

Potential use of bacterial community succession for estimating post-mortem interval as revealed by high-throughput sequencing

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Supplementary Table S1

Succession of sarcosaphagous insects attracted to the various stages of exposed rat carcasses in Changsha.

Order	Family	Species	Fresh			Bloated			Active			Advanced			Dry		
			A	L	E	A	L	E	A	L	E	A	L	P	A	L	P
Diptera	Calliphoridae	<i>Lucilia cuprina</i>	√			√	√	√	√	√	√	√	√			√	√
		<i>Lucilia sericata</i>	√			√	√	√	√	√	√	√	√			√	√
		<i>Chrysomya pinguis</i>	√			√		√	√	√		√	√			√	√
		<i>Hemipyrellia ligurriens</i>							√			√					
		<i>Achoerandrus rufifacies</i>	√			√		√	√		√	√				√	√
	Sarcophagidae	<i>Boettcherisca peregrine</i>				√			√								
		<i>Parasarcophaga crassipalpis</i>							√			√					
		<i>Phallosphaera gravelyi</i>				√			√			√					
	Muscidae	<i>Musca domestica</i>	√			√			√			√				√	
		<i>Hydrotaea chalcogaster</i>							√			√				√	
Phoridae	<i>Unident</i>				√			√	√			√				√	
Coleoptera	Staphylinidae	<i>Creophilus maxillosus</i>										√			√		
	Silphidae	<i>Calosilpha brunneicollis</i>							√			√			√		
	Nitidulidae	<i>Omosita discoidea</i>										√			√		
	Dermestidae	<i>D. maculatus</i> Degeer													√		

A, adult; L, larva; E; egg; P, pupa.

Supplementary Table S2

Numbers of adult dipterans collected at different stages of decomposition from exposed rat carcasses

Family	Species	Fresh	Bloated	Active	Advanced	Dry
Calliphoridae	<i>Lucilia cuprina</i>	6	11	24	27	0
	<i>Lucilia sericata</i>	4	17	20	19	7
	<i>Chrysomya pinguis</i>	7	15	13	21	0
	<i>Hemipyrellia ligurriens</i>	0	0	8	15	0
	<i>Achoerandrus ruffifacies</i>	13	23	27	31	0
Sarcophagidae	<i>Boettcherisca peregrine</i>	0	2	2	1	0
	<i>Parasarcophaga crassipalpis</i>	0	0	2	4	0
	<i>Phallosphaera graveleyi</i>	0	4	5	5	0
Muscidae	<i>Musca domestica</i>	5	9	7	11	2
	<i>Hydrotaea chalcogaster</i>	0	0	5	5	4
Phoridae	<i>Unident</i>	0	10	26	0	0

