A COMPUTATIONAL MODEL FOR OOCYTE GROWTH DYNAMICS IN FATHEAD MINNOWS

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Molecular biomarkers have been used in ecotoxicological studies to evaluate the effects of endocrine disrupting chemicals in fish. Changes in these molecular biomarkers must then be linked to the effects upon reproduction in individuals, and subsequently populations. To meet this need, we developed a computational model of oocyte growth dynamics (i.e., oocyte recruitment, growth, and spawning) in an asynchronous spawning fish, fathead minnow (FHM, *Pimephales promelas*). The model simulates the number and volume of oocytes in different batches within an FHM ovary. Oocyte growth was formulated to be a function of the absorption of vitellogenin (a lipoprotein precursor of egg yolk proteins used as a molecular biomarker in fish), which is known to contribute significantly to oocyte growth in fish. Model-predicted clutch sizes, spawning intervals, and average fecundity in unexposed FHMs and FHMs exposed to 17β-trenbolone matched the experimental data well. The mean and median model predictions were within 0.5 to 2.0 fold of the mean and median measurements. Overall, the model presents a novel approach to simulate oocyte growth dynamics in FHM, and provides a quantitative link between oocyte growth and the biochemical system in FHMs through vitellogenin.

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