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A high-fungi diet differentially attenuates the gut mycobiota relative to a high meat diet; consequences for chronic disease risk?

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The fungal cell wall facilitates an immune response and may be involved in intestinal immune training^(1,2). It is also fermentable by the gut microbiome, thus, consumption of fungi changes gut microbial ecology⁽³⁾. Yet, the specific effects of consuming fungal foods on the gut mycobiota (i.e., gut fungi) have not been well studied. An interesting case study is mycoprotein, a fungal based protein produced from *Fusarium Venenatum*⁽⁴⁾. We have previously reported that mycoprotein consumption attenuates faecal water genotoxicity, a surrogate marker of colorectal cancer risk, as well as modulates faecal metabolite excretion and gut bacterial composition⁽⁵⁾. Here, we aimed to evaluate the impact of consuming a diet high in mycoprotein on gut mycobial ecology, and to explore relationships between mycobial composition and faecal genotoxicity.

Here we leverage stool samples from Mycomeat: a randomised crossover-controlled trial, recruiting 20 healthy male adults to adhere to 2-week diets comprising 240 g/day of mycoprotein based foods or red and processed meat, separated by a 4-week washout. Internal transcriber spacer (ITS) sequencing was performed to characterise the mycobiota. Alpha diversity before and after study phases was compared using Wilcoxon tests. Beta diversity was compared by permutational multivariate analysis of variance (PERMANOVA) based on Bay-Curtis dissimilarities. Differences in mycobial taxa within and between study phases were compared using Wilcoxon tests. Changes in mycobiota composition was then regressed against faecal excretion of metabolites using mixed-effects models to understand the impact of myco-ecology on the wider colonic environment. Finally, given the abundance of mycobial genotoxins in nature, we regressed mycobial taxa against faecal water genotoxicity.

There were significant shifts in the abundance of several taxa following both diets. Notably, mycoprotein consumption was associated with an increase in the abundance of *Malasseziales* sp. ($P = 0.02$) and a reduction in *Candida Albicans* ($P = 0.01$). Meat consumption was associated with an increase in *Phaeoacremonium Tuscanum* ($P = 0.01$) and *Rhodotorula Mucilaginosa* ($P = 0.008$), and reduction in *Penicillium Commune* ($P = 0.02$). In addition, *Aspergillus Caesiellus* was associated with lower faecal genotoxicity ($P = 0.04$), whereas *Penicillium Commune* ($P = 0.04$) and *Penicillium Olsonii* ($P = 0.03$) were both associated with higher genotoxicity. Regressing mycobial taxa against faecal metabolites revealed a number of significant associations, including between *Penicillium Commune* and a putative mycotoxin ($P < 0.001$) as well as 1-methyladenine, a methylated DNA base with cytotoxic properties ($P = 0.001$).

The gut mycobiota is malleable through a fungi rich diet alongside changes within the wider microbiome. Members of the gut mycobiota predicted faecal genotoxicity and faecal excretion of toxins in this model, and there may be value in further exploring the gut mycobiota and the contribution of mycotoxins in gut health and colorectal cancer risk.

References

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