ΙΤΕ/ΙΕΧΜΗ

Κύκλος Σεμιναρίων ΒΙΟΕΠΙΣΤΗΜΕΣ/ΒΙΟΤΕΧΝΟΛΟΓΙΑ

ΟΜΙΛΗΤΗΣ: **Δημήτρης Θάνος,** Καθηγητής – Πρόεδρος Επιστημονικού Συμβουλίου
Ίδρυμα Ιατροβιολογικών Ερευνών
Ακαδημία Αθηνών

ΘΕΜΑ: **Συντονισμός του μεταγραφικού προγράμματος αντι-ιϊκής προστασίας από τυχαίες διαχρωμοσωμικές αλληλεπιδράσεις.**

Stochastic interchromosomal interactions coordinate the antiviral transcriptional program .

ΤΟΠΟΣ: Αίθουσα Σεμιναρίων ΙΤΕ/ΙΕΧΜΗ

ΗΜΕΡΟΜΗΝΙΑ: **Τετάρτη, 27 Ιουνίου 2012**

ΩΡΑ: **12:00**

ΠΕΡΙΛΗΨΗ:

Gene transcription is a stochastic process because most of the proteins required to regulate this process exist in small amounts. One of the best characterized examples of stochastic transcriptional activation is the virus infection- induced expression of the human IFN-b gene, playing a key role in the antiviral response of mammals. Transcriptional activation of the IFN-β gene is a biphasic process requiring three distinct sets of transcription factors bound to the enhancer. During the early phase of virus infection, the limiting transcription factor NF-κB is captured by 3 defined genetic elements termed NRCs (NF-κB Reception Centers) in a small percentage of infected cells and subsequently it is delivered via interchromosomal interactions to only a single IFN-β allele, thus triggering enhanceosome assembly and monoallelic gene expression. The produced IFN-β protein amplifies the infection signal by stimulating expression of the IFN-β gene further from both alleles and in a larger fraction of the cell population. We have identified 41 additional

NF-kB regulated genes that are affected by NRCs. DNA FISH experiments using probes for NRCs and these genes revealed that the NRCs associate with each one of these genes, and this association correlates with their stochastic monoallelic RNA expression. Remarkably, we found that each expressing cell organizes 2-4 NRC conglomerates in which many virus-induced genes are recruited to receive NF-κB and initiate monoallelic gene expression. Single cell PCR analysis verified these data by showing that all NRC-regulated genes are expressed simultaneously in the same cell and in a stochastic manner. Taken together, these experiments strongly suggest that stochastic patterns of gene expression are due to interchromosomal interactions occurring in a small proportion of cells.