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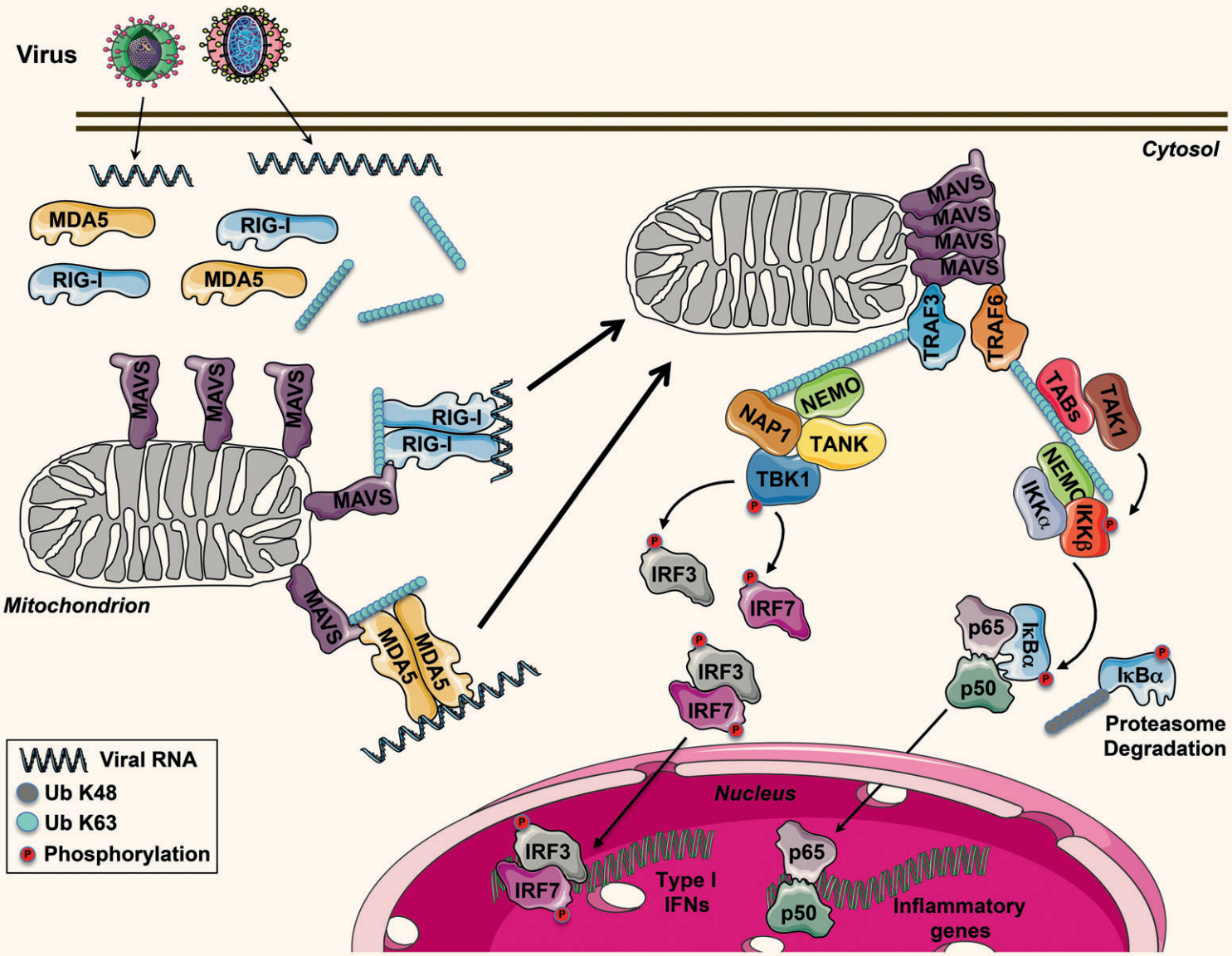

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FREE **Special Sessions (pages 56–64)**

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Keywords: BMP signalling, Drosophila embryogenesis, Post-translational modifications.

MON-204
Analysis of human and rabbit metallothioneins by Brdicka reaction and mass spectrometry

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Metallothioneins (MTs) form a large family of evolutionarily conserved low-molecular-weight proteins (~6 kDa), found in practically all life forms, in vertebrates, invertebrates, fungi and even in plants. MT plays a special role in maintaining the homeostasis of metals essential for the proper functioning of the human body, including Zn, Cu. MT is also responsible for detoxification of heavy metals such as Cd and Hg and removal of free radicals. Mammalian MTs were separated into two charge-separable isoforms, designated as MT fractions 1 and 2. The six amino acids of rabbit MT sequence show marked differences compared with the sequences of other mammalian MTs. The biological significance for this difference remains unclear.

