

In vitro conversion of ellagic acid to urolithin A by different gut microbiota of urolithin metabotype A

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Fuxiang He^{1,2,3}, Yingying Bian³, Yaling Zhao³, Mengjie Xia^{1,2,3}, Shu Liu^{1,2,3}, Jiajin Gui^{1,2,3}, Xiaoyue Hou^{1,2,3,*}, Yaowei Fang^{1,2,3,*}

1. Jiangsu Key Laboratory of Marine Bioresources and Environment /Jiangsu Key Laboratory of Marine Biotechnology, Jiangsu Ocean University, Lianyungang 222005, China

2. Co-Innovation Center of Jiangsu Marine Bio-industry Technology, Jiangsu Ocean University, Lianyungang 222005, China

3. College of Ocean Food and Biological Engineering, Lianyungang 222005, China

* Correspondence authors:

Xiaoyue Hou: 2020000057@jou.edu.cn.

Yaowei Fang: 2007000027@jou.edu.cn.

Supplementary Materials:

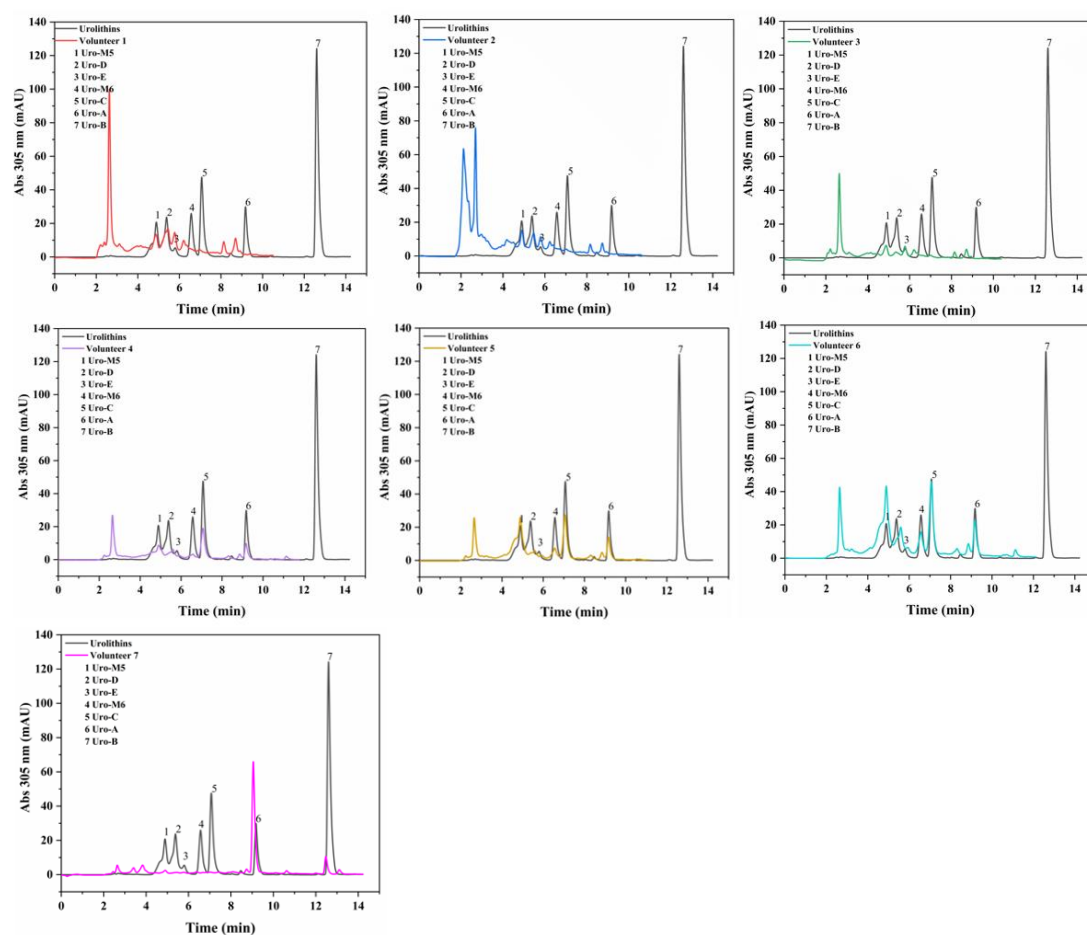


Fig. S1. HPLC identification of urolithin metabolic types in 7 volunteers. Volunteers 1-3 are UM-0, 4-6 are UM-A and 7 is UM-B.

