in vertebrates. Its functional unit, the sensory patch, contains mechanosensory hair cells innervated by sensory neurons of the vestibular and acoustic ganglia that project to the corresponding nuclei in the brainstem. How hair cells develop at specific positions, and how otic neurons are sorted to specifically innervate each endorgan and to convey the extracted information to the hindbrain is not completely understood yet. In our previous work, we studied how, when and where the formation of first-order neurons and their target hair cells takes place. We showed that the Hh pathway is crucial in coordinating the production of hair cells in the posterior macula (PM), and in the formation of its specific innervation, underlying the importance of Hh pathway in the de novo formation of a fully functional posterior sensory patch. Nevertheless, how Hh signaling is involved in defining a PM-specific identity is still unknown. One interesting question that this work highlights is how Hh confers saccular (PM) identity. Hh signaling might direct the development of both neuronal and sensory progenitors within the posteromedial otic domain. This would suggest that there is a common pool of progenitors for saccular hair cells and neurons located in the postero-medial territory in the otic epithelium. We want to address how the generation of neurons and sensory cells in this territory is coordinated – focusing on the role of proneural genes – and whether there is a common progenitor that responds to different spatial and temporal cues. Expression analysis of proneural genes in this otic territory shows that expression domains of bHLH transcription factors for neurons and sensory cells partially overlap within the posteromedial otic domain. In addition, functional experiments with neurog1 and neuroD genes suggest that neurog1 defines a posteromedial field of progenitors with competence to form PM hair cells, supporting the idea of a common pool of neurosensory precursors in the zebrafish inner ear. DS was a recipient of a postdoctoral JdC contract from MICINN (Spain) and SD is supported by a predoctoral FI fellowship from AGAUR (Generalitat de Catalunya). This work has been funded by the grant BFU2009-07010 from MICINN (Spain) to CP.

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**Program/Abstract # 250**
**Exploring the function of hair-cell-enriched microRNAs in vitro and in vivo**
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To detect sound and sense balance, animals rely on a specialized group of cells known as mechanosensory hair cells (HCs). HCs arise from the same group of progenitors as their supporting cell neighbors. The bHLH transcription factor, Atoh1, is both necessary and sufficient for HC fate acquisition, while a family of HC-enriched miRNAs, the miR-183 family, can influence HC numbers, morphology and progression of differentiation. These and other miRNAs may function to repress genes required to maintain the progenitor status, to adopt the alternative supporting cell fate, or both. If so, then the simultaneous delivery of both Atoh1 and specific miRNAs should enhance HC development. We are testing this in two ways: by validating predicted target genes of miR-182 (a miR-183 family member) in vitro and by creating gene transfer vectors that force expression of both Atoh1 and selected miRNA genes in vivo. In vitro luciferase assays show that miR-182 targets at least 14 3'UTRs, including some HC transcripts (e.g., Myosin1C and Myrip, a Rab effector that recruits myosins). For gene transfer, a bifunctional cassette was created that houses the miRNA-183 family in an artificial intron upstream of Atoh1 fused to a HA tag, all driven with the EF1α promoter. To date, the function of vector-transduced Atoh1 and the miR-183 family has been confirmed by in vitro luciferase reporter assays. For in vivo studies, bifunctional vectors are electroporated into E3 chicken otocysts and analyzed 2 days later. In vivo experiments confirm that Atoh1 alone can generate ectopic HCs. Future research is focused on analyzing otocysts injected with the entire bifunctional cassette as well as assessing what impact these miRNAs alone have on HC development.

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**Program/Abstract # 251**
**Specification of sensory progenitors: Towards a gene regulatory network**
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In the head, sense organs and sensory ganglia largely arise from the ectoderm outside of the central nervous system, the sensory placodes. During development they are derived from a pool of multipotent progenitor cells that are set aside at neural plate stages. To uncover molecular mechanisms controlling their specification we have identified the signaling pathways that induce sensory fate in naïve ectoderm as well as the transcription factors that mediate their action. Members of the Six and Eya gene families play an important role and in addition we have identified new genes that may act up-stream, down-stream or in parallel to these factors to impart sensory progenitor identity. Current experiments aim to determine their genetic hierarchy and interaction and we present a gene regulatory network that models sensory progenitor specification and diversification.

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**Program/Abstract # 252**
**The role of the zinc-finger transcription factor Sp8 in the establishment/maintenance of the dorsal lateral ganglionic eminence (dLGE)**
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The embryonic lateral ganglionic eminence (LGE) is an important progenitor domain that gives rise to olfactory bulb interneurons and striatal projection neurons. Recent work has suggested that these two neuronal subtypes arise from distinct progenitor populations within the LGE. The dorsal (d)LGE is proposed to give rise to olfactory bulb interneurons while the ventral (v)LGE generates striatal projection neurons. Previous work has shown that the zinc-finger transcription factor Sp8 marks the dLGE subventricular zone (SVZ) as well as the postnatal SVZ. Additionally, conditional deletion of Sp8 in the ganglionic eminences results in the reduction of olfactory bulb interneuron subtypes. However, it remains unclear whether Sp8 plays an active role in the establishment and/or maintenance of the dLGE SVZ. To study the role of Sp8 in defining the dLGE we have taken a gain-of-function approach. We generated a tetO-Sp8-IRES-EGFP line and expanded the expression domain of Sp8 throughout the LGE SVZ using a recently developed Dlx5/6-tTa mouse line. Our results suggest that expansion of the Sp8 domain results in the downregulation of vLGE markers such as Islet-1 at late embryonic and early postnatal stages. Furthermore, the overexpression of Sp8 leads to an enlarged SVZ/Rostral Migratory Stream (RMS) in the postnatal brain and a concomitant reduction in striatal size. Doxycline treatment of the pregnant females harboring Sp8 overexpressing embryos, delayed activation of the Sp8 transgene until E15 and did not result in respecification of vLGE to dLGE fates that was seen at early time points. Our results therefore support a role for Sp8 in establishing/maintaining dLGE identity within the LGE SVZ at early embryonic stages.

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