

GMO corn doesn't harm gut microbiome of rats, study team associated with anti-biotech geneticist Gilles-Eric Séralini finds

Safety concerns arising from the consumption of foods derived from genetically modified (GM) crops remains a controversial subject. We report here a faecal microbiota compositional analysis in Wistar rats from the GMO90 + study, which fed glyphosate-tolerant NK603 (+/? Roundup application) and Bt toxin MON810 GM maize for 6 months in comparison to their closest non-GM isogenic lines.

We first integrated the faecal microbiota compositional data with results from plasma metabolomics to understand which bacterial species can influence host metabolism. Coriobacteriaceae and Acetatifactor significantly predicted plasma metabolic profile in males, while Bifidobacterium and Ruminococcus were able to predict female plasma metabolites. We then investigated the differences in fecal microbiota composition between group of rats fed MON810 or NK603 GM maize in comparison to their isogenic lines.

[Editor's note: Co-authors of this study Robin Mesnage and Michael Antoniou [previously collaborated](#) with French geneticist Gilles-Eric Séralini, best known for his research claiming that GMO corn caused cancer in rats.]

Bacterial community richness was not altered by the test diets. There were no statistically significant differences in taxa abundance in the rat faecal microbiota that we could attribute to the consumption of either MON810 or NK603. We show that the consumption of the widely cultivated GM maize varieties NK603 and MON810 even up to 33% of the total diet had no effect on the status of the faecal microbiota compared to non-GM near isogenic lines.

Read full, original article: [Relationship between faecal microbiota and plasma metabolome in rats fed NK603 and MON810 GM maize from the GMO90+ study \(Behind Paywall\)](#)