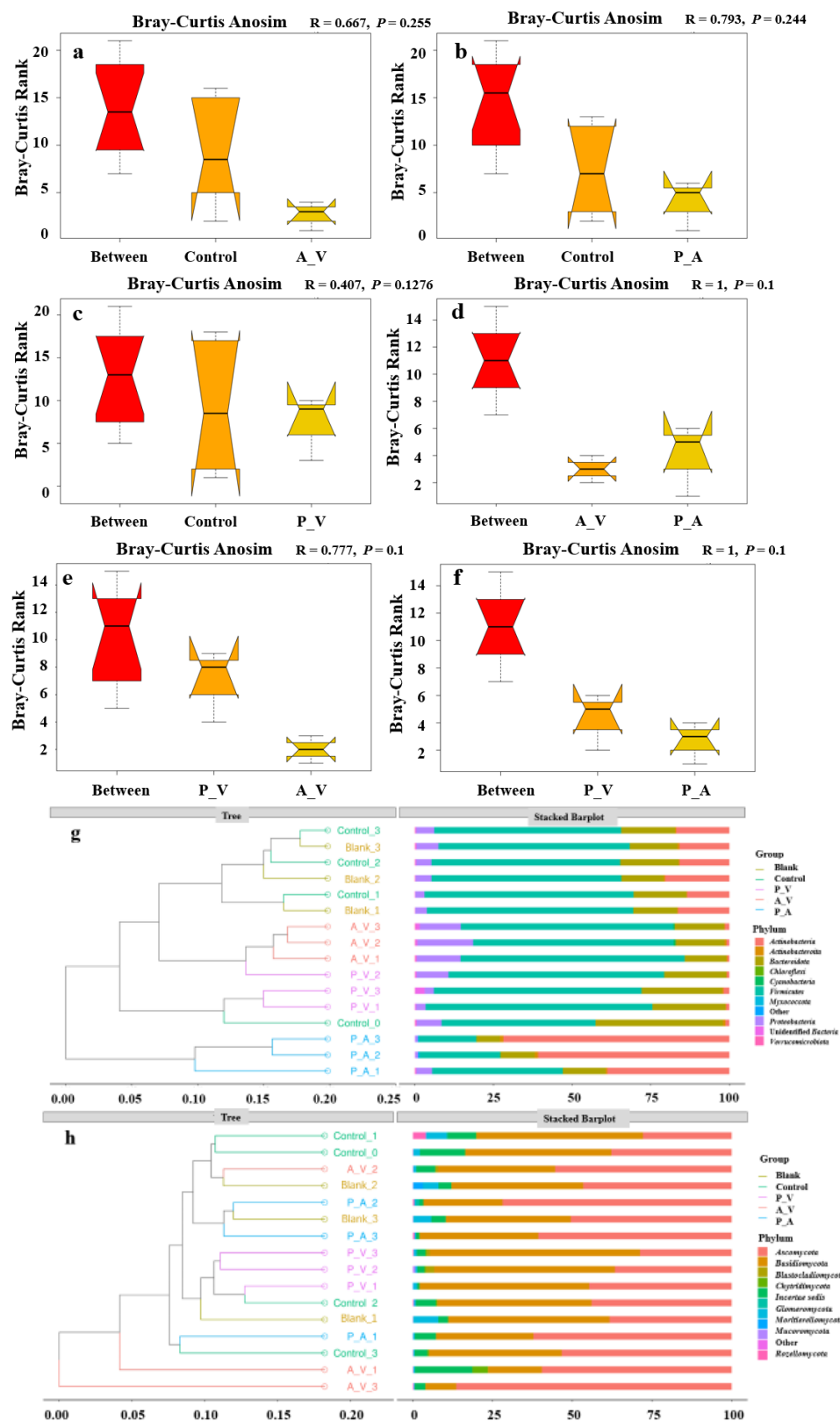


Fig. S2. Inter- and intragroup differences, the similarity analysis (Anosim). (a–f) Similarity analysis of different intestinal microbiota. (g–h) Hierarchical clustering analysis of different intestinal microbiota.

