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Characterizing the gut microbiota as a way to reduce the group size in rodent studies

Hansen, Axel Jacob Kornerup; Hansen, Camilla Hartmann Friis; Krych, Lukasz; Buschard, Karsten Stig; Lundberg, Randi; Ellekilde, Merete; Nielsen, Dennis Sandris

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Session V-2: Disease models in vivo

Co-chairs

Nicolas Dudoignon, Sanofi R&D, France

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Session V-2: Oral presentations

V-2-077

The effect of additional rodent enrichment on local and systemic bacterial infection models, hematology, clinical chemistry, and serum cortisol

J. Fernandez¹, C. McLahan², K. R. Sharp³, A. M. Queenan¹, W. Shang⁴, J. Hastings², L. Smith⁵, L. Varacallo⁵, A. Barron⁶, G. van den Dobbelsteen⁷ and A. S. Lynch⁴

¹Infectious Diseases & Vaccines, Janssen R&D, a Johnson & Johnson Company, Springhouse, USA; ²Laboratory Animal Medicine, Janssen R&D, a Johnson & Johnson Company, Springhouse, USA; ³Laboratory Animal Medicine, Janssen R&D, a Johnson & Johnson Company, LaJolla, USA; ⁴Infectious Diseases & Vaccines, Janssen R&D, a Johnson & Johnson Company, Raritan, USA; ⁵Preclinical Development and Safety, Janssen R&D, a Johnson & Johnson Company, Springhouse, USA; ⁶Nonclinical Statistics & Computing, Janssen R&D, a Johnson & Johnson Company, Raritan, USA; ⁷Bacterial Vaccines, Janssen R&D, a Johnson & Johnson Company, Leiden, The Netherlands jfernan5@its.jnj.com

Objectives: To determine the effects of foraging enrichment added to standard enrichment (SE) in a mouse skin (MS) (Fernandez et al., 2011) infection or rat endocarditis (RE) (Fernandez et al., 2012) model. Effects on hematology (H), clinical chemistry (CC) and serum cortisol (SC) were examined.

Methods: Animals were group housed into SE (mice, Nestlets™; rats, acrylic tubes) and additional enrichment (AE)(SE with autoclaved hamster food (mice) or sunflower seeds (rats)) groups. After 28 days, a group of mice or rats were euthanized and blood was collected for H, CC, and SC (rats). The remaining animals participated in a S. aureus MS or RE model. In both infection models, untreated animals were compared to vancomycin-treated animals.

Results: Additional foraging material had no apparent effect in either infection model with respect to bacterial load at the infection site or the efficacy of vancomycin. Additionally, H and CC values were similar for each group. SC in rats was lower in the AE group (p<0.03), suggesting that the animals did not experience additional stress from the added enrichment, and may have benefited.

Conclusion: Animals could benefit from the additional foraging enrichment to enable natural behavior. Clinical chemistry and hematology should be evaluated prior to implementing in a research program.

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Characterizing the gut microbiota as a way to reduce the group size in rodent studies

A. K. Hansen¹, C. H. F. Hansen¹, L. Krych², K. Buschard³, R. Lundberg^{1,4}, M. Ellekilde¹ and D. S. Nielsen²

¹Department of Veterinary Disease Biology, University of Copenhagen, Frederiksberg, Denmark; ²Department of Food Science, University of Copenhagen, Frederiksberg, Denmark; ³Bartholin Institute, Rigshospitalet (National University Hospital), Copenhagen, Denmark; ⁴Scientific Research & Development, Taconic, Ll. Skensved, Denmark

akh@sund.ku.dk

The gut microbiota of animal models has a substantial impact on the expression of and the variation in the models (Bleich and Hansen, 2012). E.g., in models of type 2 diabetes the correlation between essential parameters and the gut microbiota composition is 30-40% (Ellekilde et al., 2014), while it in the oxazolone model of atopic dermatitis is more than 80% (Lundberg et al., 2012). Today, high throughput sequencing enables a full characterization of the microbiota based upon a non-invasive fecal sample. In animal experiments group size is calculated as 2 x Z-values (Significance + power)/(Average effect level/Uncontrolled variation) (Ellekilde et al., 2014). Therefore, it is possible to characterize the microbiota composition of individual animals in sensitive studies and thereafter turn the "uncontrolled" variation into "controlled variation" by incorporating the characterization in the data evaluation model. Alternatively, only mice with a gut microbiota coding for a strong expression of the disease could be used. We have previously shown that mice might be inoculated with tailormade microbiota around weaning to achieve the immunological phenotype induced by the early life colonization (Hansen et al., 2012). A third approach might be to feed the mothers a microbiota-modulating diet that will induce a specific phenotype in their offspring (Hansen et al., 2014).

References

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M. Goldman

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R. Mokrý

European strategy for 3Rs and replacement of animal experiments

U. Marx

Human-on-a-chip a paradigm shift from animal testina

Industrial perspectives on the 3Rs and animal welfare

R. Kolar

How long must they suffer? Success and failure of our efforts to end the animal tragedy in laboratories

H. Zhengming

Future perspectives for alternatives to animal testing in China

R. Kavlock

Lessons learned from ToxCast and prospects for the future



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