Supplementary Table S3

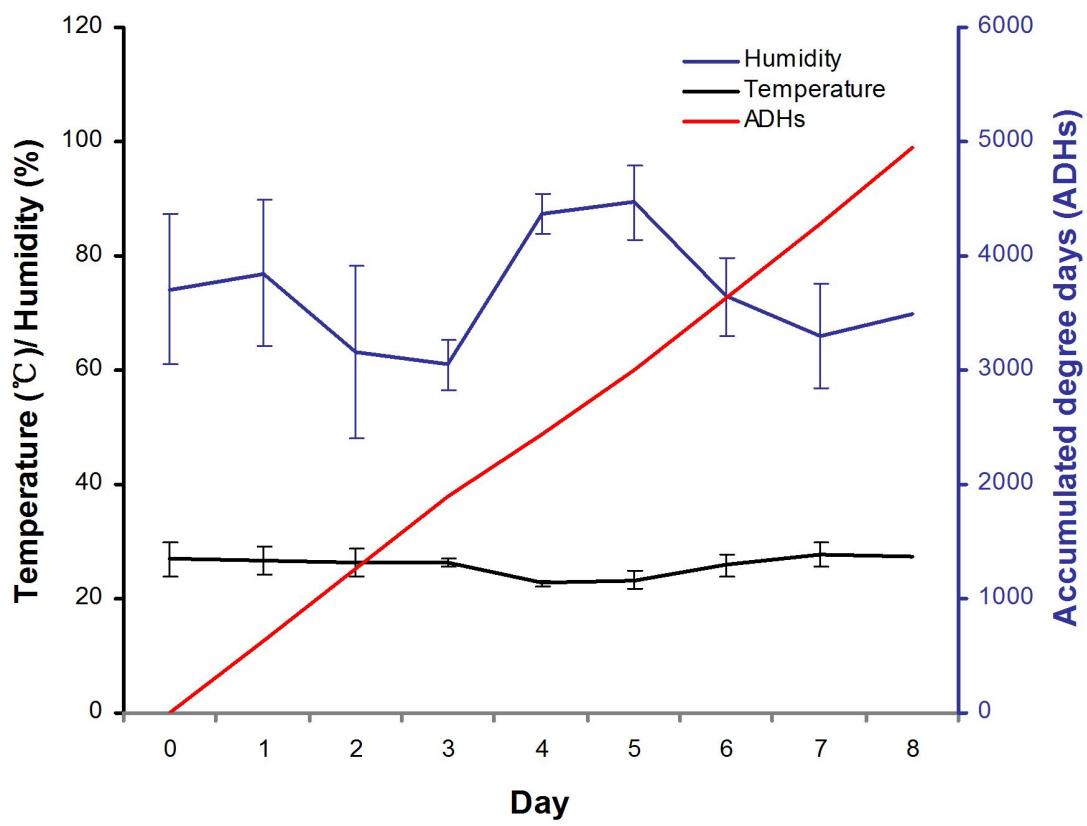
Genera with significantly different abundance in the buccal cavity between the sarcosaphagous insect exclusion group (group A) and the sarcosaphagous insect access group (group B).

Taxa	mean abundance (group A)	mean abundance (group B)	p value
<i>Escherichia</i>	0.0015649	0.0054790	0.0091
<i>Wautersiella</i>	0.0000120	0.0009286	0.0163
<i>Collinsella</i>	0.0000120	0.0001703	0.0463
<i>Deinococcus</i>	0.0000963	0	0.0114
<i>Methylocaldum</i>	0.0000843	0	0.0209
Dok59	0.0000963	0	0.0114
<i>Photobacterium</i>	0	0.0000774	0.0160
<i>Spirochaeta</i>	0.0000722	0	0.0387
SargSea-WGS	0	0.0000774	0.0160
<i>Halanaerobium</i>	0.0001204	0	0.0401
<i>Facklamia</i>	0	0.0000774	0.0160
<i>Acholeplasma</i>	0.0000722	0	0.0387

