MO259 Gene transcription ontogeny of hypothalamic-pituitarythyroid axis development in early-life stage fathead minnow and zebrafish L. Vergauwen, University of Antwerp / Zebrafishlab Dept Veterinary Sciences SPHERE; J.E. Cavallin, Badger Technical Services / National Health and Environmental Effects Research Laboratory; G.T. Ankley, U.S. EPA / National Health and Environmental Effects Research Laboratory; C. Bars, University of Antwerp / Applied Veterinary Morphology Dept Veterinary Sciences; I. Gabriëls, E.D. Michiels, University of Antwerp / Zebrafishlab Dept Veterinary Sciences; K. Nelson, U.S. EPA / Toxic Effects Branch; J. Periz Stanacev, University of Antwerp / Zebrafishlab Dept Veterinary Sciences; E. Randolph, EPA / National Health and Environmental Effects Research Laboratory; C. Robinson, Marine Scotland Science / National Health and Environmental Effects Research Laboratory; T. Saari, U.S. EPA / ORD, NHEERL; A. Schroeder, University of Minnesota-Crookston / Math, Science and Technology; E. Stinckens, University of Antwerp; J. Swintek, Badger Technical Services; S.J. Van Cruchten, University of Antwerp / Applied Veterinary Morphology, Dept Veterinary Sciences; E. Verbueken, University of Antwerp / Applied Veterinary Morphology, Dep of Veterinary Sciences; D.L. Villeneuve, U.S. EPA / National Health and Environmental Effects Research Laboratory; D. Knapen, University of Antwerp / Zebrafishlab Dept Veterinary Sciences. The hypothalamic-pituitary-thyroid (HPT) axis is known to play a crucial role in the development of teleost fish. However, knowledge of endogenous transcription profiles of thyroidrelated genes in developing teleosts remains fragmented. We selected two model teleost species, the fathead minnow (*Pimephales promelas*) and the zebrafish (Danio rerio) to describe the gene transcription ontogeny of the HPT-axis. Control embryos were sampled at several time points between fertilization and hatching, and larvae were sampled approximately every other day until 33 days post-fertilization. Total RNA was extracted from pooled, whole fish, and thyroid-related mRNA expression was evaluated using quantitative polymerase chain reaction. Gene transcripts examined included: thyrotropin-releasing hormone receptor (trhr), thyroid-stimulating hormone receptor (tshr), sodiumiodide symporter (nis), thyroid peroxidase (tpo), thyroglobulin (tg), transthyretin (ttr), deiodinases 1, 2, 3a, and 3b (dio1, dio2, dio3a and 3b), and thyroid hormone receptors alpha and beta (*thra* and ?). A loess regression method was successful in identifying maxima and minima of transcriptional expression during early development of both species. Overall, we observed great similarities between both species, including maternal transfer of almost all transcripts (confirmed in unfertilized eggs), increasing expression of most transcripts during hatching and embryo-larval transition, and indications of a fully functional HPT-axis in larvae. By making these data available to the community, we aim to aid in the development of hypotheses on the role of certain genes and pathways during development. Furthermore, it can function as a background reference dataset for designing and interpreting targeted transcriptional expression studies both for fundamental research and for applications, such as ecotoxicology.