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

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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

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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.

References

Fernandez, J. et al. (2011). *Antimicrob Agents Chemother 55*, 5522.
Fernandez, J. et al. (2012). *Antimicrob Agents Chemother 56*, 1476.

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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 tailor-made 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

Bleich, A. and Hansen, A. K (2012). *Comp Immunol Microbiol Infect Dis 35*, 81-92.
Ellekilde, M., Krych, L., Hansen, C. H. et al. (2014). *Res Vet Sci 96*, 241-250.
Hansen, C. H. F., Nielsen, D. S., Kverka, M. et al. (2012). *Plos One 7*, e34043.
Hansen, C. H., Krych, L., Buschard, K. et al. (2014). A maternal gluten-free diet reduces inflammation and diabetes incidence in the offspring of NOD mice. *Diabetes*, in press.
Lundberg, R., Clausen, S. K., Pang, W. et al. (2012). *Comparative Medicine 62*, 371-380.

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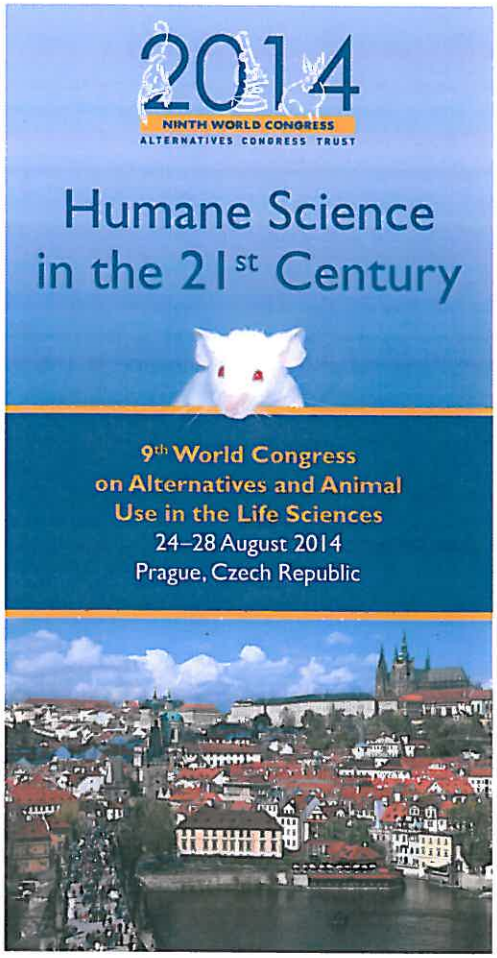

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