Supplementary Table S4

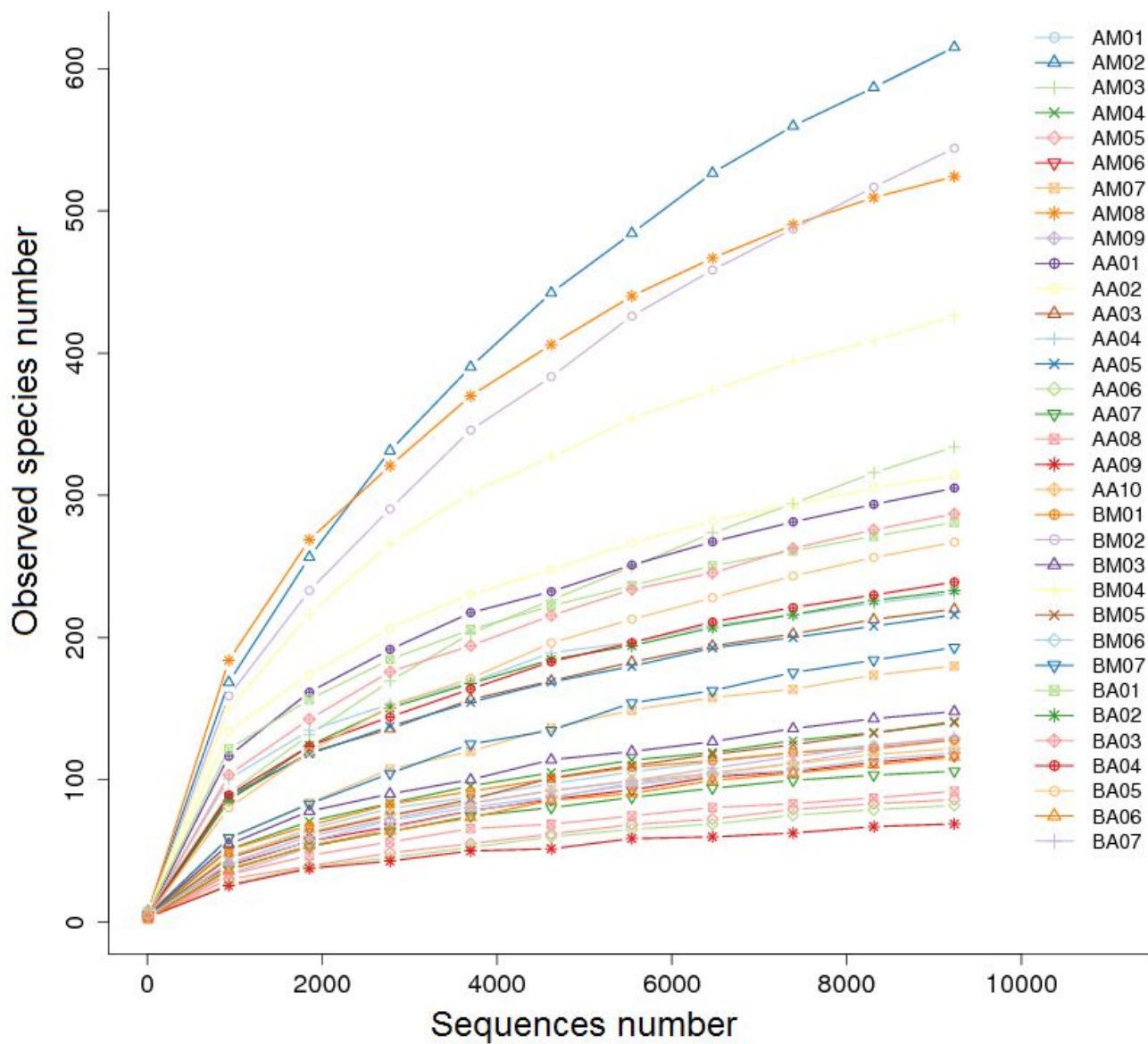
Genera with significantly different abundance in the rectum between the sarcosaphagous insect exclusion group (group A) and the sarcosaphagous insect access group (group B).

Taxa	mean abundance (group A)	mean abundance (group B)	p value
<i>Stenotrophomonas</i>	0.0000542	0.0005237	0.0005
<i>Anaerovibrio</i>	0.0204442	0.0032864	0.0402
<i>Sutterella</i>	0.0018310	0.0088299	0.0432
<i>Thiobacillus</i>	0	0.0000903	0.0074
<i>Wautersiella</i>	0	0.0001625	0.0013
<i>Collinsella</i>	0.0012026	0.0004695	0.0338
<i>Bifidobacterium</i>	0.0000542	0.0001806	0.0469
<i>Sulfurimonas</i>	0	0.0000722	0.0198
<i>Clostridium</i>	0.0001733	0	0.0129
<i>Adlercreutzia</i>	0.0000975	0	0.0169
<i>Caulobacter</i>	0.0000867	0	0.0289
<i>Lachnospira</i>	0	0.0000722	0.0198



