SCREENING OF MOLECULAR NETWORKS UNDERLYING OVARIAN AGING IN MICE FOR CLINICAL APPLICATIONS

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Although several theories have been suggested such as mitochondrial malfunction, DNA damage/repair/methylation, caloric restriction, studies regarding ovarian aging-related molecular mechanisms for development of therapeutic methods are insufficient so far. Our objective is to determine molecular pathways of ovarian aging that result in pregnancy failure and other complications in women health to develop treatment strategies. Ovaries from 10 week and 11 month-old FVB/NJ female mice with synchronized estrus cycle were collected for this study. Using the Illumina HiSeq 2000 System, preferentially expressed genes were identified. Functional annotation database-based gene-set enrichment analyses and Pathway Studio® were employed to evaluate aging-related molecular networks. In young or aged ovary, preferentially expressed 876 genes were identified and extracellular matrix (ECM; $p<0.001$) and chromatin/nucleosome-related ($p<0.001$) protein-coded genes have the majority in these genes by GOTERM analysis. Regarding molecular interactions in these genes, Pathway Studio® was employed to predict aging-involved molecular networks in mouse ovary. Here we report candidate molecular networks and medicines (chemicals) for targeting these preferentially expressed genes/proteins. Further analyses are scheduled to produce transgenic animal models and with human ovarian tissues and cell lines.[This research was supported by Mizmedi Research Fund and by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by Korean Government (NRF-2018R1D1A1B07048830)]