세미나 초록

성명	김정웅
소속	중앙대학교 생명과학과
발표 주제	Epigenomic regulation of gene expression during retinal development and aging
발표 내용	Epigenetic alterations explained by the “loss of heterochromatin” model has been proposed as a universal mechanism of aging, but the region-specific chromatin organizations are unclear. Here, we examine age-dependent transcriptomic profiling of mouse retinal neurons to identify epigenetic regulators involved in heterochromatin loss. The single-cell RNA sequencing analysis reveal a gradual down-regulation of *Kdm3b* in cone photoreceptors during retinal aging. Disruption of *Kdm3b* (*Kdm3b*$^{+/-}$) of 12-month-old mouse retina leads to the decreasing number of cones via apoptosis, and it changes the morphology of cone ribbon synapses. Integration of transcriptome profiling with epigenomic analysis demonstrate gains of heterochromatin feature in synapse assembly and vesicle transport genes that are downregulated via the accumulation of H3K9 mono-, di-methylation. Contrary, losses of heterochromatin in apoptotic genes exacerbated retinal neurodegeneration. We propose that KDM3B-centered epigenomic network is crucial for balancing of cone photoreceptor homeostasis via the modulation of gene-set specific heterochromatin features during aging.