PAPER • **OPEN ACCESS**

Effect of virgin coconut oil on caecal microbiota composition in alloxan-induced diabetic rats

To cite this article: D Mitic-Culafic *et al* 2019 *IOP Conf. Ser.: Earth Environ. Sci.* **333** 012080

Effect of virgin coconut oil on caecal microbiota composition in alloxan-induced diabetic rats

D Mitic-Culafic[1], S Djurasevic[1], Z Todorovic[2], J Knezevic-Vukcevic[1], J Djordjevic[1] and B Nikolic[1]

[1] University of Belgrade Faculty of Biology, Belgrade, Serbia
[2] University of Belgrade Faculty of Medicine, and University Medical Center Bezanijska kosa, Belgrade, Serbia

E-mail: mdragana@bio.bg.ac.rs; biljanan@bio.bg.ac.rs

Abstract. The gut microbiota is a complex community of a diverse population of obligate and facultative anaerobic microorganisms that could affect host metabolism and immune homeostasis. The effects of virgin coconut oil on the mean weekly fasting glycaemia, weekly body mass gains and daily water and food intakes after 16 weeks, as well as on the changes in composition of caecal microbiota in both non-diabetic and alloxan-induced diabetic rats, were investigated. The beneficial effects of virgin coconut oil were observed for all examined parameters. Additionally, this oil's potential to positively affect the caecum microbiome, with significant increase in the abundance of beneficial bacteria such as *Lactobacillus*, *Allobaculum* and *Bifidobacterium* species, was proven.

1. Introduction

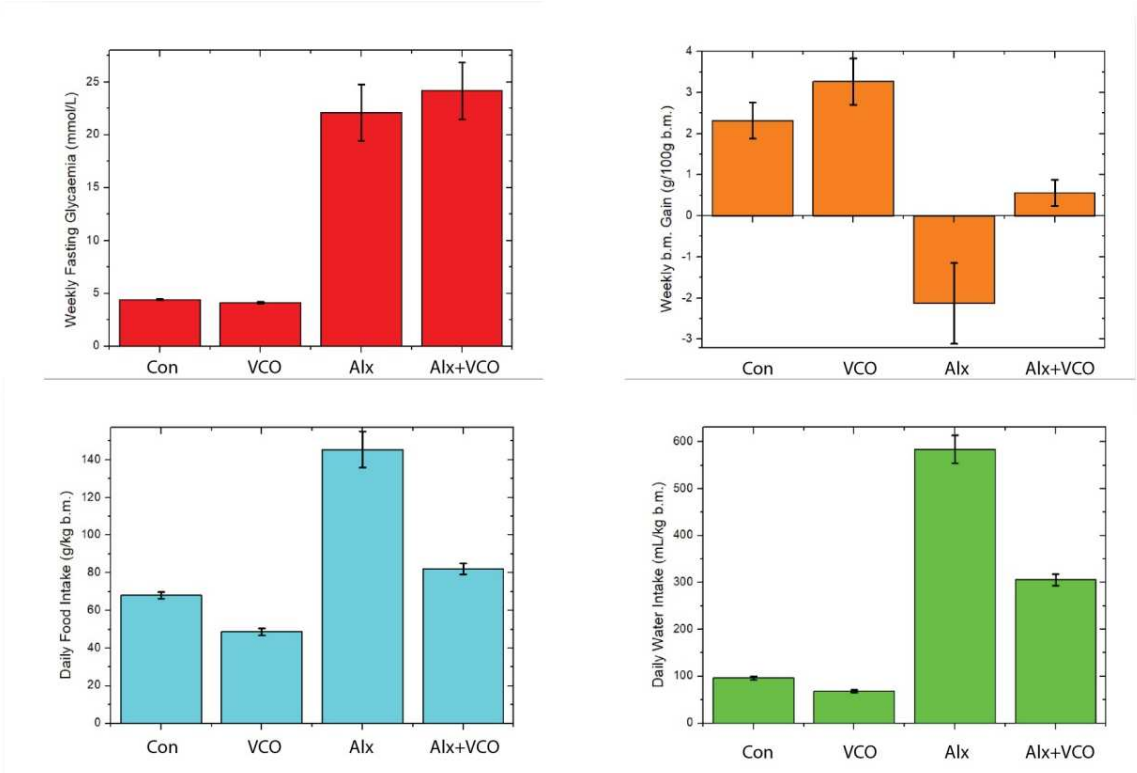
Coconut (*Cocos nucifera*) is known as one of the most popular natural sources of short and medium chains fatty acids with lauric acid as dominant. Coconut oil is thought to have anti-obesity effects, and due to the presence of lauric acid, antimicrobial effects as well.

