

Identification of amnion progenitor-like cells at the amnion-epiblast boundary in the primate peri-gastrula

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ABSTRACT

Amniogenesis is triggered in a collection of pluripotent epiblast cells as the human embryo implants. To gain insights into the critical, but poorly understood, transcriptional machinery governing amnion fate determination, we examined the evolving transcriptome of a human pluripotent stem cell (hPSC)-derived amnion model at the single cell level. This analysis enabled the identification of several markers specific to the different stages of amnion lineage progression, and revealed a previously unrecognized CLDN10⁺ amnion progenitor cell type, as well as formation of some primordial germ cell-like cell (PGCLC) in this model. Strikingly, in peri-gastrula cynomolgus macaque embryos the expression of CLDN10 is restricted to the amnion-epiblast boundary region. This bolsters the notion that, at this stage, the amnion-epiblast boundary is a site of active amniogenesis. Bioinformatic analysis of published primate peri-gastrula single cell sequencing data further confirmed that CLDN10 is expressed in cells progressing to amnion. Notably, in the absence of CLDN10 in the hPSC-amnion model, more PGCLC are formed at the expense of amnion formation. Overall, this study identifies a previously unrecognized CLDN10⁺ amnion progenitor-like cell population and validates the presence of these fate transitioning cells at the boundary of the developing amnion.