E3-4
Enhanced dendritic cell differentiation from pluripotent stem cells by ectopic expression of Runx3

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Dendritic cells (DCs) are professional antigen-presenting cells (APCs) of the immune system. Their major functions related to the immune responses are clearly proven. They are required for the capturing, processing and presentation of antigens on the cell surface, thus together with co-stimulatory molecules can regulate the immune responses. Furthermore, one additional key role of DCs is the maintenance of B cell functions and recall responses. Thus, DCs are critical in the establishment of immunological memory. Clinical applications of DCs related to prime responses to tumor antigens could act as a key tool of cancer immunotherapies. Well known issue of the current protocols is that only a limited number of DCs can be obtained from adult precursors. In contrast, embryonic stem (ES) cells could serve as unlimited source of DC generation. The major challenge is to achieve the properly governed differentiation because immaturation and impaired functional characteristics are common traits of these ES derived cells. Consistent with this, our results indicated that ES derived DCs showed less mature cells compared to the bone-marrow (BM) derived DCs. This finding led us to examine the gene expression profile of ES and BM derived DCs. Quantification of 17 DC specific transcription factors revealed that three of these, namely Runx-3, Spi-B and Irf4 showed lower expression in ES derived DCs. In the light of our results we tested the effects of these three transcription factors in developing mouse ES-DCs with an isogenic expression screen. Our results revealed that forced expression of Irf4 in ES-DC negatively modulates, but Spi-B and Runx3 are both enhancers of the early myeloid commitment. Moreover, overexpression of Runx3 improved the maturation as well as the T cell activation capacity of ES derived DCs.

E4 - Regulation of gene expression, regulatory RNA, epigenetics

E4-1
Transcriptional outcomes (fates) in response to DNA damage

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Various types of DNA damage interfere with key vital processes which use DNA as a template, like replication and transcription. Upon large amount of genotoxic impacts, transcription is over-activated and probably results in the activation of several DNA damage recognition processes. During transcription, numerous components of the transcription machinery may act as a platform to recruit repair proteins at break sites. In contrast to that, when DNA damage occurs at a transcribing unit, it leads to transcriptional block. This multistep process involves several kinases and the ubiquitin ligases like NEDD4 and CUL3 leading to proteasome dependent degradation of RNA polymerase II (RNAPII) which happens at the site of the damage. Finally, at the break site ddRNA (a new class of noncoding RNA) production could be observed by controlling the DDR activation at sites of DNA damage. Taken together these results support an uncharacterized function of RNAPII complexes which allow the recognition of DNA damages and like this enhance cell survival following DNA damage. This work was supported by OTKA-PD [112118], and the János Bolyai Research Scholarship of the Hungarian Academy of Sciences.

E4-2
SUMOylation regulates light-induced signaling in Arabidopsis thaliana

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The red/far-red light absorbing photoreceptor phytochrome-B (phyB) cycles between the biologically inactive (Pr, λ_{max}=660nm) and active (Pfr, λ_{max}=730 nm) forms and functions as a light quality and quantity controlled switch to regulate photomorphogenesis in Arabidopsis. At the molecular level, phyB interacts in a conformation-dependent fashion with a battery of downstream regulatory proteins, including PHYTOCHROME INTERACTING FACTOR (PIF) transcription factors, and by modulating their activity/abundance it alters expression patterns of genes underlying photomorphogenesis. We found