

POSTERS

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P.15-028-Mon**Peptidoglycan can induce expression of CD44 on lymphocytes during inflammatory response of bovine mammary gland**P. Slama¹, L. Kratochvilova¹, K. Kharkevich¹, J. Y. Kwak²¹Mendel University in Brno, Brno, Czech Republic, ²Ajou

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CD44 is a proteoglycan that is expressed by different cell types. CD44 plays a role in leukocyte trafficking to extra lymphoid sites of inflammation or as a non-specific accessory adhesion molecule. The aim of this study was to inquire development over time of the surface expression of CD44 on lymphocytes during an inflammatory response of bovine mammary gland induced by peptidoglycan. Intramammary instillation of peptidoglycan resulted in an increase in the proportion of CD44-positive lymphocytes after 24 and 48 h. During resolution of the inflammatory response, there was observed a decrease in the proportion of CD44-positive lymphocytes. The results suggest that the cell surface receptor CD44 can play an important role in the inflammatory response of bovine mammary gland to bacteria and their components.

P.15-029-Tue**Expression and functional activity of specific membrane transport of serotonin in the mouse ovary**D. Nikishin^{1,2}, N. Alyoshina^{1,2}, Y. Shmukler¹¹Koltzov Institute of Developmental Biology, Russian Academy of Sciences, Vavilov Street 26, 119334, Moscow, Russia, ²M.V.

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Along with the classical function of serotonin as the neurotransmitter, it performs the regulation of female reproductive function. Serotonin is present in the female reproductive system and affects the maturation of oocytes, the synthesis of sex steroid hormones, as well as the processes of early embryonic development, which is shown in a variety of animals, including mammals. However, the mechanisms of serotonergic regulation of the female reproductive function have been poorly studied. The serotonin transporter *Sert* (*Sls6a4*) is of particular interest in this respect, which carries out the uptake of the serotonin from the extracellular medium. The mRNA of the *Sert* gene is expressed in the ovary, including follicular cells and oocytes at different stages of folliculogenesis. A quantitative study have shown that the expression level of the transporter is constant and does not depend on the development stage of the ovarian follicle. Immunostaining revealed that the transporter is localized in ovarian follicles, with immunoreactivity much more pronounced in the oocytes. There was an increase of the immunostaining intensity in all compartments of the ovary, including mouse follicles and oocytes after subcutaneous injections of serotonin during five days. According to the data obtained by HPLC, the concentration of serotonin in the ovaries of mice in the experimental group increased more than 4-fold. Thus, the ovary actively seizes exogenous serotonin from the bloodstream, probably through the membrane transporter *Sert*. The transmitter was accumulated in oocytes during cultivation of isolated ovarian follicles in vitro in the presence of serotonin but the addition of a selective serotonin reuptake inhibitor fluoxetine reverses the effect, which indicates the specificity of membrane transport. Thus, expression of the specific membrane serotonin transporter *Sert* in the ovary, and its specific functional activity in the oocytes of preantral follicles are revealed.

P.15-030-Wed**Protein sorting upon exit from the endoplasmic reticulum**S. Rodriguez-Gallardo¹, S. Sabido-Bozo¹, A. M. Perez-Linero¹, J. Manzano-Lopez¹, K. Funato², K. Kurokawa³, A. Nakano³, M. Muñiz¹¹Department of Cell Biology, University of Seville. IBiS (Instituto de Biomedicina de Sevilla) HVR/CSIC/US, Sevilla, Spain,²Department of Bioresource Science and Technology, Hiroshima University, Hiroshima, Japan, ³Live Cell Molecular Imaging Research Team, RIKEN Center for Advanced Photonics, Hirosawa, Wako, Saitama, Japan

Protein sorting upon vesicular transport through the secretory pathway is essential to dynamically maintain functional compartmentalization and homeostasis in eukaryotic cells. During many years it was generally thought that all newly synthesized secretory proteins travel together in the same COPII vesicles from the endoplasmic reticulum (ER) to the Golgi, where they are sorted to different destinations. However, we found in yeast that glycosylphosphatidylinositol (GPI)-anchored proteins (GPI-APs), a special category of lipid-anchored secretory proteins, are segregated from transmembrane cargos at the level of the ER and then incorporated into distinct COPII vesicles. We have developed in yeast a genetic assay that allows visualization of cargo sorting in ER exit sites (ERES) by using super-resolution confocal live imaging microscopy. Our data suggest that GPI-AP sorting into specific ERES is driven by the acquisition of ceramide C:26 (a very long and saturated lipid) by the GPI anchor. GPI-ceramide remodeling might induce a strong hydrophobic mismatch in the ER membrane leading to the clustering of GPI-APs into specific lipid domains. We also show that the specific ER export machinery is recruited after GPI-AP sorting at ERES to produce specialized COPII vesicles.

P.15-031-Mon**Study of the PFNA cluster in bifidobacteria: structure, evolution and possible functions**

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Signaling through STPK appears to be the dominant prokaryotic signaling system. STPK Pkb2 is the receptor-type kinase, with an extracytoplasmic sensor domain and an intracellular kinase domain, that indicates this kinase to transduce the external signals. Using the phylogenetic profiling method, we found an evolutionarily stable cluster of genes linked to *pkb2* gene in the *Bifidobacterium* genus. The operon organization of the cluster in *B. longum* GT15 was confirmed with transcriptional analysis. The transcription start site was determined by 5'-RACE method. The cluster named PFNA was found in most bifidobacterial species obtained from various sources. The cluster contains genes that encode, mainly, membrane proteins, among which a protein with a cytokine receptor motif is annotated. Genes in the PFNA cluster show high sequence divergence between species which may be an indicator of rapid evolution in response to the rapid evolution of host's cytokine genes. To investigate the molecular evolution of the cluster we tested in silico hypotheses concerning positive and relaxed negative selection. The molecular evolution analysis of the cluster showed the presence of episodic positive selection as well as the relaxed negative selection in some phylogenetic clades. This allowed us to determine the structurally and functionally significant sites under the pressure of selection. The presence of episodic positive selection can indirectly indicate a possible role of the cluster in interacting with the host's immune