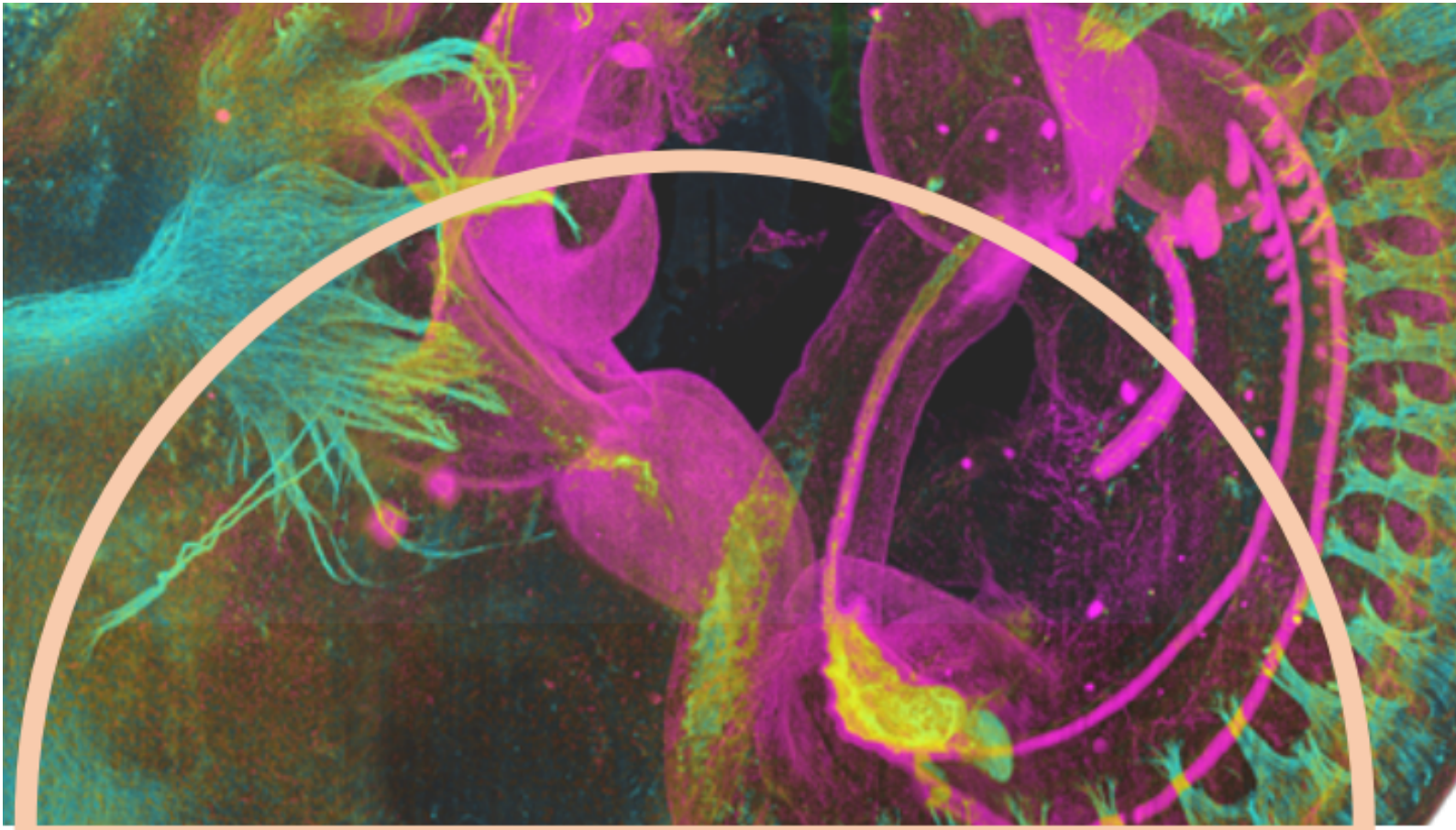

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ABSTRACT BOOK

Poster Abstracts

P001 - P115

P082

Implementation of transgenic platform based on the application of CRISPR/Cas9 technology in mouse zygotes

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In recent years, the development of CRISPR technologies has provided an excellent tool for genomic editing. We have taken advantage of this technology to set up a CRISPR service at our Institute that based on the electroporation of mouse zygotes (day 0.5) generates desired mouse genomic modifications in a highly efficient, rapid and unexpensive manner.
We have applied this methodology to the generation of several mouse models of human congenital hand malformations, especially focussing on the Split Hand Foot Malformation (SHFM), a rare and highly variable malformation characterized by the loss or deformity of the central digit rays. We have previously shown the involvement of Sp6 and Sp8 transcription factors in the generation of SHFM phenotypes in mouse and the interaction of these two factors with Dlx family members. Dlx genes are the genes involved in human SHFM types 1 (Dlx5/Dlx6) and 5 (Dlx1/Dlx2). With the aim of fully investigating the implication of the Dlx-Sp interactions in the pathogenesis of SHFM, we have generated a couple of mouse models: the Dlx5/Dlx6 double deletion and the Sp6-V5 tagged knock-in. Additionally, and based on studies in Drosophila indicating that Sp factors control appendage development through the Notch pathway, we have also generated a Jag2 KO mutant.
We are currently using the generated animal models to advance our understanding of the mechanisms subjacent to the SHFM.