**Table S1.** A selection of 45 quotations that, implicitly or explicitly, convey the view that all animals host and depend upon a microbiome.

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| **Quotation** | **Reference** |
| Like all animals, butterflies also host internal communities of microorganisms... | Hammer, T. J., McMillan, W. O. & Fierer, N. 2014 Metamorphosis of a butterfly-associated bacterial community. PLoS One 9, e86995. |
| Mammals host gut microbiomes that are immensely important to the health, and likely fitness, of the host. | Sanders, J. G., Beichman, A. C., Roman, J., Scott, J. J., Emerson, D., McCarthy, J. J. & Girguis, P. R. 2015 Baleen whales host a unique gut microbiome with similarities to both carnivores and herbivores. Nat. Commun. 6, 8285. (doi:10.1038/ncomms9285) |
| Like nearly all plants and animals, humans host a large number of microorganisms... | Fierer, N. et al. 2011 From Animalcules to an Ecosystem: Application of Ecological Concepts to the Human Microbiome. Annu. Rev. Ecol. Evol. Syst. 43, 120830113150004. (doi:10.1146/annurev-ecolsys-110411-160307) |
| Animals and plants are no longer viewed as autonomous entities, but rather as "holobionts"...Symbiotic microbes are fundamental to nearly every aspect of host form, function, and fitness... | Bordenstein, S. R. & Theis, K. R. 2015 Host biology in light of the microbiome: Ten principles of holobionts and hologenomes. PLoS Biol. 13, e1002226. (doi:10.1371/journal.pbio.1002226) |
| Today we realize that any multicellular organism must be considered a metaorganism comprising the macroscopic host and its synergistic interdependence with bacteria, archaea, fungi, and numerous other microbial and eukaryotic species including algal symbionts. | Bosch, T. C. G. & McFall-Ngai, M. J. 2011 Metaorganisms as the new frontier. Zoology 114, 185–190. (doi:10.1016/j.zool.2011.04.001) |
| The gut microbiota of animals exert major effects on host biology. | Bourguignon, T., Lo, N., Dietrich, C., Šobotník, J., Sidek, S., Roisin, Y., Brune, A. & Evans, T. A. 2018 Rampant Host Switching Shaped the Termite Gut Microbiome. Curr. Biol. 0, 1–6. (doi:10.1016/j.cub.2018.01.035) |
| The host-microbiome supraorganism appears to have coevolved and the unperturbed microbial component of the dyad renders host health sustainable. This coevolution has likely shaped evolving phenotypes in all life forms... | Dominguez-Bello, M. G., Godoy-Vitorino, F., Knight, R. & Blaser, M. J. 2019 Role of the microbiome in human development. Gut , gutjnl-2018-317503. (doi:10.1136/gutjnl-2018-317503) |
| Eukaryotes do not live alone. They bear living cells of bacteria (Eubacteria and Archaea), and often eukaryotic microorganisms, on their surfaces and internally... | Douglas, A. E. 2014 Symbiosis as a general principle in eukaryotic evolution. Cold Spring Harb. Perspect. Biol. 6, 1–14. (doi:10.1101/cshperspect.a016113) |
| Animals establish mutually beneficial interactions with micro-organisms. This is particularly true for commensal bacterial communities that colonize the intestinal tract of most animal species. | Erkosar, B. & Leulier, F. 2014 Transient adult microbiota, gut homeostasis and longevity: Novel insights from the Drosophila model. FEBS Lett. 588, 4250–4257. (doi:10.1016/j.febslet.2014.06.041) |
| Animals are colonized by coevolved bacterial communities, which contribute to the host’s health. | Franzenburg, S., Walter, J., Kunzel, S., Wang, J., Baines, J. F., Bosch, T. C. G. & Fraune, S. 2013 Distinct antimicrobial peptide expression determines host species-specific bacterial associations. Proc. Natl. Acad. Sci. 110, E3730–E3738. (doi:10.1073/pnas.1304960110) |
| Animals cannot be considered individuals by anatomical or physiological criteria because a diversity of symbionts are both present and functional in completing metabolic pathways and serving other physiological functions. Similarly, ...animal development is incomplete without symbionts. | Gilbert, S. F., Sapp, J. & Tauber, A. I. 2012 A symbiotic view of life: We have never been individuals. Q. Rev. Biol. 87, 325–341. (doi:http://www.jstor.org/stable/10.1086/668166) |
| All animals have associated microbial communities called microbiomes that influence the physiology and fitness of their host. | Gould, A. L., Zhang, V., Lamberti, L., Jones, E. W., Obadia, B., Gavryushkin, A., Carlson, J. M., Beerenwinkel, N. & Ludington, W. B. 2018 Microbiome interactions shape host fitness. Proc. Natl. Acad. Sci. 115, E11951–E11960. (doi:10.1101/232959) |
| …animal guts are colonized by diverse microbial classes, including bacteria and archaea, fungi, oomycetes, as well as viruses. These communities can be regarded as the host’s extended genome, providing a huge range of potential functional capacities. | Hacquard, S. et al. 2015 Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host Microbe 17, 603–616. (doi:10.1016/j.chom.2015.04.009) |
| Eukaryotic hosts generally obtain fitness benefits through association with specific microbes. | Hoang, K. L., Gerardo, N. M., Morran, L. T. 2019 The effects of Bacillus subtilis on Caenorhabditis elegans fitness after heat stress. Ecol Evol 9, 3491-9. (doi:10.1002/ece3.4983) |
