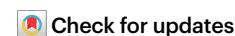


Decomposer communities are universal in death

Michael S. Strickland & Laurel Lynch



Decomposer microbiomes are universal across cadavers regardless of environmental conditions, and they use complex cross-feeding and interkingdom interactions to break down organic matter.

All life invariably ends in death, but what happens after is arguably just as important. Decomposition is fundamental across all of Earth's ecosystems and is driven largely by microorganisms. Although decomposition is one of the most studied biogeochemical processes in ecosystem ecology, much of this research focuses on the decay of plant litter¹. This plant-centric focus arose because in most environments, plant inputs are ubiquitous, abundant and resistant to degradation. Plant biomass is primarily composed of cellulose macromolecules, a feature that exerts strong selective pressure on microbial decomposers. As a result, litter decomposition typically follows a broadly predictable successional pattern, where fungal specialists first deploy oxidative enzymes that depolymerize carbon-rich macromolecules and then bacterial communities catalyse the turnover of smaller molecules via hydrolytic enzymes. In contrast to litter, animal inputs (including humans) represent smaller

amounts of biomass that tend to decompose more rapidly and are thus assumed to have limited ecological consequences. However, there is a growing realization that the often-overlooked decomposition of animal inputs plays a critical role in ecosystem and community ecology.

As we enter the sixth mass extinction event in Earth's history, animal biomass represents an estimated 2 billion metric tons of decomposable carbon². Climate-driven increases in mass mortality events, disease and human conflicts will only increase the relevance of this resource to ecosystem productivity and resilience³. In contrast to plant litter, animal carcasses are enriched in lipids and proteins that more closely match microbial stoichiometry and metabolic demand. This means that macronutrients, such as nitrogen and phosphorus – which typically limit rates of biological productivity – are alleviated during animal decomposition. Although the influx of cadaver-derived nutrients could release constraints on microbial metabolism, it also represents a major ecological disturbance that probably selects for decomposers with the genomic potential and metabolic repertoire needed to capitalize on high-quality resources that are both spatially and temporally dispersed⁴. Furthermore, the flow of carcass-derived fluids belowground seeds the soil microbiome with carcass-derived microorganisms, setting the stage for interactions among taxonomically distinct communities. Additionally, the miasma of carcass-derived

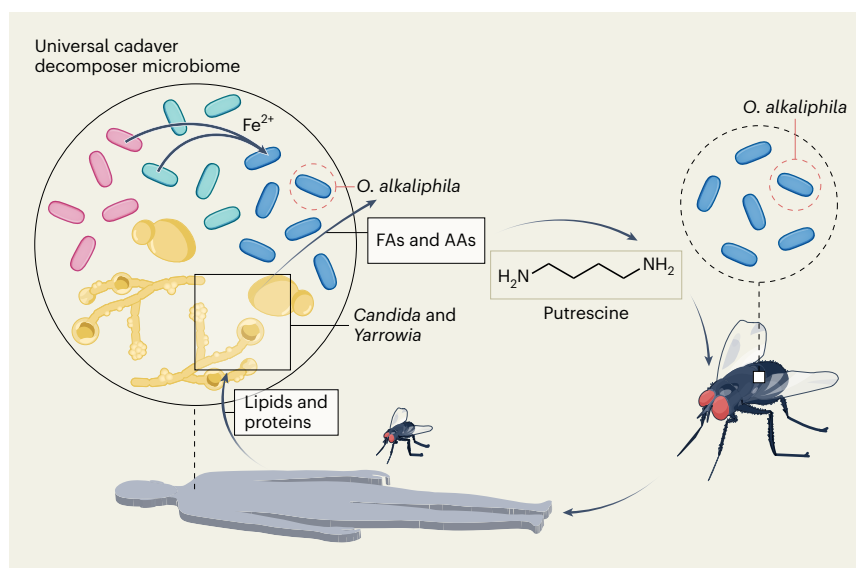


Fig. 1 | Interkingdom interactions associated with cadaver decomposition.

The cadaver decomposer microbiome is universal across geographic scales and is unique when compared with other environmental microbiomes. The cadaver decomposition microbiome also represents a series of interkingdom interactions. These interactions include cross-feeding, whereby *Candida* and *Yarrowia* fungi break down complex lipids and proteins into fatty acids (FAs)

and amino acids (AAs), which can be utilized by bacteria such as *O. alkaliphila* (which also receives ferrous ions from other bacteria). *O. alkaliphila* has the capacity to produce putrescine (from fungal-derived ornithine), a key volatile compound used by insects such as blow flies to locate cadavers. *O. alkaliphila* is also detected on blow flies, suggesting a potential dispersal mechanism of the cadaver decomposer microbiome.

volatiles (for example, putrescine) can either attract or repel scavengers, leading to a suite of interkingdom interactions⁵. Because few studies have used DNA-based techniques to track changes in microbial decomposer composition or function during animal decay, the extent to which animal decomposition departs from plant decomposition and whether it can affect ecosystem-scale processes remains unclear.