The microbiota of the intestine consists of a diverse population of obligate and facultative anaerobic microorganisms with a wide range of metabolic activities that provide essential nutrients for the host [1]. Consumption of particular types of food produces predictable shifts in the host's bacterial genera. There is a substantial body of evidence that dysbiosis or imbalance in gut microbiota is associated with various diseases, including colorectal cancer, liver cirrhosis, arthritis, atherosclerosis, ulcerative colitis, Crohn's disease, metabolic syndrome, allergy, asthma, eczema and autism [2-5]. Furthermore, the connection of type 2 *diabetes mellitus* (DM) and obesity with alterations in gut microbiome is well established. DM is a metabolic endocrine disorder resulting from a deficiency in insulin secretion and insulin action. Despite the large number of medicines for the treatment of diabetes, the complications caused by this disease remain a major medical problem [6]. Therefore, the search for oral herbal medicinal products for long-term blood glucose control in patients with DM is very important.

Consequently, in our recent work, we focused on determining the effects of *Cocos nucifera* virgin oil (VCO) on the caecum microbiota composition changes in both non-diabetic and alloxan-induced diabetic rats, as well as on determining mean fasting glycaemia, weekly body mass gains and daily water and food intakes [7]. Alloxan is widely used to induce DM in experimental animals, due to its generation of excess reactive oxygen species, which lead to destruction of pancreatic β-cells [8]. The main goal of this study was to present the most important findings of this research.

2. Physiological parameters

Four groups of rats, differing from each other by the combinations of alloxan treatment and coconut oil administration (Control (con), VCO, Alloxan (Alx) and Alx+VCO groups) were included in the investigation. We studied the glycaemic level by using tail fresh capillary whole blood samples and handy Wellion CALLA Light blood glucose test strips. In addition, body mass gain was measured weekly, while food and water intake was measured daily. The results obtained are presented in Figure 1.



* b.m. - body mass; data are given as mean ± standard error of the mean (X-bar ± SEM), with the $p < 0.05$ as the minimal significant level. Significantly different: [a] in respect to Con; [b] in respect to VCO; [c] in respect to ALX. Control (con), virgin coconut oil (VCO), alloxan (Alx) and Alx+VCO groups.

Figure 1. Mean weekly fasting glycaemia, daily food and water intakes and weekly body mass gains, after 16 weeks

Coconut oil supplementation significantly increased mean body mass gain, and lowered glycaemia, and food and water intake in the VCO group compared to the control. This effect was partly noticed in the alloxan-induced diabetes: there was a significant decrease in the food and water intake, and an increase in the body mass gain in the Alx+VCO group compared to Alx group. The beneficial effect of coconut oil supplementation in the Alx+VCO group lies in the fact that this oil is an energetically highly efficient food, with a high content of fatty acids that can be metabolized into metabolic water. The hypoglycaemic effect of coconut oil could be due to the presence of lauric acid, which has insulin tropic properties and the content of which is particularly high in VCO [9,10]. Furthermore, VCO polyphenols may enhance the

sensitivity to insulin and reduce insulin resistance and damage of pancreatic β-cells by scavenging reactive oxygen species [11, 12].

3. Caecal microbiota composition

The abundance and composition of the caecal microbiota of all tested groups was investigated in an *in vitro* study performed under the 16S rRNA NGS sequencing lllumina platform. The effect of VCO on intestinal community richness was also evaluated, and the maximum value of unique Operational Taxonomic Units (OTUs) was found in the control group, while the minimum value of OTUs was found in the VCO group. The overlap between the groups is shown in the Venn diagram (Figure 2), and it is noticeable that 1250 (13%) of the total 9614 taxa were divided among all groups.

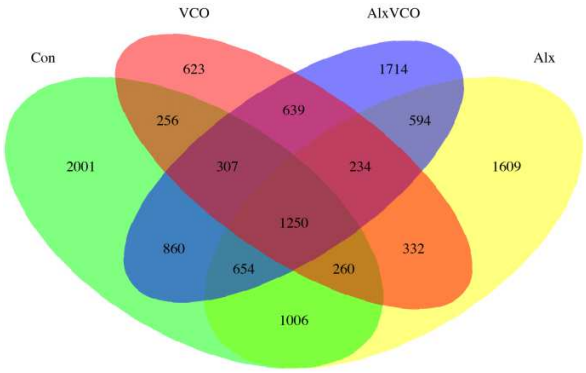


Figure 2. Venn diagram, taken from [7], depicts the overlap of OTUs in caecal microbiota between the groups. Control (con), virgin coconut oil (VCO), alloxan (Alx) and Alx+VCO groups.

The structure of caecal microbiota at the phylum level showed the dominant bacteria in all rat groups were Gram-negative Bacteroidetes and Gram-positive Firmicutes, accounting for 77% to 90% of total bacterial rRNA-targeted sample sequences. At a family level, the caecal microbiomes of all four groups of rats demonstrated similar richness, but different bacterial abundances (Figure 3).

