



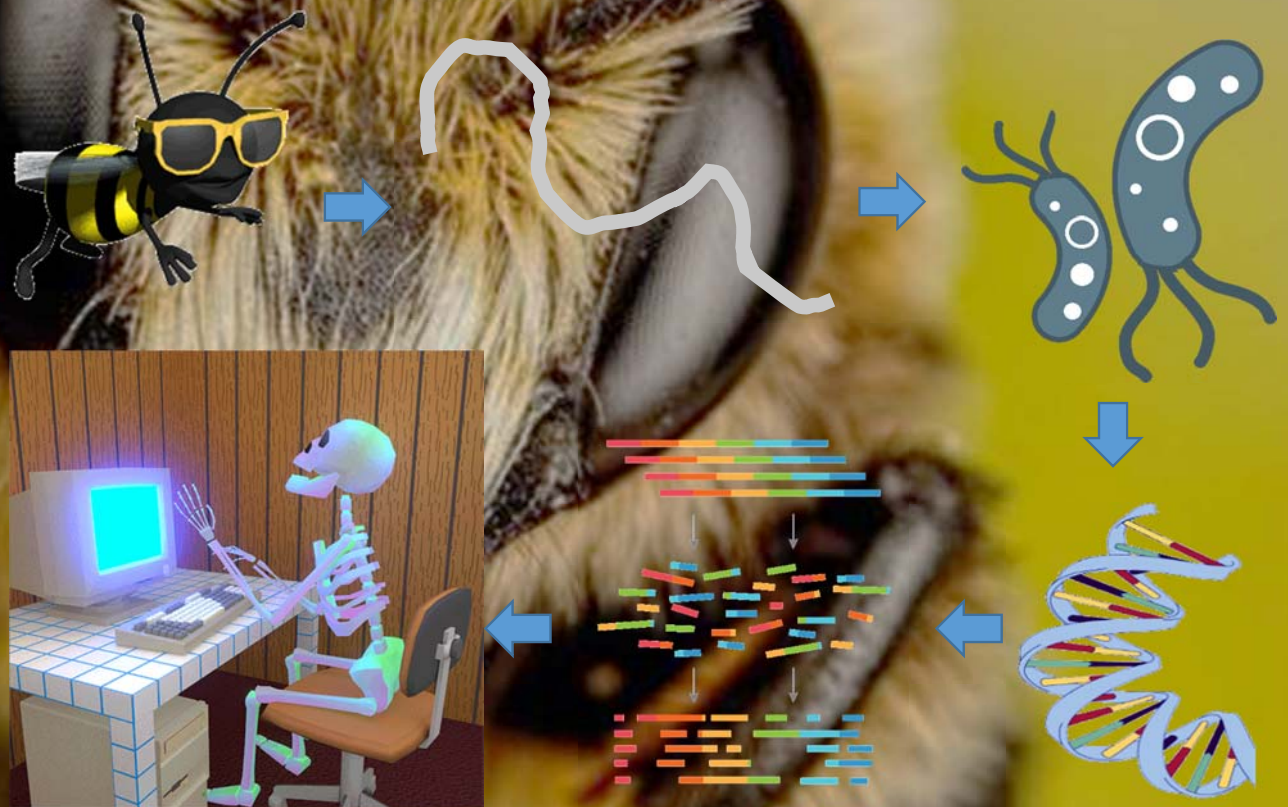
Snapshot of the bacterial microbiota within the gastrointestinal tract of the honeybees from 4 different locations in Bulgaria

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Agricultural production strongly depends on pollinators, and among them one of the central roles is played by the honeybees *Apis mellifera*, which are negatively influenced by the anthropogenic pressure and industrialization of the agriculture. In order to partially assess the role of the anthropogenic factors on the health of the hives we performed an NGS-based metagenomics research of the eubacterial microbiota composition within the gastrointestinal tract of the honeybees from 4 different locations in Bulgaria which are differently influenced by human activities. Total DNA was isolated from the content of the stomach of the bees and intestines which were subjected to 16S rRNA metagenomics based on the V3-V4 region, and performed on the Illumina 2 x 150 paired end reads. Despite the fact that within the four locations the most predominant genera were *Lactobacillus*, *Gilliamella*, *Bifidobacterium* and *Snodgrassella*, differences were observed not only in their relative abundances, but also in the total number of the bacterial species observed. A clear tendency of an inversely proportional dependence between the anthropogenic pressure and microbiota richness was observed.

