

**Polysaccharides from *Callerya speciosa* alleviate metabolic disorders and gut
microbiota dysbiosis in diet-induced obese C57BL/6 mice**

Dongli Li^{1,4}, Zhaonan Xu², Yuanyuan Li², Lishe Gan^{1,4}, Panpan Wu^{1,4}, Rihui Wu^{1,4}, Jingwei
Jin^{1,4}, Xi Zheng^{1,4}, Kun Zhang¹, Hang Ma^{1,3,*}, Liya Li^{2,*}

¹ School of Biotechnology and Health Sciences, Wuyi University, Jiangmen 529020, China

² Institute of Microbial Pharmaceuticals, College of Life and Health Sciences, Northeastern
University, Shenyang 110819, China

³ Bioactive Botanical Research Laboratory, Department of Biomedical and Pharmaceutical
Sciences, College of Pharmacy, University of Rhode Island, Kingston, RI, 02881, United States

⁴ International Healthcare Innovation Institute (Jiangmen), Jiangmen 529040, China

Table S1. Primer sequences for real-time PCR

Genes	Forward	Reverse
18S	AGTCCCTGCCCTTTGTACACA	CGATCCGAGGGCCTCACTA
Atgl	GGATGGCGGCATTTTCAGACA	CAAAGGGTTGGGTTGGTTCAG
Cebp α	CAAGAACAGCAACGAGTACCG	GTCACTGGTCAACTCCAGCAC
Hsl	GATGTCACAGTCAATGGAGACAC	GGTGAAACCCCTCAGGGAAAG
Mgl	CAGAGAGGCCAACCTACTTTTC	ATGCGCCCCAAGGTCATATTT
Srebplc	GCAGCCACCATCTAGCCTG	CAGCAGTGAGTCTGCCTTGAT

Table S2. Body weight, body weight gain, food and energy intake in three groups of mice (n = 9)

Parameter	SD	HFD	HFD +NP
Body weight (g)	26.21 ± 0.36	32.34 ± 0.80 ^{###}	27.13 ± 0.44 ^{**}
Body weight gain (g)	6.24 ± 0.30	12.85 ± 0.75 ^{###}	8.00 ± 0.35 ^{***}
Food intake (g/day/mice)	3.34 ± 0.12	2.19±0.14 ^{###}	1.77 ± 0.06 ^{***}
Energy intake (kcal/day/mice)	12.12 ± 0.42	11.73 ± 0.63	9.23 ± 0.31 ^{**}

^{###}, $p < 0.001$, HFD vs. SD group; ^{***}, $p < 0.001$, ^{**}, $p < 0.01$, HFD+NP vs. HFD group.

Table S3. Relative abundance of the top 30 genera in fecal samples collected from three groups of mice at week 10

Bacterial name	SD (%)	HFD (%)	HFD +NP (%)
<i>Anaerotruncus</i>	0.172 ± 0.011	0.567 ± 0.025 ^{###}	0.605 ± 0.045
<i>Lachnospiraceae_UCG-006</i>	0.215 ± 0.017	0.726 ± 0.033 ^{###}	0.977 ± 0.052
<i>Intestinimonas</i>	0.353 ± 0.023	2.718 ± 0.139 ^{###}	2.332 ± 0.091
<i>Romboutsia</i>	0.023 ± 0.001	0.382 ± 0.034 [#]	0.755 ± 0.063 [*]
<i>Odoribacter</i>	1.380 ± 0.089	4.258 ± 0.247 ^{###}	7.694 ± 0.586 [*]
<i>Ruminiclostridium</i>	0.349 ± 0.033	2.184 ± 0.061 ^{###}	2.590 ± 0.183
<i>Tyzzerella</i>	0.044 ± 0.002	0.627 ± 0.036 ^{###}	0.523 ± 0.039
<i>Ruminiclostridium_9</i>	0.479 ± 0.018	2.696 ± 0.050 ^{###}	2.645 ± 0.100
<i>Oscillibacter</i>	0.099 ± 0.001	1.651 ± 0.002 ^{###}	1.168 ± 0.003
<i>Rikenellaceae_RC9_gut_group</i>	0.396 ± 0.064	1.471 ± 0.078 [#]	2.058 ± 0.143
<i>Mucispirillum</i>	0.719 ± 0.004	5.477 ± 0.010 ^{###}	2.075 ± 0.007 ^{**}
<i>Acetatifactor</i>	0.092 ± 0.018	0.574 ± 0.048 ^{##}	0.244 ± 0.034 [*]
<i>Lachnoclostridium</i>	0.855 ± 0.038	1.484 ± 0.039 ^{###}	1.284 ± 0.051
<i>Faecalibaculum</i>	0.605 ± 0.105	2.692 ± 0.288 [#]	3.713 ± 0.534
<i>Roseburia</i>	1.013 ± 0.139	1.468 ± 0.093	1.109 ± 0.085
<i>Akkermansia</i>	0.194 ± 0.044	0.327 ± 0.113	0.006 ± 0.001
<i>Erysipelatoclostridium</i>	0.017 ± 0.002	0.028 ± 0.003	0.196 ± 0.064
<i>Bacteroides</i>	1.543 ± 0.232	1.393 ± 0.106	2.105 ± 0.166
<i>Ruminococcaceae_UCG-014</i>	0.323 ± 0.030	0.488 ± 0.088	0.290 ± 0.034
<i>Alloprevotella</i>	1.328 ± 0.115	2.982 ± 0.726	7.333 ± 1.863
<i>Helicobacter</i>	7.531 ± 0.777	4.296 ± 0.255 [#]	2.745 ± 0.223
<i>Lachnospiraceae_NK4A136_group</i>	14.662 ± 0.633	10.800±0.615	9.606±0.612
<i>Candidatus_Saccharimonas</i>	0.342 ± 0.037	0.273 ± 0.065	0.164 ± 0.014
<i>Ruminiclostridium_6</i>	0.278 ± 0.043	0.016 ± 0.003 [#]	0.017 ± 0.002
<i>Lactobacillus</i>	1.914 ± 0.276	0.374 ± 0.062 [#]	1.994 ± 0.499
<i>Alistipes</i>	2.443 ± 0.153	1.104 ± 0.053 [#]	1.108 ± 0.061
<i>Prevotellaceae_UCG-001</i>	0.678 ± 0.063	0.009 ± 0.001 [#]	0.018 ± 0.002

<i>Dubosiella</i>	1.209 ± 0.060	0.030 ± 0.002 [#]	0.222 ± 0.008 [*]
<i>Lachnospiraceae_UCG-001</i>	0.931 ± 0.075	0.011 ± 0.001 ^{###}	0.011 ± 0.001
<i>[Eubacterium]xylanophilum_group</i>	0.673 ± 0.025	0.157 ± 0.016 ^{###}	0.164 ± 0.018

n = 8 per group. [#] $p < 0.05$, ^{##} $p < 0.01$, ^{###} $p < 0.001$, HFD vs. SD group; ^{*} $p < 0.05$, ^{**} $p < 0.01$, HFD+NP vs. HFD group.