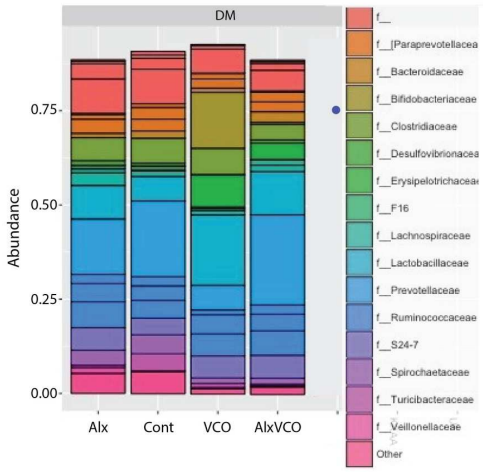


Figure 3. Percentage abundance at the family level in the caecal microbiomes of four rat groups. Only taxa with total percentage abundance above 0.5% across all samples were included. Alloxan (Alx), control (Cont), virgin coconut oil (VCO), and Alx+VCO groups

Particularly, coconut oil supplementation was positively correlated with family Lactobacillaceae (*Lactobacillus)* and Erysipelotrichaceae (*Allobaculum).* The effect of VCO on family Prevotelaceae, with detected *Prevotella* genus, was clearly dependant on the glycaemic status of the rats. In healthy animals, the oil radically decreased the abundance of this genus, but in diabetic animals, the effect was opposite. The effect on Bifidobacteriaceae (*Bifidobacterium* species) is worth mentioning, because an extremely high percentage of *Bifidobacterium* spp. was observed only in the VCO group. On the other hand, reductions of the number of bacteria from the Spirochaetaceae family, in this case, *Treponema* genus, were detected in VCO and Alx+VCO groups, while in the case of Turicibacteriaceae (*Turicibacter* species) a significant decrease in the abundance in the VCO group was observed.

In conclusion, we proved the beneficial effect of virgin coconut oil on some physiological parameters associated with diabetes in rats, i.e. food and water intakes and average body mass gain. In addition, the positive effect of coconut oil on the caecum microbiome, with significant increase in the abundance of beneficial bacteria *Lactobacillus*, *Allobaculum* and *Bifidobacterium* species, was detected. Additional research is needed to examine the variety of microbial species in the gastrointestinal tract and the diversity of microbial genes and their functions.

Acknowledgement
This work was supported by the Ministry of Education, Science and Technological Development of Republic of Serbia, Projects No. 173023 and 172058.

References

[1] Martínez N, Prieto I, Hidalgo M, Segarra A B, Martínez-Rodríguez A M, Cobo A, Martínez-Cañamero M 2019 *Microorganisms* **7** 61
[2] Lecomte V, Kaakoush N O, Maloney C A, Raipuria M, Huinao K D, Mitchell H M, Morris M J 2015 *PLoS One* **10** e0126931 doi:10.1371/journal.pone.0126931
[3] Etxeberria U, Arias N, Boque N, Macarulla M T, Portillo M P, Martinez J A and Milagro F I 2015 *J. Nutr. Biochem.* **26** 651
[4] Li H, Zhu Y, Zhao F, Song S, Li Y, Xu X, Zhou G and Li C 2017 *Sci. Rep.* 7 826
[5] Bressa C, Bailen-Andrino M, Perez-Santiago J, Gonzalez-Soltero R, Perez M, Montalvo-Lominchar M G, Mate-Munoz J L, Dominguez R, Moreno D and Larrosa M 2017 *PLoS One* **12**(2) e0171352 doi:10.1371/journal.pone.0171352
[6] Upadhyaya S and Banerjee G 2015 *Gut Microbes* **6** 85
[7] Djurasevic S, Bojic S, Nikolic B, Dimkic I, Todorovic Z, Djordjevic J, Mitic-Culafic D 2018 *Plant Food Hum. Nutr.* **73** 295
[8] Lachin T and Reza H 2012 *Recent* Pat. Endocr. Metab. *Immune. Drug. Discov*. **6** 67
[9] Garfinkel M, Lee S, Opara EC and Akwari O E 1992 *J. Surg. Res.* **52** 328
[10] Iranloye B, Oludare G, Olubiyi M 2013 *J. Diabetes Mellit.* **3** 221
[11] Siddalingaswamy M, Rayaorth A and Khanum F 2011 Anti-diabetic effects of cold and hot extracted virgin coconut oil *J. Diabetes Mellit.* **1** 118
[12] Narayanankutty A, Mukesh R K, Ayoob S K, Ramavarma S K, Suseela I M, Manalil J J, Kuzhivelil B T and Raghavamenon A C 2016 *J. Food Sci. Technol.* **53** 895