The 3D Mitochondrial Networks in the Lineage of Goat Large Luteal Cells during Folliculogenesis and Luteal Formation

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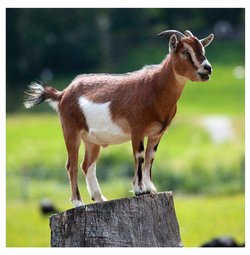
Introduction

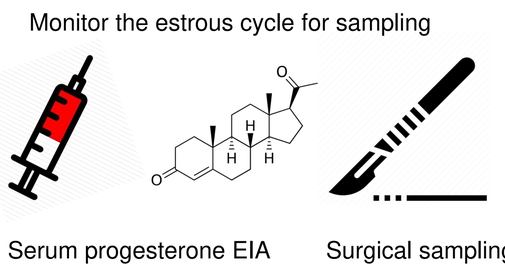
The development of follicles and formation of corpus luteum (CL) are the major processes that define the two phases of the ovarian cycle. During these phases, endocrine function of the ovary rely heavily on the differentiation of the large luteal cell (LLC) lineage. Development of this lineage begins when follicle cells (FCs), which reside in primordial follicles (PFs), proliferate and stratify into granulosa cells (GCs) during folliculogenesis. As a mature follicle (MF) escapes from follicular atresia, estrogen production by a maximal number of GCs triggers a surge of luteinizing hormone (LH) to stimulate ovulation. Shortly after ovulation, the GCs differentiate into LLCs during maturation of the corpus hemorrhagicum (CH) into the CL. Secretion of progesterone (P_4) from the CL then provides necessary support for development of an embryo[(1)].

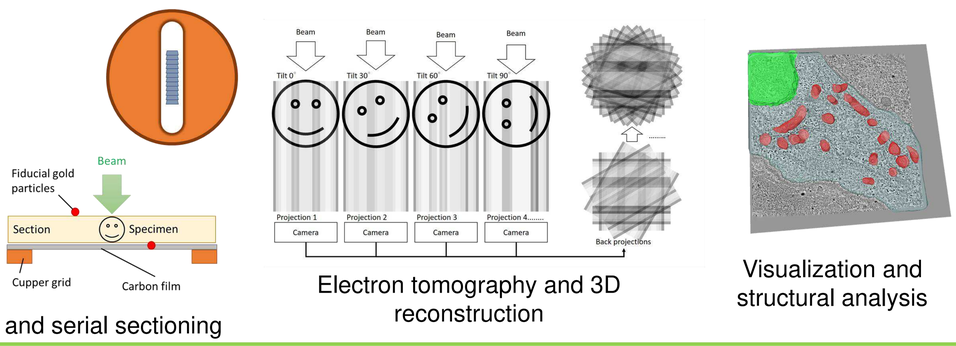
In post-ovulation ovarian tissues, the CH undergoes dramatic tissue remodeling with rapid proliferation and differentiation of GCs, and during this time, signs of hypoxia and angiogenesis can be observed[(2)]. Since ischemia and reperfusion is known to cause mitochondrial dysfunction and cellular damage, differentiating GCs may recruit certain adaptive mechanisms to survive in the microenvironment. However, specific roles for mitochondria in survival of LLCs within the CH by LLCs in the CL have not been defined.

In the present study, we sampled goat ovaries based on estrous cycle prediction and investigated the structural changes of mitochondria in the LLC lineage during follicle-luteal transitions. To examine fine structural details, 3D reconstructions of cellular structures and enzyme activities were made at an ultrastructural level.

Material and Methods







Result

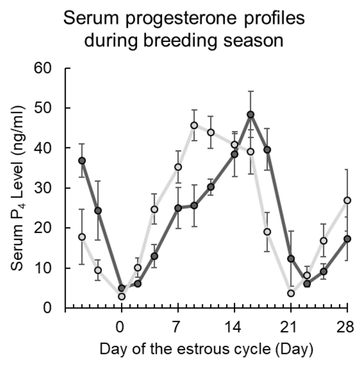


Figure 1. Two representative curves of goat serum progesterone profiles (21-day and 23-day cycle, Mean ± SEM).

