



Studies of oocytes and eggs; mining the proteome

Keywords: *Xenopus*, eggs, activation, apoptosis, bioinformatics, human proteome

● 研究概要

Oocytes and eggs are unique totipotent cells that can develop into complete organisms. Our present focus is set on dissection of the meiotic oocyte maturation, egg activation and apoptosis. In addition, proteome mining helps to understand coordination of these processes, as well as general principles of protein function.

● 研究テーマ

・Coordination of oocyte maturation and follicular rupture

Frog oocytes have been extensively used to study maturation and meiotic progression. Most of the control mechanisms that operate in meiosis, including MPF and CSF, were first established in frogs. A number of key signaling molecules, such as membrane receptors, protein kinases, protein phosphatases, their substrates, inhibitors and activators, adaptor proteins, etc., have been characterized (Figure 1). The focus of our recent studies is set on the coordination of oocyte maturation and follicle rupture, the two interdependent and highly synchronized ovulatory processes. Specifically, involvement of the MAPK pathway in the orchestration of these processes is being scrutinized.

・Molecular mechanisms of egg activation and apoptosis

Apoptosis develops in ovulated matured eggs after their activation and meiotic exit in the absence of fertilization. Spontaneous egg activation has been implicated as a probable trigger of egg apoptosis and a major factor responsible for the loss of fertilization capacity of ovulated eggs. Egg activation can be induced by various environmental and developmental factors. It was shown to occur by calcium-dependent and -independent mechanisms. Egg aging and increased production of reactive oxygen species (ROS) were found to initiate intracellular apoptotic events (Figure 2). Thus, our studies are aimed at the identification of natural inducers of the spontaneous egg activation, elucidation its molecular mechanisms and delineation of intracellular events that link egg activation to apoptosis. In addition, the phenomenon of egg over-activation is thoroughly investigated to reveal a non-apoptotic cell death scenario.

・Mining the human proteome for localization-specific traits

Availability of whole-genome sequences allows comparative proteome-wide studies of intracellular protein distributions in different cellular organelles and compartments. Physicochemical properties of proteomes and sub-proteomes vary significantly at different subcellular locations, reflecting differences in intracellular environmental conditions and local functional requirements (Figure 3). Revealing the correlations between physicochemical parameters of proteins and their subcellular localization will help to understand the principles of protein targeting and spatial organization of the human proteome.



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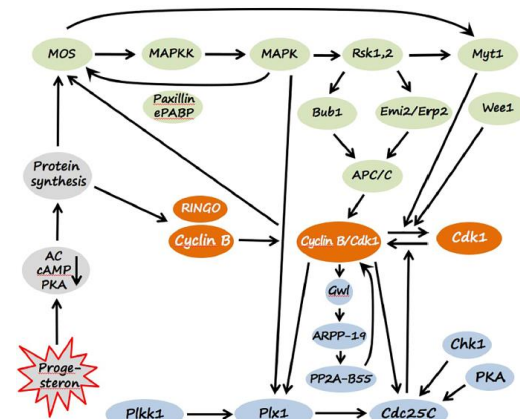


Figure 1. Signaling pathways of *Xenopus* oocyte maturation (Tokmakov et al., 2020).

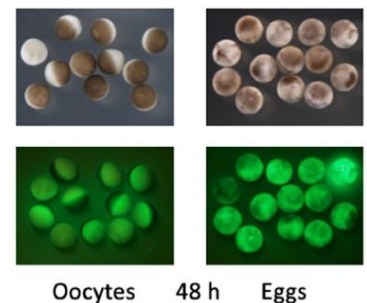


Figure 2. Detection of intracellular ROS in aging oocytes and eggs (Tokmakov et al., 2021).

| Protein pI | ← Acidic | Neutral | Basic → |
|--------------|---------------------------------------|---|-------------------------------------|
| Localization | Cytoplasm Cytoskeleton Lysosome | Plasma membrane Extracellular Endoplasmic reticulum | Nucleus Mitochondria |
| Environment | Low pH, Low membrane Charge | Moderate pH and membrane charge | High pH, High membrane charge |

Figure 3. Relationships between protein pI and subcellular localization (Kurotani et al., 2019)

● 論文.特許等

【論文】

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