| All multicellular organisms benefit from their own microbiota, which play important roles in maintaining the host nutritional health and immunity. | Ikeda-Ohtsubo W, Brugman S, Warden CH et al. 2018 How Can We Define “Optimal Microbiota?”: A Comparative Review of Structure and Functions of Microbiota of Animals, Fish, and Plants in Agriculture. Front Nutr 5, 1–18. |
| Virtually every multicellular organism hosts beneficial microbes. | Janson, E. M., Stireman, J. O., Singer, M. S. & Abbot, P. 2008 Phytophagous insect-microbe mutualisms and adaptive evolutionary diversification. Evolution 62, 997–1012. (doi:10.1111/j.1558-5646.2008.00348.x) |
| Virtually all animals have a gut which is partly to nearly totally (ruminants) filled with a complex coterie of other organisms (microbes, yeast, nematodes, protozoans, etc.). | Janzen DH. The natural history of mutualisms. In: Boucher DH (ed.). The Biology of Mutualism. Oxford University Press, 1985, 40–99. |
| Virtually all animals associate with smaller organisms, primarily prokaryotes (bacteria and archaea) that digest complex organic substrates, fix CO2, fix N2, stimulate ontogeny, affect behaviour, compete against pathogens, synthesize growth factors or serve as prey. | Kieft, T. L. & Simmons, K. A. 2015 Allometry of animal-microbe interactions and global census of animal-associated microbes. Proc. R. Soc. B 282, 20150702. (doi:10.1098/rspb.2015.0702) |
| ...abundant and diverse microbial communities living in and on eukaryotic hosts are of paramount importance to the organismal phenotype, influencing everything from pathogen susceptibility and autoimmunity, to nutrient acquisition and metabolism, range expansion, and an organism’s ability to cope with stressful environments. | Koskella, B., Hall, L. J. & Metcalf, C. J. E. 2017 The microbiome beyond the horizon of ecological and evolutionary theory. Nat. Ecol. Evol. 1, 1606–1615. (doi:10.1038/s41559-017-0340-2) |
| The digestive tracts of animals are inhabited by a taxonomically and functionally diverse community of microorganisms, dominated by mutualistic and commensal prokaryotes, viruses and fungi. | Kropáčková L. Co-diversification of gastrointestinal microbiota and phylogeny in passerines is not explained by ecological divergence. Mol Ecol 2017, DOI: 10.1111/ijlh.12426. |
| Complex ecosystems have been forged by co-adaptation over millennia between animals and microbes to create stable and specific microbiomes... | Lee, S. M., Donaldson, G. P., Mikulski, Z., Boyajian, S., Ley, K. & Mazmanian, S. K. 2013 Bacterial colonization factors control specificity and stability of the gut microbiota. Nature 501, 426–429. (doi:10.1038/nature12447) |
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| All animals live in intimate association with communities of microorganisms, known as microbiota, composed of bacteria, archaea, anaerobic fungi, protozoa, and viruses. | Macke, E., Tasiemski, A., Massol, F., Callens, M. & Decaestecker, E. 2017 Life history and eco-evolutionary dynamics in light of the gut microbiota. Oikos 126, 508–531. (doi:10.1111/oik.03900) |
| Virtually all eukaryotes associate with mutualistic bacteria. | Maire, J., Vincent-Monégat, C., Balmand, S. et al. 2019 Weevil pgrp-lb prevents endosymbiont TCT dissemination and chronic host systemic immune activation. Proc. Natl. Acad. Sci. 116, 5623-32. (doi:10.1073/pnas.1821806116) |
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| Coelomate animals...have coevolved with a diverse range of symbiotic gut bacteria and other 26microorganisms collectively known as the gut microbiota. | Nicholson, J. K., Holmes, E., Kinross, J., Burcelin, R., Gibson, G., Jia, W. & Pettersson, S. 2012 Host-gut microbiota metabolic interactions. Science 336, 1262–7. (doi:10.1126/science.1223813) |
| Almost every living macroorganism has symbiotic interactions with microorganisms... | Nougué, O., Gallet, R., Chevin, L.-M. & Lenormand, T. 2015 Niche limits of symbiotic gut microbiota constrain the salinity tolerance of brine shrimp. Am. Nat. 186, 390–403. (doi:10.1086/682370) |
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| It is increasingly recognized that all animals are chronically infected by microorganisms, and that the resident microbiota, especially the substantial microbial community in the alimentary tract, has major effects on nutrient processing, metabolic signaling and, ultimately, the health and well-being of the animal host | Ridley, E. V., Wong, AC-N., Westmiller, S. et al. Impact of the resident microbiota on the nutritional phenotype of Drosophila melanogaster. PLoS One 2012;7:e36765. |
| Microbial symbioses with eukaryotic hosts are ubiquitous. | Rio, R. V. M., Symula, R. E., Wang, J. et al. 2012 Insight into the Transmission Biology and Species-Specific Functional Capabilities of Tsetse (Diptera: Glossinidae) Obligate Symbiont Wigglesworthia. MBio 3, e00240-11. (doi:10.1128/mBio.00240-11) |
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| The intestinal microbiome of animals is essential for health, contributing to digestion of foods, proper immune development, inhibition of pathogen colonization, and catabolism of xenobiotic compounds. | Sherrill-Mix, S. et al. 2018 Allometry and Ecology of the Bilaterian Gut Microbiome. MBio 9, e00319-18. (doi:10.1128/mBio.00319-18) |
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