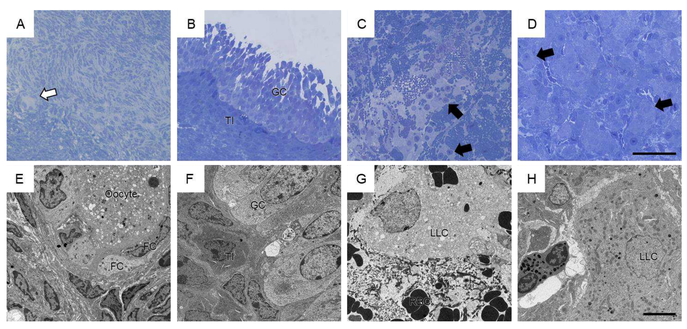


Figure 2. Representative images show the lineage of LLCs in goat ovarian tissues at a cellular level. A-D: The images depict PF (white arrow, A), MF (B), CH (C) and CL (D). The black arrow indicates LLCs. Bar: 100 μm. E-H: The TEM images show FCs (E), GCs (F), LLCs in CH (G) and LLCs in CL (H) in corresponding tissues at low magnifications. TI: theca interna cells. RBC: red blood cells. Bar: 5 μm.

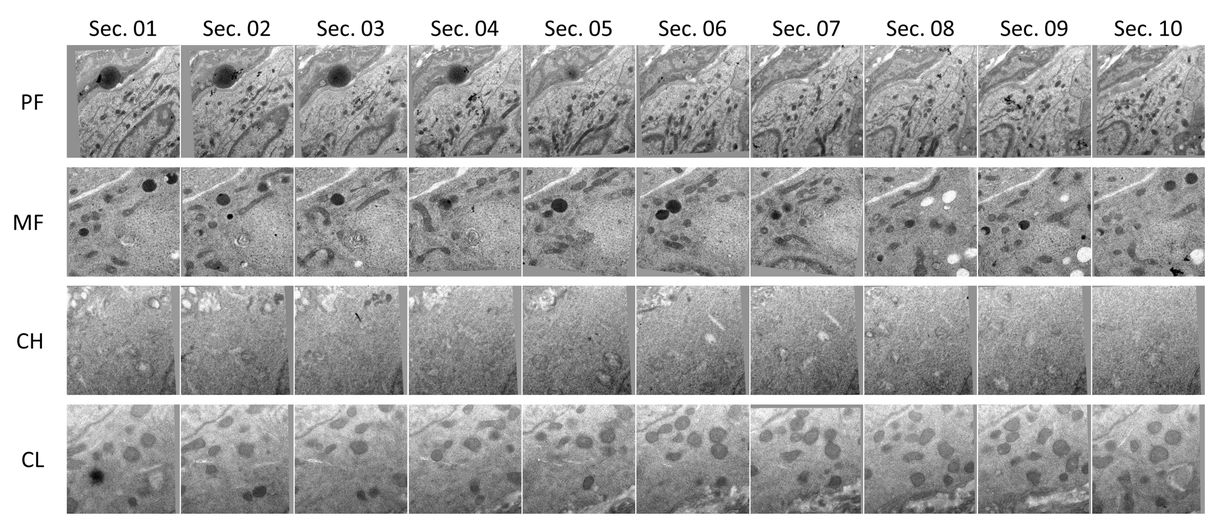


Figure 3. The serial sections from the goat LLC lineage for electron tomography. For each specimen, 10 sections (thickness: 200nm each) containing target cells are shown (Sec. 01-10).

