illustrated that the effects of *irx1a* on *shh* expression are both cell-autonomous and non-cell-autonomous. We also found that *irx2a* is expressed in the developing retina and that knockdown of *irx2a* results in a retinal phenotype strikingly similar to that of *irx1a* morphants. The expression of *irx2a* in retina ganglion cells was shown to be *irx1a*- and *ath5*-dependent suggesting that *irx1a* and *ath5* are transcriptional regulators of *irx2a*. Furthermore, *irx2a* expression could rescue impaired propagation of *shh* waves in *irx1a* morphants. Together, these observations suggest that *Irx2* functions downstream of *irx1a* to control *shh* expression in the retina. We proposed a novel transcriptional cascade of *ath5*-*irx1a*-*irx2a* in the regulation of hedgehog waves during vertebrate retinal development. We are currently exploring whether similar regulatory mechanisms are controlled by the *irx* genes in embryonic heart. Our preliminary data supports a necessary role of *irx* genes in the transcriptional control of cardiogenesis

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