



# BIOLOGY COLLOQUIUM

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Hosted by Professor Gong Zhiyuan

## The STAT Pathway: From the Beginning to Now



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The Stat family of genes was originally discovered in the interferon system. First two STAT proteins were identified as p91 (STAT1) and p113 (STAT2) activated by interferon-alpha. The molecular cloning of genes encoding for p91 and p113 revealed the existence of the STAT gene family. The existence of a SH2 domain in STAT proteins leads the realization that they are not only transcription factors but also signal proteins in response to external stimuli. Now we present evidence that a major function of STAT proteins is to regulate epigenetic modeling of the genome. Thus, this integrated and regulatory process from external signals to transcription mediators that eventually cause specific epigenetic modeling of genome is defined as "Perigenetics".

In this seminar, I will present evidence that STAT proteins regulate epigenetic event. In particular, we will demonstrate that STAT3 regulates a novel family of "epigenetic factors" in regulation of cell fate. We propose that this integrated perigenetic process is essential for regulating stem cells, oncogenesis and involved in development in general.