Now, writing in *Nature Microbiology*, Burcham and colleagues⁶ suggest mammal decomposition is driven by a universal microbial network that is predictable across a broad range of environmental conditions. The authors collected skin and underlying soil samples from 36 human cadavers decomposing in temperate or semi-arid environments. They sequenced community DNA and built metagenome-assembled genomes from the cadaver samples, and then reconstructed genome-scale metabolic models across the environments and stages of cadaver decomposition. They found preferential utilization of energy-rich compounds (for example, amino acids, carbohydrates) followed by slower catabolism of less labile compounds (for example, lipids). In temperate ecosystems, microbial metabolic efficiencies were strongly correlated with cadaver decomposition rates. In the semi-arid ecosystem this correlation was weaker, probably because the lack of water constrained microbial growth. However, these communities also displayed greater cross-feeding throughout decomposition, where metabolic byproducts of one strain were utilized as a resource by another. As decomposition progressed in both environments, the potential for metabolic exchanges via cross-feeding also increased, while phylogenetic turnover and microbial richness declined. These results suggest that factors such as microbial interactions and succession play a deterministic role in community assembly during cadaver decomposition, with implications for microbial network stability under disturbance and for the maximum rates of carcass decomposition. For instance, moisture limitation in semi-arid environments muted microbial responses, both in terms of taxonomic composition and metabolic potential, illustrating complex feedbacks with climate and weather conditions.

The decomposing carcass is the intense focus of a complex milieu of species that interact across the domains and kingdoms of life⁷ to catalyse cadaver decomposition (Fig. 1). Using DNA sequencing techniques, Burcham and colleagues identified key organisms and interkingdom interactions that catalysed cadaver decomposition. For instance, the genomes of two key fungal decomposers, *Yarrowia* and *Candida*, contained arginine and ornithine biosynthesis pathways, and both taxa converted lipids and proteins into forms that were efficiently assimilated by co-occurring bacterial consumers, such as *Oblitimonas alkaliphila*. In turn, *O. alkaliphila* utilized fungal-derived ornithine to generate putrescine, a ubiquitous byproduct of mammalian tissue decomposition that also serves as a critical volatile signalling compound. *O. alkaliphila* was largely responsible for increasing the efficiency of amino acid metabolism, suggesting interkingdom cross-feeding can influence soil nutrient cycling. Along with other key bacterial consumers, *O. alkaliphila* has been detected on blow flies, suggesting insects can ferry microorganisms from one cadaver resource to another, aiding microbiome dispersal to an ephemeral resource and setting the trajectory of cadaver decomposition. Notably,

insects may not transfer just microorganisms but also other organisms, such as mites, setting the stage for distinct communities across the domains and kingdoms of life associated with cadavers⁸. These findings illustrate that cadaver inputs do not simply represent a resource pulse for resident communities, but also serve as an important nexus of community reshuffling that could influence resident soil communities across larger spatial and temporal scales than expected⁹. However, the ability of cadaver communities to coexist with the native soil community remains an open question.

Burcham and colleagues provide a much-needed, genome-resolved view of microbial dynamics during cadaver decomposition. Their findings reveal a core mammalian decomposer network that is phylogenetically unique and rare in the environment until cadaver-derived nutrients are introduced. Results of this work have implications for the fields of forensic science, criminology and ecology. For instance, by leveraging a series of machine learning and network approaches they identified conserved links between taxonomy and function that precisely predict post-mortem interval. The ability to predict post-mortem interval will enable crime scene investigators to determine an individual's time of death more accurately, providing important evidence for solving crimes. This work is likewise relevant to the applied aspects of green burials and composting of livestock carcasses, whereby microbial inoculants could be used to mediate rates and stages of decomposition. Furthermore, the authors were able to demonstrate how interactions among mammalian decomposer communities fuel the turnover and exchange of resources, with implications for biogeochemical cycling and trophic cascades. The interplay between vertebrate, invertebrate and microbial scavengers on cadaver decomposition and ecosystem resilience in the face of global change presents an exciting arena for future investigation¹⁰.

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References

1. Moore, J. C. et al. *Ecol. Lett.* **7**, 584–600 (2004).
2. Bar-On, Y. M., Phillips, R. & Milo, R. *Proc. Natl Acad. Sci. USA* **115**, 6506–6511 (2018).
3. Barton, P. S., Cunningham, S. A., Lindenmayer, D. B. & Manning, A. D. *Oecologia* **171**, 761–772 (2013).
4. Morant, J. et al. *Ecosystems* **26**, 383–396 (2023).
5. von Hoermann, C. et al. *R. Soc. Open Sci.* **9**, 220555 (2022).
6. Burcham, Z. M. et al. *Nat. Microbiol.* <https://doi.org/10.1038/s41564-023-01580-y> (2024).
7. Benbow, M. E. et al. *Ecol. Monogr.* **89**, e01331 (2019).
8. Gibbs, J. P. & Stanton, E. J. *Ecol. Appl.* **11**, 79–85 (2001).
9. Singh, B. et al. *Front. Microbiol.* **8**, 2616 (2018).
10. Bartel, S. L. et al. *Trends Ecol. Evol.* <https://doi.org/10.1016/j.tree.2023.09.008> (2023).

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Competing interests

The authors declare no competing interests.