EXPERIMENTAL WORKFLOW:

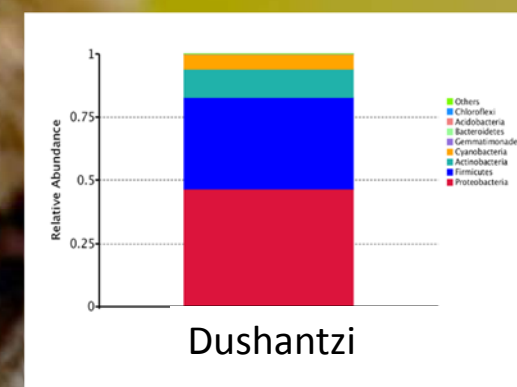
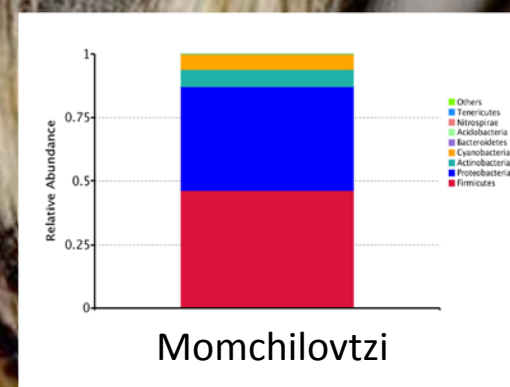
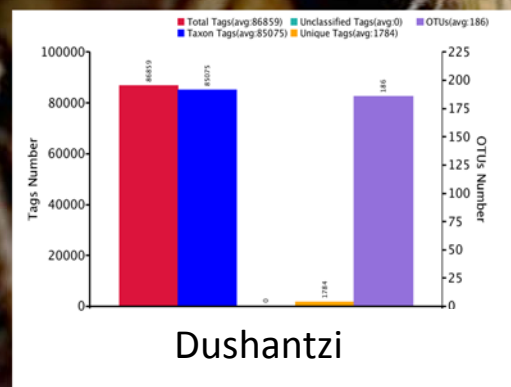
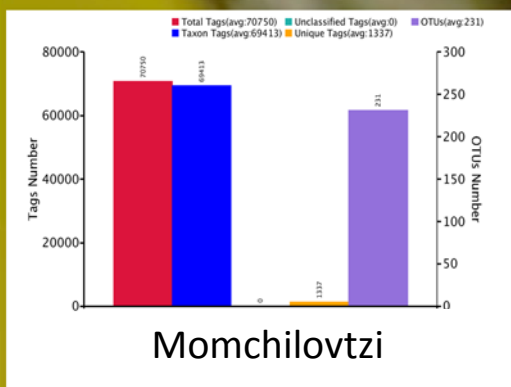
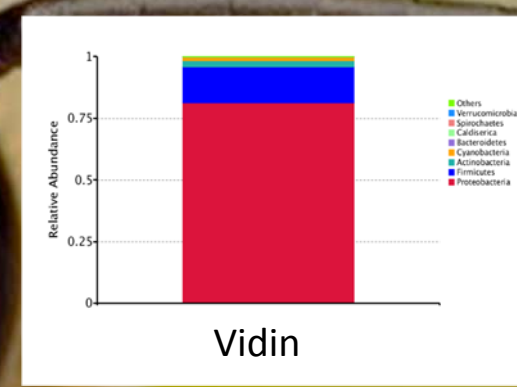
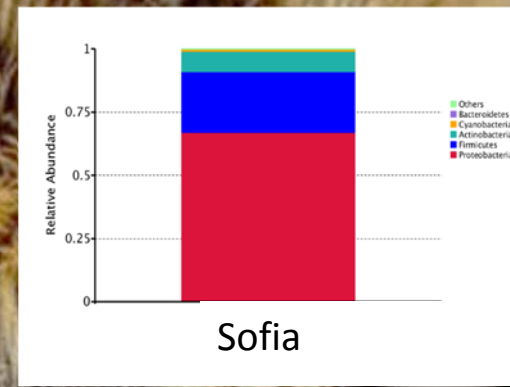
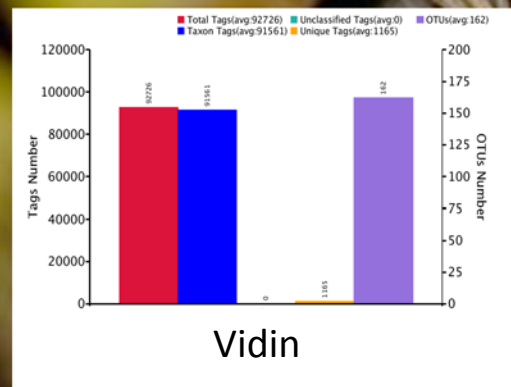
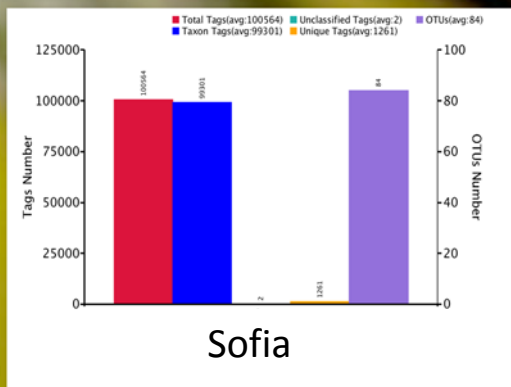