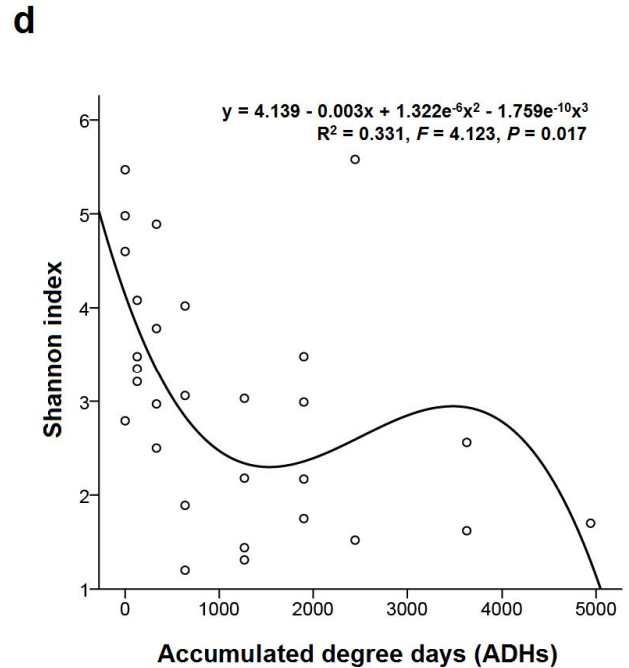
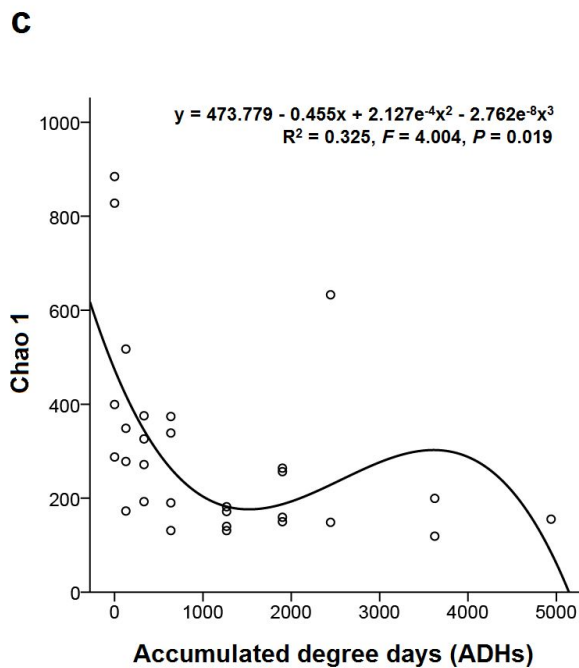
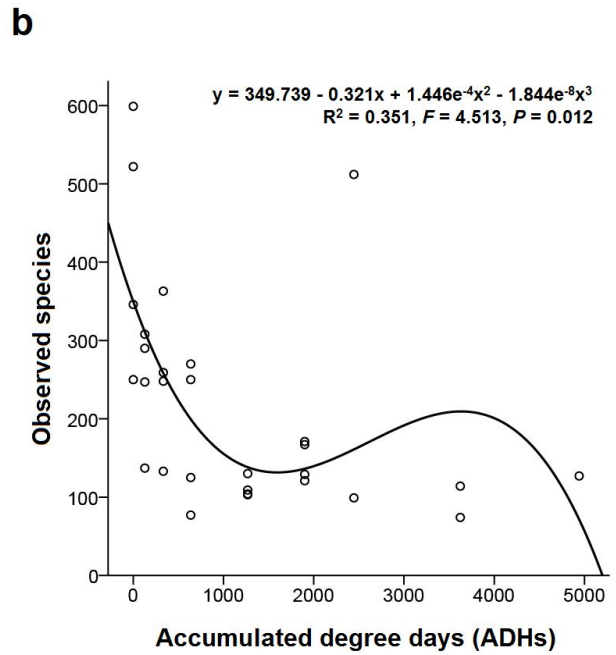
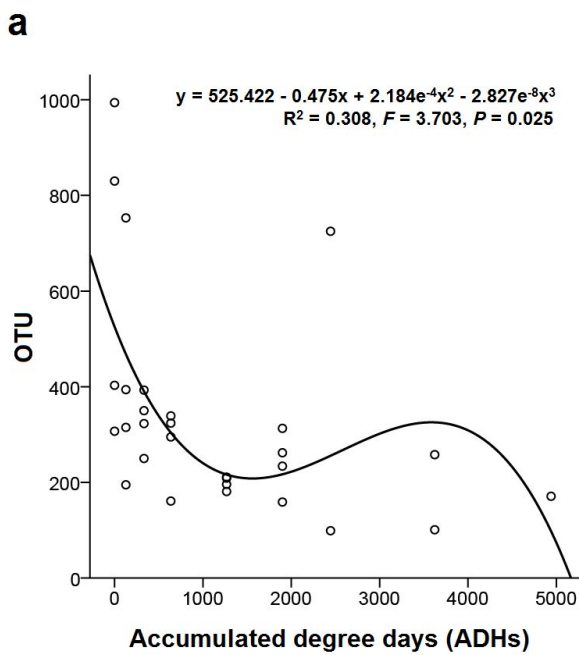
Supplementary Figure S1

