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以去氧核糖核酸微陣列分析小鼠卵子及著床前胚胎中基因表現之研究		
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囊胚; cDNA 微陣列; 基因晶片; 基因表現; 孵化; 著床		
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在早期胚胎發育過程中,囊胚(Blastocyst)的孵化(Hatching)是非常重要的一個步驟。在胚胎著床過程中,母體的子宮內膜與胚胎之間,有許多的基因表現的調控和交互作用。然而,其間的分子機轉仍是不太明瞭。在本計畫中,結合體外 RNA 放大技術(in vitro RNA amplification; T7-based RNA amplification)和 cDNA 基因晶片的技術,我們得到囊胚在 Hatching 前後時期,胚胎所表現的基因表現圖譜。我們搜集 ICR 小鼠的 2-cell 胚胎,在體外培養約四天後取 Blastocyst,並於 6 至 12 小時後收取 Hatched blastocyst。這些胚胎用來抽取 RNA 後進行 RNA 放大,然後進行基因晶片的分析(約25 個胚胎用於三重復的實驗)。我們使用含 6,144 個基因的基因晶片來分析基因表現。根據基因晶片的研究顯示,胚胎在 Blastocyst 時期有 1,193 個基因的表現能被偵測得到,其中有 13 個基因表現在還沒 Hatching 的 Blastocyst 表現量較高;而有 85 個基因在 Hatching 的 Blastocyst 表現量增加。這些基因可被分類成與細胞附著、荷爾蒙、免疫反應、細胞骨架或細胞外基質相關的基因,其中還包括一些 EST。這個研究提供許多資訊讓我們能更深入去探討這些基因在胚胎 hatching 與著床的機轉中可能扮演的角色。		
	以去氧核糖核酸微陣列分析小鼠卵子及著床前胚胎中基因表現之一 行政院國家科學委員會 臺北醫學大學婦產科 9008 ~ 9107 8 頁 曾啓瑞 Tzeng, Chii-Ruey 囊胚; cDNA 微陣列;基因晶片;基因表現;孵化;著床 Blastocyst; cDNA microarray; Gene biochip; Gene expression; Hatc 在早期胚胎發育過程中,囊胚(Blastocyst) 的孵化(Hatching)是非常 現的調控和交互作用。然而,其間的分子機轉仍是不太明瞭。 amplification)和 cDNA 基因晶片的技術,我們得到囊胚在 Hatch 外培養約四天後取 Blastocyst,並於 6 至 12 小時後收取 Hatched 25 個胚胎用於三重復的實驗)。我們使用含 6,144 個基因的基因 基因的表現能被偵測得到,其中有 13 個基因表現在還沒 Hatchi 些基因可被分類成與細胞附著、荷爾蒙、免疫反應、細胞骨架理	以去氧核糖核酸微陣列分析小鼠卵子及著床前胚胎中基因表現之研究 一 行政院國家科學委員會 臺北醫學大學婦產科 9008 ~ 9107 8 頁

• 英文摘要

Blastocyst hatching stage is very important for implantation in early embryo development. Several gene expressions are highly regulated and cross-talked between embryo and maternal endometrium during implantation process. However the molecular mechanisms were still unclear. In this study, the global gene expression profiles in blastocysts before and after hatching were analyzed and compared by integrating the technologies of T7-based RNA amplification and cDNA microarray. Two-cell ICR-mouse embryos were cultured for 4 days to collect the pre-hatched blastocysts and then the hatched blastocysts were harvested after another 6~12 h. These embryos were collected for RNA extraction and amplification for microarray analysis (twenty-five blastocysts were used in each group in the triplicate experiments). The mouse cDNA microarray system (6,144 genes, including known regulatory genes and expressed sequence

tags, ESTs) with colorimetric detection system was used to identify differentially expressed genes between pre-hatched and hatched blastocyst. According to cDNA microarray analysis, we have identified 1193 genes were detectable during blastocyst stage, 13 genes whose expression was higher in pre-hatched blastocyst, and 85 genes were higher at hatching stage. The differentially expressed genes were further grouped into categories by their putative functions, including: cell adhesion molecules, hormones/cytokines, immuno-response related factors, cytoskeleton/extracellular matrix proteins and related enzymes, and some expressed sequence tags (ESTs). This work adds to our understanding in the mechanisms of blastocyst hatching and provides the information for studying the cross-talk of blastocyst and endometrium by reporting the global gene expression profiles of blastocyst hatching process.