Supplemental Material

Supplemental Tables

Table S1. Megyesi table of decomposition. State of decomposition is described from visual inspection of the carcass. Points for each visual state at each body site are indicated in the table. 'NA' indicates the category is not applicable to that body site.

Decomposition Stage and Grade	Head	Trunk	Limbs
Fresh			
No discoloration	1	1	1
Early Decomposition			
Discoloration	2	2	2
Purging of fluids from eyes, nose, mouth	3	NA	NA
Bloating of neck and/or face	3	3	NA
Rupture and/or purging	NA	4	NA
Advanced Decomposition			
Sagging of flesh	5	5	NA
Sinking of flesh	6	6	NA
Caving in of flesh	7	7	NA
Mummification	8	8	NA
Dessication and/or mummification	NA	NA	3

Table S2. Faith's Phylogenetic Diversity (PD) of eukaryotic and bacterial communities. Mean and SEM (in parentheses) are presented for treatment and stage of decomposition at each body site and for the soil. Means without SEM had on one sample for analysis. NA indicates the samples did not produce sequences for analysis.

	18S Mean PD (SEM)	16S Mean PD (SEM)
Abdominal Cavity		
Sterile-Early	17 (7.1)	11 (1.9)
Sterile-Late	NA	9.6 (0.85)
Untreated-Early	NA	13
Untreated-Late	83 (0.07)	9.3 (1.3)
Skin of Head		
Sterile-Early	NA	NA
Sterile-Late	36 (10)	5.8 (0.25)
Untreated-Early	77	10 (2)
Untreated-Late	61 (13)	7 (0.27)
Skin of Torso		
Sterile-Early	62 (33)	11 (0.24)
Sterile-Late	47 (13)	5.3 (0.25)
Untreated-Early	NA	6.2
Untreated-Late	26 (4.4)	4.8 (0.3)
Soil		
Sterile-Early	36 (9.9)	5.2 (0.5)
Sterile-Late	NA	7.6 (0.78)
Untreated-Early	102 (2.3)	25 (2.2)
Untreated-Late	107 (1.7)	24 (0.84)

Table S3. The number of samples that were used for 18S and 16S analyses. Only late stage decomposition samples were compared by statistical methods. 'NA' indicates no sample produced enough sequences for analysis after quality filtering and rarefaction.

	Treatment			
	Early Sterile	Late Sterile	Early Untreated	Late Untreated
18S				
Abdominal Cavity	NA	5	NA	2
Skin of Torso	NA	7	NA	9
Skin of Head	NA	10	NA	8
Soil	NA	8	5	10
16S				
Abdominal Cavity	2	8	1	8
Skin of Torso	3	8	1	7
Skin of Head	1	10	1	10
Soil	2	4	3	8

Table S4. Mean and (SEM) of eukaryotic taxa classified to the species level for sterile and untreated soils with abundances greater than 0.5%. Early samples correspond to T0, late samples include T3 and 4 for the untreated soil, T5 and 6 for sterile soils. Asterisks (*) indicate a significant difference in abundance at late stage decomposition for sterile and untreated soil using a bootstrapped Mann-Whitney U test with Bonferroni correction of the p-value.

	Treatment			
	Early Sterile	Late Sterile	Early Untreated	Late Untreated
Abominal Cavity				
Eurotiomycetes		99 (0.2)		9.9 (1.4)
Saccharomycetales		0.3 (0.2)		65 (23)
Polar-centric-Coscinodiscophyceae		0 (0)		7.6 (7.6)
Opisthokonta		0 (0)		6.9 (6.9)
Basidiomycota		0 (0)		5.9 (3.9)
Agaricomycetes		0 (0)		2.9 (2.9)
Skin of Torso				
Eurotiomycetes*	0.5 (0.4)	73 (13.4)		0.5 (0.2)
Mucoromycotina*	0.1 (0.1)	0 (0)		62 (10)
Sordariomycetes	0 (0)	9.6 (9.5)		20 (8.4)
Chromadorea	0 (0)	0.1 (0)		15 (8.8)
Tritrichomonadidae	7.5 (5.3)	0 (0)		0 (0)
Dothideomycetes*	0.1 (0.1)	15 (10.2)		0 (0)
Cristamonadida	18 (13)	0 (0)		0 (0)
Saccharomycetales	27 (19)	0.2 (0.1)		0.4 (0.2)
Skin of Head				
Eurotiomycetes*		98 (1.2)		0.2 (0.1)
Chromadorea		1.2 (0.9)		37 (14)
Mucoromycotina*		0.1 (0)		36 (14)
Agaricomycetes		0 (0)		16 (11)
Oomyceta		0 (0)		8.1 (8.1)
Soil				
Eurotiomycetes*		66 (13)	0.6 (0.1)	0.5 (0)
Gregarines*		0.1 (0.1)	13 (1.8)	16 (2.5)
Agaricomycetes*		0.3 (0.3)	8.2 (0.5)	15 (2.5)
Leotiomycetes*		0.2 (0.1)	5.3 (1)	1.8 (0.2)
Mucoromycotina*		0 (0)	3.9 (0.9)	17 (2.9)
Dothideomycetes		11 (5)	2.8 (0.3)	1.3 (0.3)
Oomyceta*		0 (0)	7.5 (0.8)	8.5 (1.7)
Chromadorea*		0 (0)	3.2 (0.5)	7.6 (2.8)
Sordariomycetes		12 (11.3)	0 (0)	0 (0)
Pezizomycotina*		8.2 (8.2)	1.1 (0.2)	0.1 (0)
Stichotrichia*		0 (0)	7.5 (3.3)	2.8 (0.5)
Clade-C*		0 (0)	3.3 (0.3)	2.3 (0.3)
Haptoria*		0 (0)	2.6 (0.5)	2.2 (0.7)
Cercomonadidae*		0 (0)	3 (0.3)	1.6 (0.1)
Chytridiomycetes*		0 (0)	1.9 (0.5)	2 (0.7)
Conosa*		0 (0)	2.3 (0.7)	0.8 (0.1)
Glomeromycotina*		0 (0)	1.9 (0.3)	0.9 (0.1)
Tremellomycetes*		0 (0)	1.3 (0.6)	0.8 (0.3)
Plasmodiophorida*		0 (0)	1.1 (0.3)	1 (0.1)
Hyphochrytriaceae*		0 (0)	1.1 (0.4)	0.7 (0.1)
Microsporidiomycotina*		0 (0)	0.7 (0.2)	0.8 (0.2)