Average daily temperature (°C), humidity (%) and accumulated degree hours (ADHs) during the experiment



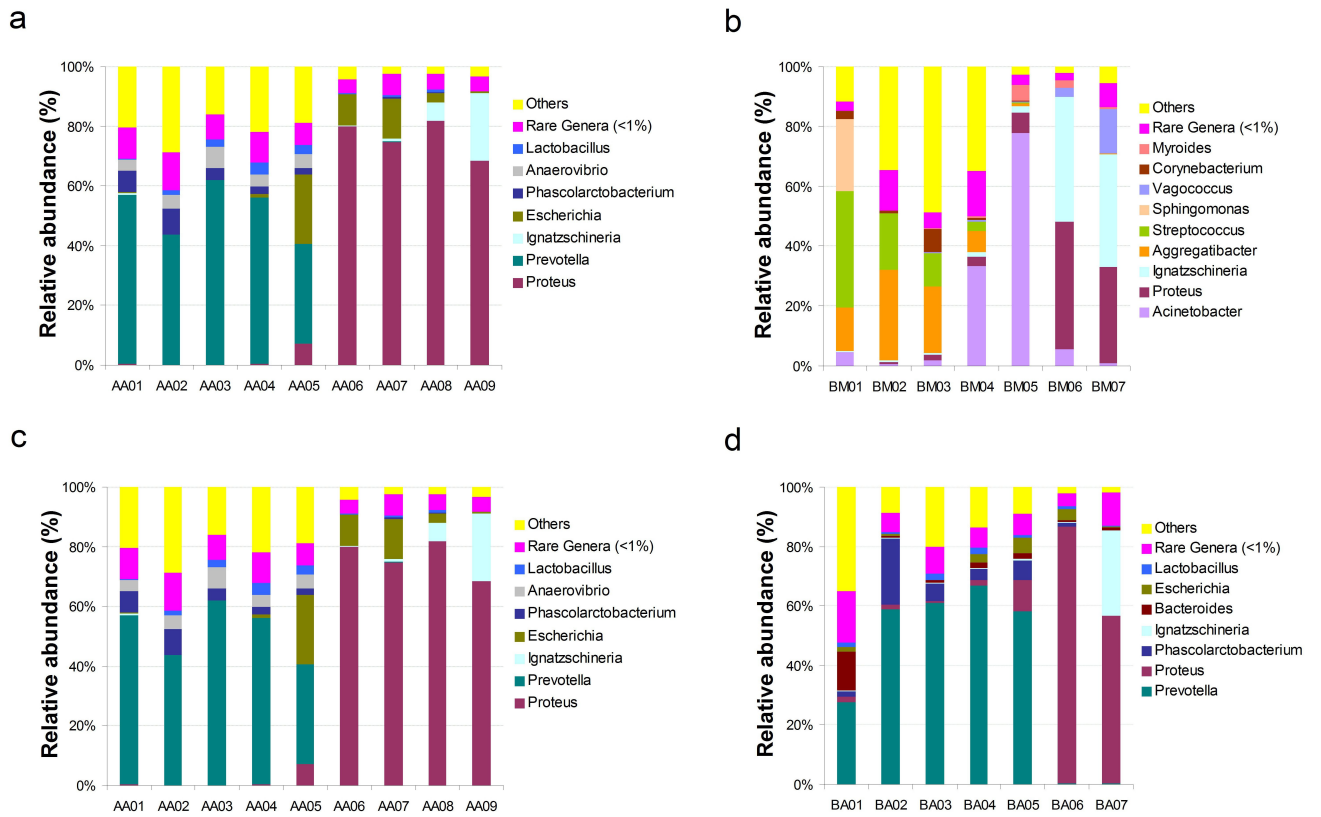
Supplementary Figure S2

Rarefaction curves of observed species number clustered at 97% sequence identity across all samples. Sample names refer to samples as described in Table 1.



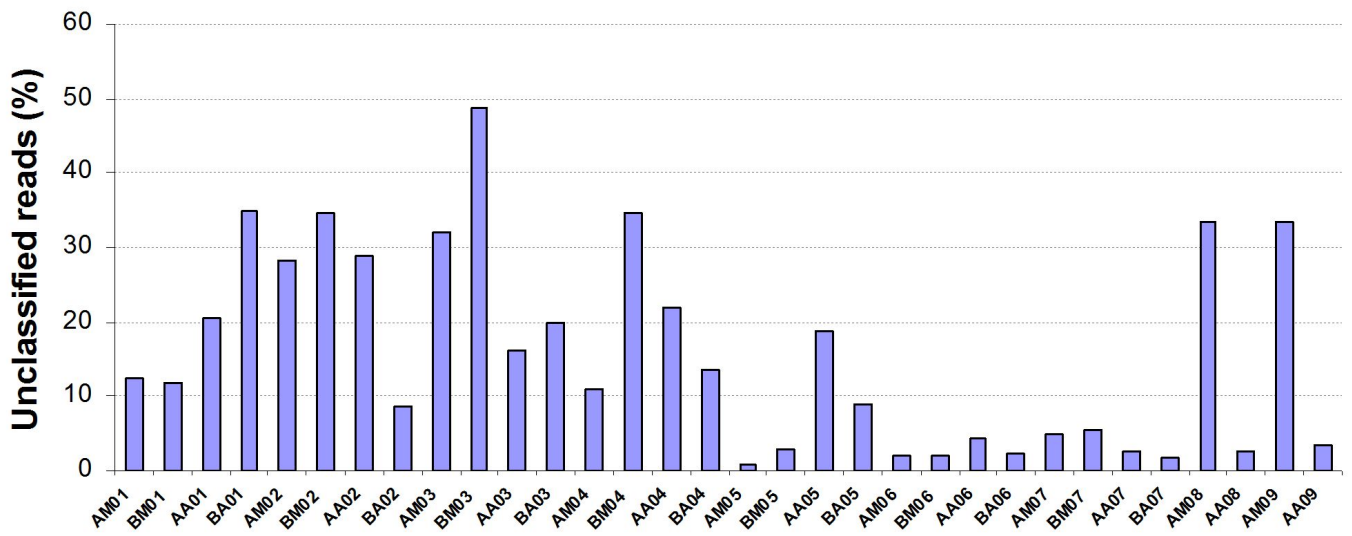
Supplementary Figure S3

Non-linear regression curves of operational taxonomic unit (OTU) richness (a), observed species index (b), Chao1 index (c) and Shannon index (d) during decomposition. Each open circle represents the bacterial community of a single sampling body site (i.e., buccal cavity or rectum) from rat carcasses.



Supplementary Figure S4

Bacterial community structure variation during decomposition at the genus level. Relative abundance of bacterial genera during decomposition in the buccal cavity in group A (a), buccal cavity in group B (b), rectum in group A (c) and rectum in group B (d). Sample names refer to samples as described in Table 1.



Supplementary Figure S5

Proportion of the unclassified reads in different samples. Sample names refer to samples as described in Table 1.