Table S1. LC-MS/MS (G2-XS QTOF) characteristics of 15 μ M urolithins and EA detected in the present work or used as standards.

Standards	Formula	[M-H] (m/z)	Retention time (min)	Area
Urolithin A	C ₁₃ H ₈ O ₄	227.0346	11.47	556.1195
Urolithin C	C ₁₃ H ₈ O ₅	259.0245	8.15	1060.1349
Urolithin M5	C ₁₃ H ₈ O ₇	275.0192	6.10	7889.9680
Urolithin M6	C ₁₃ H ₈ O ₆	300.9982	7.61	2980.3081
Iso Urolithin A	C ₁₃ H ₈ O ₄	243.0296	8.89	667.8921

Table S2. Intestinal microbiome richness in all the samples. Metagenomic bacterial taxonomic distribution based on relative abundance of clean metagenomic reads at family level.

Taxonomy	Blank	Control	P_V	A_V	P_A
<i>Lactobacillaceae</i>	0.001993	0.001715	0.063682	0.008576	0.006859
<i>Rhodobacteraceae</i>	0.029337	0.027298	0.016808	0.026129	0.008082
<i>Enterobacteriaceae</i>	0.008626	0.006959	0.029864	0.108445	0.002219
<i>Prevotellaceae</i>	0.025962	0.111025	0.128654	0.037561	0.037025
<i>Bacteroidaceae</i>	0.095933	0.094424	0.072015	0.073288	0.041681
<i>Ruminococcaceae</i>	0.100657	0.098129	0.10971	0.033633	0.099124
<i>Veillonellaceae</i>	0.189873	0.130433	0.037703	0.112524	0.015954
<i>Selenomonadaceae</i>	0.143611	0.119975	0.117825	0.399285	0.006323
<i>Lachnospiraceae</i>	0.14377	0.190198	0.301266	0.089233	0.113554
<i>Bifidobacteriaceae</i>	0.170527	0.113399	0.009505	0.007487	0.567065
Others	0.089711	0.106446	0.112968	0.103839	0.102114

Table S3. Intestinal microbiome heat map of species abundance in all the samples. Metagenomic bacterial taxonomic distribution based on relative abundance of clean metagenomic reads at genus level. The values corresponding to the heat map are relative quantitative data standardized by Z-Score.

