MATEMAATIKA-LOODUSTEADUSKOND
INTEGREERITUD SÜSTEEMIDE BIOLOOGIA KESKUS
TEADUS- JA ARENDUSTEGEVUSE AASTAARUANNE 2013

1. Struktuur

Struktuuriüksuse nimetus eesti ja inglise keeles, direktori /juhataja nimi

Integreeritud Süsteemide Bioloogia Keskus/Centre for Biology of Integrated Systems, Acting head: Anu Aaspõllu

2. Teadus- ja arendustegevuse (edaspidi T&A) iseloomustus

2.1 Struktuuriüksusesse kuuluvad uurimisgrupid *(kõik uurimisgrupid näidatakse aruandes eraldi, järgides alltoodud ülesehitust).*
Uurimisgrupi nimetus *(eesti ja inglise keeles)* **ja juhi nimi**

- uurimisgrupi teadustöö kirjeldus *(inglise keeles*);
- uurimisgrupi aruandeaastal saadud tähtsamad teadustulemused *(inglise keeles);*
- uurimisgrupi kuni 5 olulisemat publikatsiooni aruandeaastal.

In 2014 the research was focused on several directions:

1) We continued development and validation of bioinformatic tools for 18S marker based NGS data management for forensic purposes, especially for soil sample analysis.
2) We used high-throughput small RNA sequencing of paired samples of peritoneal endometriotic lesions and matched healthy surrounding tissues together with eutopic endometria of the same patients. We found with colleagues five miRNAs (miR-34c, miR-449a, miR-200a, miR-200b and miR-141) specific to epithelial cells showing significantly higher expression in peritoneal endometriotic lesions compared to healthy peritoneal tissues. We also determined the expression levels of miR-200 family target genes E-cadherin, ZEB1 and ZEB2 and found that the expression level of E-cadherin was significantly higher in endometriotic lesions compared to healthy tissues. As a conclusion the studied miRNAs could be used as diagnostic markers for confirming the presence of endometrial cells in endometriotic lesion biopsy samples. In addition we demonstrated that the miRNA profile of peritoneal endometriotic lesion biopsies is largely masked by the surrounding peritoneal tissue, challenging the discovery of an accurate lesion-specific miRNA profile. Our findings indicate that only particular miRNAs with a significantly higher expression in endometriotic cells can be detected from lesion biopsies, and can serve as diagnostic markers for endometriosis.
3) We described the profile of gut microbiota in 50 extremely low birth weight (<1200 g) critically ill infants at three different time points during the first two months of life. Stool samples were collected in collaboration with our colleagues at the age of one week, one month and two months. Bacterial community profiling was done using partial 16S rRNA gene sequencing. The diversity of gut microbiota in preterm neonates in the first week of life was low but increased significantly over two months. The gut microbiota was dominated by facultative anaerobic bacteria (Staphylococcus spp. and Enterobacteriaceae) and lacked colonization with bacteria known to provide resistance against pathogens (Bacteroides, Bifidobacterium, and Lactobacillus) throughout the study. Colonization of Escherichia coli and uncultured Veillionella was positively correlated with maturity. Infants born to mothers with chorioamnionitis had significantly higher bacterial diversity than those

without. We found that high prevalence and abundance of potentially pathogenic Enterobacteriaceae and Staphylococcaceae with low prevalence and abundance of colonization resistance providing taxa bifidobacteria, Bacteroides and lactobacilli may lead to high infection risk via microbial translocation from the gut. Additionally, our data suggest that maternal chorioamnionitis may have an effect on the diversity of infants' gut microbiota.
4) We were involved in the study related to the evolution of bacterial consortia in six semi-solid rye sourdoughs during long-term backslopping at different temperatures. The changes in bacterial diversity over time were studied by DGGE coupled with partial 16S rRNA gene sequencing. Four species from the genus Lactobacillus (brevis, crustorum, plantarum, and paralimentarius) were detected in different combinations in all sourdoughs after 56 propagation cycles. Facultative heterofermentative lactic acid bacteria dominated in sourdoughs fermented at 30°C, while both obligate and facultative heterofermentative LAB were found to dominate in sourdoughs fermented at 20°C. After 56 propagation cycles, Kazachstania unispora (formerly Saccharomyces unisporus) was identified as the only yeast species that dominated in sourdoughs fermented at 20°C, while different combinations of strains from four yeast species (Kazachstania unispora, Saccharomyces cerevisiae, Candida krusei and Candida glabrata) were detected in sourdoughs propagated at 30°C.
5) We implemented approach for detection of Aleutian mink disease virus in Euroean minks (Mustela lutreola) living in Tallinn Zoo. The pilot study performed by another group has shown presence of the ADMV in individual animals in Tallinn Zoo. We collected samples from all 97 animals: blood samples were used for viral DNA detection and for immunological analysis (detection of virus specific antibodies). In addition stool samples were collected for a reference analysis. We found the reason why results of pilot study were wrong and by our results it was possible to contradict the AMDV infection occurrence among European minks at Tallinn Zoo, thus this European mink population will not spread the AMDV to the wild nature.

Year 2014 was relatively productive despite of limited number of staff members; several publications were published and submitted, were participated in international meetings with presentations.

2014 tähtsamad teadustulemused on kokku võetud järgnevates publikatsioonides:

Saare M, Rekker K, Laisk-Podar T, Sõritsa D, Roost AM, Simm J, Velthut-Meikas A, Samuel K, Metsalu T, Karro H, Sõritsa A, Salumets A, Peters M.High-throughput sequencing approach uncovers the miRNome of peritoneal endometriotic lesions and adjacent healthy tissues. PLoS One. 2014 Nov 11;9(11):e112630. doi: 10.1371/journal.pone.0112630. eCollection 2014.

Drell T, Lutsar I, Stšepetova J, Parm U, Metsvaht T, Ilmoja ML, Simm J, Sepp E. The development of gut microbiota in critically ill extremely low birth weight infants assessed with 16S rRNA gene based sequencing. Gut Microbes. 2014 May-Jun;5(3):304-12. doi: 10.4161/gmic.28849.

Bessmeltseva M, Viiard E, Simm J, Paalme T, Sarand I. Evolution of bacterial consortia in spontaneously started rye sourdoughs during two months of daily propagation. PLoS One. 2014 Apr 18;9(4):e95449. doi: 10.1371/journal.pone.0095449. eCollection 2014.