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7th Annual congress on

Probiotics, Nutrition and Microbes

July 18-19, 2018 Prague, Czech Republic

Sex-dependent impact of roundup on the rat guts microbiome

Veronica L Lozano¹, Nicolas Defarge^{3, 1}, Louis-Marie Rocque^{2, 3}, Robin Mesnage^{3, 4}, Didier Hennequin¹, Renaud Cassier², Joël Spiroux de Vendômois³, Jean-Michel Caroline Amiel^{1, 3}, Panoff^{1, 3}, Gilles-Eric Séralini^{1, 3} and

¹University of Caen Normandy, France

²Adgène Laboratoire, France
³Information Indépendantes Sur Le Génie Génétique – CRIIGEN, France
⁴Guy's Hospital, UK

A growing body of research suggests that dysbiosis of the gut microbiota induced by environmental pollutants, such as pesticides, could have a role in the development of metabolic disorders. We have examined the long-term effects of three doses of the roundup (R) herbicide (made of glyphosate and formulants) on the gut microbiota in male and female Sprague-Dawley rats. A total of 141 bacteria families were identified by a 16S sequencing analysis approach. An OPLS-DA analysis revealed an increased bacteroidetes family S24-7 and a decreased Lactobacillaceae in eight out of the nine females treated with three different doses of R (N=3). These effects were confirmed by repetitive sequence-based PCR fingerprinting showing a clustering of treated females. A culture-based method showed that R had a direct effect on rat gut microbiota. Cultivable species showed different sensitivities to R, including the presence of a high tolerant or resistant strain identified as Escherichia coli by 16S rRNA sequencing. The high tolerance of this E. coli strain was explained by the absence of the EPSPS gene (coding glyphosate target enzyme) as shown by DNA amplification. Overall, these gut microbiome disturbances showed a substantial overlap with those associated with liver dysfunction in other studies. In conclusion, we revealed that even an environmental concentration of R (0.1 ppb) has a sex-dependent impact on rat gut microbiome composition and thus warrants further investigation.

caroline.amiel@unicaen.fr

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