

Characterization of the fecal microbiome of sheep after administration of *Tanacetum vulgare L.* extract.



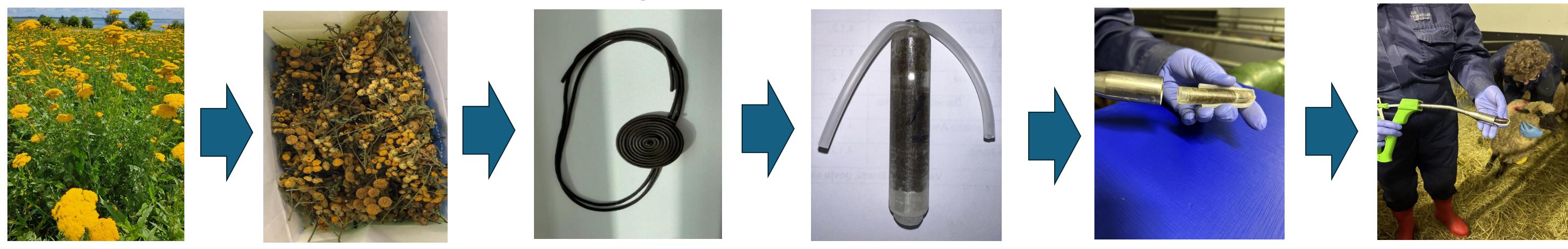
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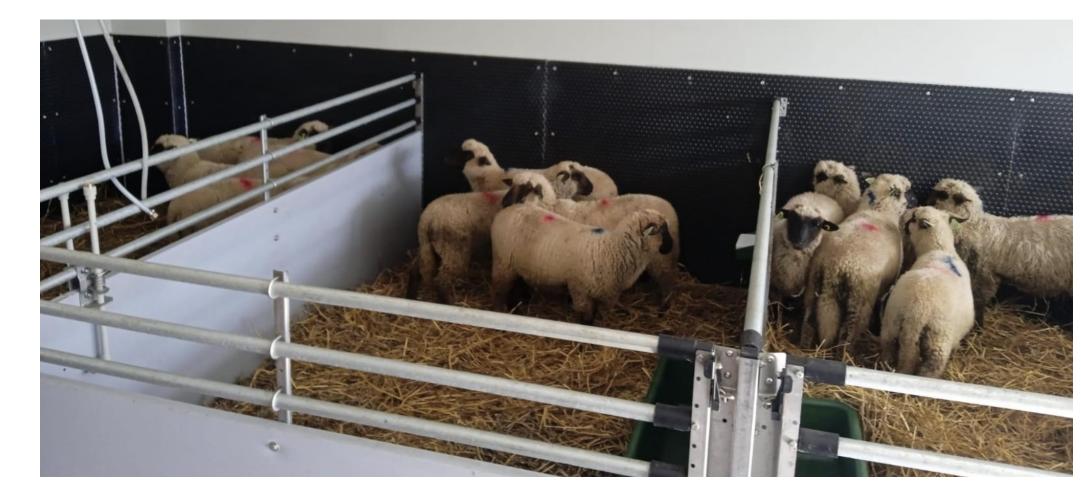
Introduction: *Tanacetum vulgare* extract has shown some antiparasitic effects, but its potential effects on the gastrointestinal microbiome (GIM) need further clarification.

Aims: To determine the effect of *Tanacetum vulgare* extract on the sheep GIM.



From Tansy plant to Tansy extract and its incorporation in intraruminal bolus

Materials and Methods: Thirty Latvian Dark-Headed sheep (4-5 months old) were randomly assigned to groups A to E in a controlled experiment. On day 0, groups A and B received 3D-printed intraruminal boluses of tansy extract in different concentrations, group C received tansy granules for 40 days. Group D served as a negative control, group E as a positive control treated with levamisole (5 mg/kg). Fecal samples were collected before treatment and on day 56, then frozen and sent for DNA isolation, microbiome profiling by targeting bacterial 16S rDNA using next-generation sequencing (NGS).



Example from sheep groups during study

Group

Post_mortem

Pre_mortem

Feeding

Bolus_1

Bolus_2

Granules

NC

PC

Axis.1 [4.8%]

Beta diversity between groups, before treatment and day 56 after it

Lachnospiraceae Family, Ruminococcaceae UCG-010, Ruminococcaceae Family, Clostridiales Order, Christensenellaceae R-7 group, Treponema 2, Bacteroidales Order, p-251-o5 Family, Bacteroides. There were no difference between the groups in the beta diversity score before the study, (p<0,05). At the end of the study, differences were observed between groups C and A (p=0.015), E and A, B, C, D (p=0.001). Differences before and at the end of the study were observed for group A (p=0.011) and E (p=0.004).

Results: The ten most frequently detected genera were

Ruminococcaceae UCG-005, Rikenellaceae RC9 gut group,

Post_mortem_Bolus_1 Post_mortem_Granules -Genus Ruminococcaceae UCG-005 Phascolarctobacterium Pre_mortem_Granules -Rikenellaceae RC9 gut group Akkermansia Pre_mortem_PC [Eubacterium] coprostanoligenes group Lachnospiraceae Family Ruminococcaceae UCG-010 Ruminococcus 1 Pre_mortem_NC Ruminococcaceae Family Alistipes Clostridiales Order Unassigned Kingdom Post_mortem_PC Christensenellaceae R-7 group Ruminococcaceae UCG-002 Treponema 2 Bifidobacterium Post_mortem_NC · Bacteroidales Order Prevotellaceae UCG-003 Post_mortem_Bolus_2 · p-251-o5 Family Bacteroides Pre_mortem_Bolus_1 Microbial diversity on genera level Pre_mortem_Bolus_2 -

0.75

Conclusion: The GIM is modulated using tannin-containing preparations. Further studies using larger numbers of animals should be conducted.

Relative abundance

0.25

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