Short taxonomy	P_V	Control	Blank	A_V	P_A
<i>Enterococcus</i>	-0.77443	-0.4869	0.683944	-0.83575	1.41313
<i>Bifidobacterium</i>	-0.71114	-0.26089	-0.0133	-0.71989	1.705225
<i>Ruminococcus</i>	0.950331	-0.38662	-0.80992	-0.94017	1.186381
<i>Alistipes</i>	0.475636	-0.50098	-0.76026	-0.75529	1.540889
<i>Barnesiella</i>	1.335383	-0.14368	-0.97477	-0.89026	0.673326
Unidentified <i>Clostridia</i>	1.391566	-0.32126	-0.84446	-0.8945	0.668652
<i>Fusicatenibacter</i>	1.700032	0.022878	-0.42627	-0.85691	-0.43973
<i>Lachnospira</i>	1.685967	0.016041	-0.56984	-0.87563	-0.25654
<i>Lachnoclostridium</i>	1.560053	0.338004	-0.59165	-1.00576	-0.30065
Unidentified <i>Prevotellaceae</i>	1.255609	0.908047	-0.88128	-0.6419	-0.64048
<i>Agathobacter</i>	1.602977	0.247992	-0.22819	-0.80168	-0.8211
Others	1.446624	0.528233	-0.3031	-0.57225	-1.0995
<i>Paraprevotella</i>	1.618875	0.267248	-0.60526	-0.39428	-0.88658
Unidentified <i>Lachnospiraceae</i>	1.531569	0.490239	-0.80307	-0.49452	-0.72422
<i>Desulfovibrio</i>	1.626541	-0.59526	-0.66828	0.312235	-0.67523
<i>Dorea</i>	1.7245	-0.50676	-0.40345	-0.77794	-0.03634
<i>Weissella</i>	1.774317	-0.50348	-0.51954	-0.22373	-0.52757
<i>Roseburia</i>	1.763337	-0.19978	-0.39025	-0.51554	-0.65776
<i>Subdoligranulum</i>	1.200427	0.580674	0.178031	-1.34767	-0.61146
<i>Blautia</i>	1.015028	0.251897	0.365323	-1.66485	0.032606
<i>Bacteroides</i>	-0.15696	0.861534	0.930144	-0.0991	-1.53562
<i>Allisonella</i>	-0.86527	0.465799	1.366791	0.107259	-1.07458
<i>Ruegeria</i>	-0.5224	0.623337	1.005248	0.373244	-1.47943
<i>Ilumatobacter</i>	-0.93217	0.486349	0.902305	0.765786	-1.22227
Unidentified <i>Erysipelotrichales</i>	-0.69657	0.620094	1.469611	-0.70378	-0.68935
<i>Faecalibacterium</i>	-0.21881	0.666112	1.285792	-1.28687	-0.44622
Unidentified <i>Oscillospiraceae</i>	1.031377	1.047442	-0.48945	-0.38449	-1.20488
<i>Coproccoccus</i>	0.576551	1.423261	-0.29111	-0.63374	-1.07496
<i>Coprobacter</i>	-0.28371	1.478064	-0.14069	0.234724	-1.28839
<i>Raoultella</i>	-0.02414	-0.55375	-0.48659	1.734207	-0.66973
<i>Citrobacter</i>	-0.05643	-0.53128	-0.56483	1.744891	-0.59235
Unidentified <i>Enterobacteriaceae</i>	-0.15591	-0.50486	-0.47605	1.761725	-0.62491
<i>Megamonas</i>	-0.27229	-0.25763	-0.09487	1.664302	-1.03951
<i>Parabacteroides</i>	-0.34989	-0.32013	-0.35928	1.762905	-0.7336
<i>Dialister</i>	-0.08075	0.236116	-0.14667	1.394972	-1.40366

Table S4. Intestinal microbiome richness in all the samples. Metagenomic bacterial taxonomic distribution based on relative abundance of clean metagenomic reads at species level.

Taxonomy	Blank	Control	P_V	A_V	P_A
<i>Metagenome</i>	0.013148	0.013743	0.019756	0.004112	0.012788
<i>Weissella cibaria</i>	0.000636	0.001024	0.055433	0.007671	0.000435
<i>Bacteroides plebeius</i>	0.021883	0.02177	0.009397	0.006549	0.007722
<i>Bacteroides vulgatus</i>	0.014019	0.012813	0.022654	0.033072	0.010293
<i>Bifidobacterium. bifidum</i>	0.009648	0.006193	0.004171	0.001172	0.073874
<i>Ruminococcus. sp. N15 MGS 57</i>	0.011557	0.017059	0.044746	0.011574	0.054269
<i>Allisonella histaminiformans</i>	0.064444	0.039847	0.006407	0.032142	0.000904
<i>Bifidobacterium longum</i>	0.112331	0.074877	0.002454	0.003283	0.131945
<i>unidentified Prevotellaceae</i>	0.023985	0.108035	0.124374	0.035233	0.035249
<i>Bifidobacterium adolescentis</i>	0.043105	0.029634	0.00242	0.002311	0.30434
Others	0.685242	0.675004	0.708189	0.86288	0.368181