The present study demonstrates an analytical approach of employing two detection techniques: Brdicka reaction and matrix-assisted laser desorption/ionization - mass spectrometry analysis (MALDI-MS) to characterize MTs from human and rabbit liver.

By MALDI-MS, rabbit and human MT were identified and additionally to monomers of MTs (~6 kDa), which are the major peaks in mass spectrum, small signals from the dimers of MTs were also observed, which are present both in human and rabbit MT.

During MT analysis by Brdicka reaction, changes in signals - RS_2Co (−1.25V which represents current response of MT complex with components of Brdicka electrolyte), Cat1 (−1.35V) and Cat2 (−1.48V) correspond to hydrogen evolution from the supporting electrolyte catalyzed by the MT - were observed. Concentrations of MT – 0.025, 0.5 and 0.1 mg/ml were analyzed. With decreasing MT concentration, RS2Co and Cat signals decreased and shifted to more positive potential. Signals Cat1 and Cat2 are more exposed with decreasing MT concentration. Character of the mentioned MT signals changed with different MT concentrations. The best signal for human MT was observed in concentration 0.025 mg/ml and for rabbit MT in concentration 0.05 mg/ml.

Methods used in this report allow MTs identification, permit to quantify the purity and content of its isoforms, and allow studying its quantification and polymerization.

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Keywords: Brdicka reaction, mass spectrometry, metallothionein.

MON-205
Brk regulates wing disc growth in part via repression of Myc expression

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The biological and molecular mechanisms, which regulate tissue size, represent an essential but unresolved problem in developmental biology. The main question is how developing growing tissues know when they have reached their correct final size and therefore should stop growing. The developing wing of Drosophila melanogaster is one model system that has been extensively used to address this question. One signaling pathway that strongly influences wing tissue size is the TGFß pathway, which is activated by Dpp – a gradient morphogen member of the TGFβ family growth factors. Flies lacking Dpp in the wing have extremely small wings, whereas overactivation of the Dpp pathway leads to excessive tissue overgrowth, clearly indicating that Dpp signaling is required to support tissue growth and also that the size of the wing correlates with the activity of the Dpp pathway. Dpp promotes growth via repression of the transcription factor Brinker. Although the transcriptional targets of Brinker that control the patterning of the wing, like vg, salm and omb, are known, the transcriptional targets and processes for cell growth and proliferation are not yet fully elucidated. In this project, a genome-wide approach was used to identify Brinker transcriptional targets, performing a ChIP-Seq of endogenous Brinker from wing imaginal discs. I identified the growth regulator Myc as a target of Brinker and showed that myc together with the microRNA bantam explain a significant fraction of the growth inhibition caused by Brinker. This work sheds light on the mechanisms by which Dpp signaling controls tissue growth.

Keywords: Dpp, Drososphila, Wing growth.

MON-206
Cell cycle analysis of neural progenitors in the developing ferret neocortex

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The evolutionary expansion of the neocortex reflects an increase in neurogenesis, which in turn is due to increased numbers and rounds of cell division of cortical progenitors. The length of the cell cycle is known to be an important parameter determining the proliferative versus neurogenic potential of cortical progenitors. Here, we have studied the length of the individual cell cycle phases of the various progenitor populations in the developing neocortex of a gyrencephalic mammal, the ferret (*Mustela putorius furo*), in order to gain further insight into possible causes underlying neocortical expansion.

Progenitor types were identified by immunofluorescence for Pax6 and Tbr2. These two transcription factors are sequentially expressed by cortical progenitors, in correlation with their progressive restriction towards a neurogenic fate. We identified an abundant progenitor population positive for both of these markers, found in all germinal zones during neurogenesis. We propose these progenitors to be capable of transit-amplification and to include proliferative intermediate progenitors. These Pax6- plus Tbr2-positive progenitors would thus have the potential to expand the progenitor pool and the total number of neurons of gyrencephalic brains.

The length of each cell cycle phase of the four different cortical progenitor populations (Pax6+Tbr2−, Pax6+Tbr2+, Pax6−Tbr2+, Pax6−Tbr2−) was determined by cumulative EdU labeling of postnatal day 1 (P1) ferrets. The greatest difference between these

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