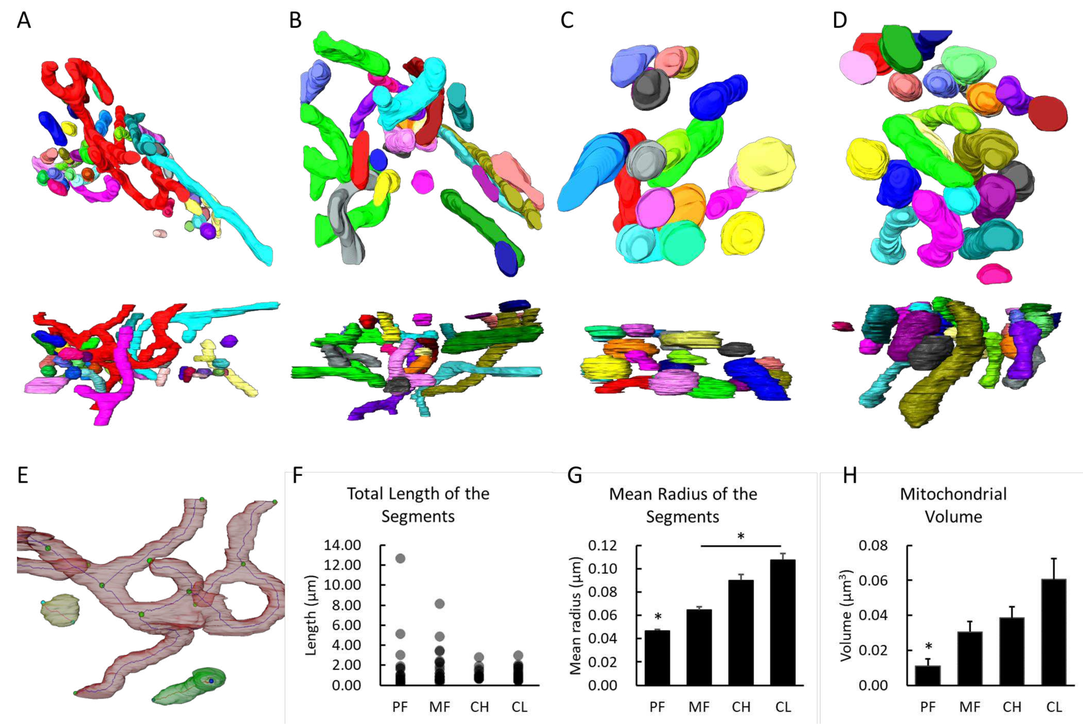


Figure 4. Visualization and quantitative analysis of 3D mitochondrial networks in the goat LLC lineage. A-D: The top view (the upper panel) and side view (the lower panel) of mitochondrial networks in FC (A), GC (B), LLC in CH (C) and LLC in CL (D). Mitochondria without physical connections are labeled with different colors. Bar: 1μm. E: The diagram shows nodes (colored spheres) and central line segments (the line between two nodes) of mitochondria (labeled in transparent red color) in FC. F: The distributions of total length of the central line segments in mitochondria from the LLC lineage. G: The mean radius (H) of the mitochondrial segments in the LLC lineage. H: The average volumes of mitochondria in the LLC lineage. Data are presented as the mean ± SEM (n = 39 for PF, 22 for MF, 21 for CH, and 24 for CL). Statistical analysis was done with one-way ANOVA and Dunn's multiple comparison test. *P < 0.05.

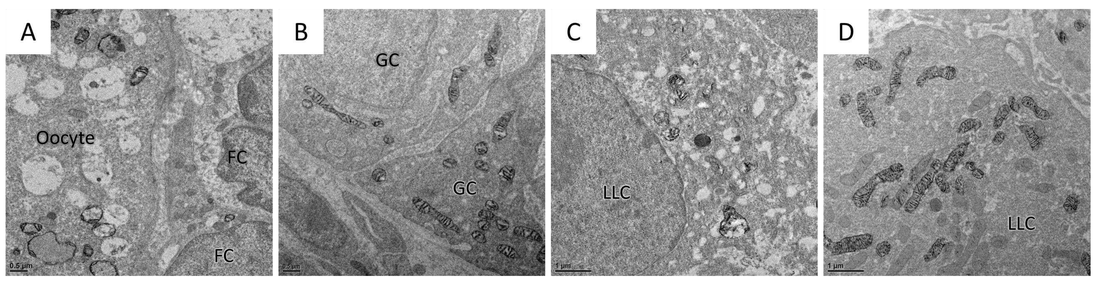
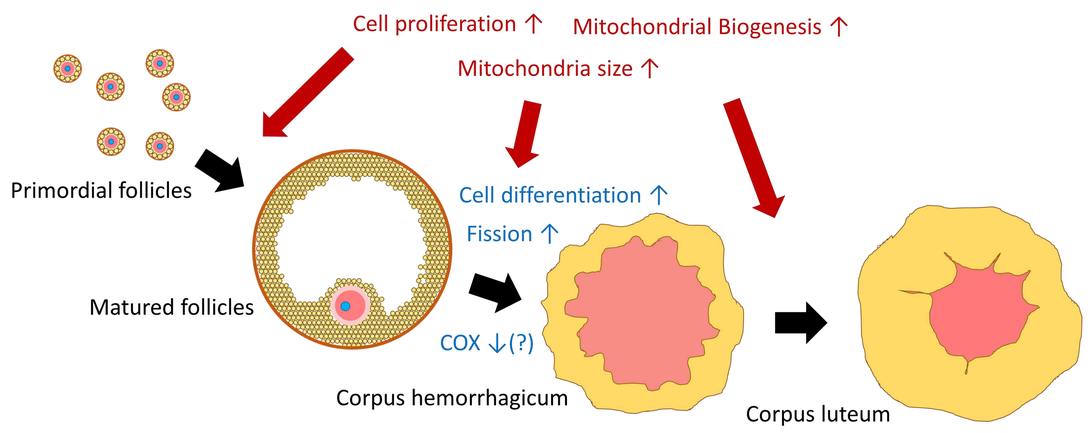


Figure 5. The distributions of COX signals in the goat LLC lineage. Images of COX signals (dark densities) were obtained in FC (A), GC (B), LLC in CH (C) and LLC in CL (D).

Conclusion



Reference

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