ATGTCCTCATGAGAAAGCTATCTGCACTGCTGATCTCAAAAAGGAGGAGAA

Snapshot of the bacterial microbiota within the gastrointestinal tract of the honeybees from 4 different locations in Bulgaria

OTUs analyses:

Bacterial taxa distribution:



	VIDIN	SOFIA	MOMCHILOVTZI	DUSHANTZI
Total number of bacterial OTUs detected	162	84	231	186

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The most abundant bacterial genera found into the gastrointestinal tract of the honeybees in June 2020 at the four different locations *

	Dushantzi	Momchilovtzi	Sofia	Vidin
<i>Bifidobacterium</i>	12,99 %	7,90 %	9,94 %	6,08 %
<i>Lactobacillus</i>	41,87 %	52,12 %	29,06 %	30,67 %
<i>Commensalibacter</i>	2,26 %	3,76 %	1,77 %	6,50 %
<i>Snodgrassella</i>	6,09 %	7,92 %	9,63 %	29,70 %
<i>Hafnia-Obesumbacterium</i>	3,67 %	6,84 %	0,50 %	0,00 %
<i>Providencia</i>	0,77 %	0,00 %	0,00 %	0,00 %
<i>Frischella</i>	1,58 %	1,16 %	3,00 %	1,21 %
<i>Gilliamella</i>	27,94 %	16,85 %	43,82 %	20,89 %
<i>Enterobacter</i>	0,00 %	0,87 %	0,00 %	2,63 %
<i>Megamonas</i>	0,00 %	0,00 %	0,70 %	1,13 %
<i>Escherichia-Shigella</i>	0,00 %	0,00 %	0,66 %	0,00 %
<i>Acinetobacter</i>	0,00 %	0,00 %	0,93 %	0,00 %
<i>Polynucleobacter</i>	0,00 %	0,00 %	0,00 %	1,46 %

* The overall % could be lower than 100% because certain amount of chloroplast and mitochondrial 16S rRNA genes were also detected



Conclusions:

1. The richness of the bacterial community found in the honeybees gastrointestinal tract diverge within the different locations;
2. The richness of the the bacterial community in the honeybees gastrointestinal tract is inversely proportional to the anthropogenic pressure on the environment;
3. The most predominant bacterial genera within the gastrointestinal tract, despite the differences observed, are *Lactobacillus*, *Gilliamella*, *Bifidobacterium* and *Snodgrassella*.

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