Table S5. Mean and (SEM) of bacterial taxa classified to the species level for sterile and untreated soils with abundances greater than 0.5%. Early samples correspond to T0, late samples include T3 and 4 for the untreated soil, T5 and 6 for sterile soils. Asterisks (*) indicate a significant difference in abundance at late stage decomposition for sterile and untreated soil using a bootstrapped Mann-Whitney U test with Bonferroni correction of the p-value.

	Treatment			
	Early Sterile	Late Sterile	Early Untreated	Late Untreated
Abdominal Cavity				
Enterococcus*	0.37 (0.3)	24 (6)	0	6.3 (2.2)
Morganella	0	0.01 (0)	0	30 (14)
Clostridium	0	0	0	11 (11)
Bacteroides	0.13 (0.1)	2.2 (1.1)	0.63	5 (3.1)
Lactobacillus	0.03 (0)	0.76 (0.5)	0.07	2 (1.5)
Mucispirillum	0.93 (0.9)	0.67 (0.5)	5.1	1.2 (0.5)
Proteus	0.02 (0)	0	0	2.6 (1.2)
Ruminococcus	0.93 (0.9)	0.87 (0.4)	2.1	0.64 (0.2)
Oscillospira	0.92 (0.9)	0.57 (0.4)	3.5	0.5 (0.2)
Parabacteroides	1.5 (1.2)	0.61 (0.3)	0.23	0.42 (0.3)
Skin of Toroso				
Morganella*	0	0.35 (0.3)	54	48 (16)
Bacillus	0	20 (12)	0.1	13 (13)
Lactobacillus	12 (1.9)	0	0	0
Proteus*	0	0	4.9	4.2 (1.4)
Burkholderia	0	2.2 (1.2)	0	0
Enterococcus	0	1.9 (1.9)	0	0
Novosphingobium	0	1.8 (1.3)	0	0
Allobaculum	4.4 (3.6)	0	0	0
Escherichia	0	1 (0.6)	0.33	0.65 (0.4)
Skin of Head				
Morganella	0	0 (0)	0	32 (11.2)
Staphylococcus*	0	12 (6)	0.1	0.07 (0.1)
Campylobacter	0	0 (0)	62	0
Bacillus	3.0	3.2 (3.1)	0.03	2.3 (1.9)
Proteus*	0	0 (0)	0	5.1 (1.8)
Pseudomonas	0	1.5 (1)	0	3.6 (1.4)
Enterococcus	0	3.3 (1.2)	0	0.05 (0)
Burkholderia	0	3.2 (2.7)	0	0
Novosphingobium	0	2.6 (2.3)	0	0
Stenotrophomonas	0	2.2 (2.2)	0	0
Escherichia	3.4	1.5 (0.5)	0	0.28 (0.2)
Acinetobacter	0.63	1.9 (1.9)	0.27	0.06 (0.1)
Sphingobacterium	0	0	0	1.8 (1)
Soil				
Bacillus*	81 (1)	17 (3.2)	0 (0.2)	3.3 (0.7)
DA101*	0	0	8.5 (0.9)	7.6 (0.9)
Morganella	0	0	0	6.5 (6.5)
Rhodoplanes	0	0.09 (0.1)	4.6 (0.3)	4.4 (0.7)
Stenotrophomonas	0	8.3 (7.6)	0	0.08 (0)
Kaistobacter	0	0.09 (0.1)	2.4 (0.3)	3.1 (0.5)
Candidatus Solibacter*	0	0	2.3 (0.3)	2.2 (0.3)
Novosphingobium	0	5.8 (4.8)	0	0
Burkholderia	0	5 (3.8)	0	0
Staphylococcus	0	4.8 (4.8)	0	0.08 (0.1)
Pedobacter	0	2.5 (2.5)	0.24 (0.2)	0.56 (0.2)
Candidatus Nitrososphaera*	0	0	1.5 (0.3)	1.2 (0.2)
Arthrobacter	0	0.63 (0.6)	0.29 (0.1)	1.3 (0.2)
A4	0	0	1.6 (0.2)	1 (0.2)
Brochothrix	4.6 (0.1)	0.06 (0)	0	0.16 (0.1)
Flavisolibacter	0	0	0.69 (0.1)	0.76 (0.2)
Acinetobacter	0.2 (0.2)	0.06 (0)	0.51 (0.4)	0.72 (0.6)
Paenibacillus	0	1.7 (0.7)	0.1 (0.1)	0
Thermomonas	0	0	0.86 (0.2)	0.56 (0.1)