TS-07/P-047: Dissecting the regulation of olfactory receptor expression in the mouse.

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Detection of odorants occurs in the main olfactory epithelium (MOE), which contains olfactory sensory neurons (OSNs) that express olfactory receptors (ORs). These bind the odorants and then transmit an electrical signal to the brain. Each OSN expresses only one OR, from a repertoire of over 1,200 genes, and silences all the others. Therefore, the mouse nose has over 1,200 different OSN types, each patterned by a different OR gene. High levels of genomic variation have been reported both in the mouse and human OR repertoire. This is thought to contribute to the unique sense of smell each individual has, but the mechanisms responsible are not known.

We have devised an RNAseq-based approach to quantify the OSN repertoire of three inbred strains of mice (C57BL/6, 129S5 and CAST/EiJ) via their OR gene expression levels. We found that each strain has a unique and reproducible distribution of OSNs in their noses, and that this is directly instructed by genomic variation.

Additionally, OR expression in the MOE is susceptible to olfactory experience. Exposure to an enriched olfactory environment results in the differential expression of dozens of OR genes in a reproducible and specific manner. These changes increase with time and are reversible. These data allows, for the first time, to comprehensively explore and dissect the effects of genetic and environmental variation in the regulation of OR expression and OSN repertoire. Together they generate an olfactory sensory system that is individually unique.

TS-08/P-144: Horses: an underutilized animal model

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Horses provide an opportunity to study unique phenotypes that can lead to fundamental biological insights as well as help to decipher mechanisms underlying biological and disease processes. At present, we have three horse projects with preliminary results that may serve as models for investigating gene functions in mammals. A GWAS of equine insect bite hypersensitivity (IBH), an allergic recurrent seasonal dermatitis classed as a type I and type IV hypersensitive reaction, suggests the importance of two genomic regions on Chromosome 8 (ECA8). An increased knowledge of the genes involved in the manifestation of IBH is expected to not only improve prevention, diagnosis, and treatment of equine IBH, but may also broaden our understanding of the biology underlying type I and type IV hypersensitive reactions across species. Observed in a wide range of species including humans, a second project concerns polydactyly, a genetic defect that presents as an increased number of digits. Preliminary analyses of a family of ponies suggest a recessive mode of inheritance in horses. Through whole-genome re-sequencing of this family (n=5) we aimed to confirm this mode of inheritance and identify the causative locus. Additionally, Delta F_{ST} analyses of harness racing breeds have identified specific candidate regions that harbor genes selected for athletic performance. These regions contain genes known to be involved in energy metabolism and cell growth. Genes that regulate energy metabolism and other biological processes that impact racing performance have the potential to improve our understanding of metabolic defects and diseases in horses as well as in other species. At the meeting we will present results from the three aforementioned studies and comment on the fact that in some circumstances the horse may provide unique knowledge of biological pathways that may not otherwise be fully understood.

TS-09/P-132: Higher expression of *Adcyap1* gene is associated with altered behavioral and prolonged physiological responses to stress in wild-derived MSM mice

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