

Publication record (peer-reviewed, chronological order)

In review

- Meyer M*, Schmid DW*, Baldwin H, Wilhelm K, Nkrumah EE, Badu EK, Oppong SK, Schwensow N, Vallo P, Corman VM, Tschapka M, Drosten C, **Sommer S**. Bat species assemblage predicts coronavirus prevalence.
- Risely A, Müller-Klein N, Schmid DW, Wilhelm K, Clutton-Brock T, Manser MB, **Sommer S**. Climate change and tuberculosis drive non-adaptive shifts in the faecal microbiota of wild meerkats.
- Schmid DW*, Meyer M*, Wilhelm K, Tilley T, Link-Hessing T, Fleischer R, Badu EK, Nkrumah EE, Oppong SK, Schwensow N, Tschapka M, Baldwin HJ, Vallo P, Corman VM, Drosten C, **Sommer S**. MHC class II genes mediate susceptibility and resistance to coronavirus infections in bats.

2023

- Fackelmann G, Pham CK, Rodríguez Y, Mallory ML, Provencher JF, Baak JE, **Sommer S** (2023) Current levels of microplastic pollution impact wild seabird gut microbiomes. *Nature Ecology & Evolution*.
- Heni AC, Fackelmann G, Eibner G, Kreinert S, Schmid J, Schwensow NI, Wiegand J, Wilhelm K, **Sommer S** (2023) Wildlife gut microbiomes of sympatric generalist species respond differently to anthropogenic landscape disturbances. *Animal Microbiome*.
- Schmid DW, Capilla-Lasheras P, Dominoni D, Müller-Klein N, **Sommer S**, Risely A (2023) Circadian rhythms of hosts and their gut microbiomes: implications for animal physiology and ecology. *Functional Ecology*, 37, 476–487. doi: 10.1111/1365-2435.14255.
- Veith T, Bleicker T, Eschbach-Bludau M, Brünink S, Mühlemann B, Schneider J, Beheim-Schwarzbach J, Rakotondranary SJ, Ratovonamana YR, Tsagnangara C, Ernest R, Randriantafika F, **Sommer S**, Stetter N, Jones TC, Drosten C, Ganzhorn JU, Corman VM (2023) Non-structural genes of novel lemur adenoviruses reveal codivergence of virus and host. *Virus Evolution*.

2022

127. Carranco AS, Gillingham MAF, Wilhelm K, Romo D, de Lourdes Torres M, **Sommer S***, Romo D* (2022) Transcending sea turtles: first report of hatching failure in eggs of an Amazonian freshwater turtle with symptoms of the fungal emerging disease fusariosis. *Transboundary and Emerging Diseases*, 69, e3282–e3288. doi: 10.1111/tbed.14596. * contributed equally to the study.

126. Carranco AS, Romo D, de Lourdes Torres M, Wilhelm K, **Sommer S***, Gillingham MAF* (2022) Egg microbiota is the starting point of hatchling gut microbiota the endangered yellow-spotted Amazon river turtle. *Molecular Ecology*, 31(14), 3917-3933. doi: 10.1111/mec.16548. * contributed equally to the study.
125. Donadio J, Risely A, Müller-Klein N, Wilhelm K, Clutton-Brock T, Manser MB, **Sommer S** (2022) Characterizing tuberculosis progression in wild meerkats (*Suricata suricatta*) from faecal samples and clinical signs. *Journal of Wildlife Diseases*, 58(2), 309–321. doi: 10.7589/JWD-D-21-00063.
124. Fleischer R, Schmid DW, Wasimuddin, Brändel SD, Rasche A, Corman VM, Drosten C, Tschapka M, **Sommer S** (2022) Interaction between MHC diversity and constitution, gut microbiome composition and Astrovirus infections in a neotropical bat. *Molecular Ecology*, 31, 3342–3359. doi: 10.1111/mec.16491.
- 123a. Leibniz-Forschungsnetzwerk Biodiversität (2022) 10 Must-Knows aus der Biodiversitätsforschung 2022. Thonicke K, Rahner E, Arneth A, Bartkowski B, Bonn A, Döhler C, Finger R, Freitag J, Grosch R, Grossart H.-P, Grützmaker K, Hartman Scholz A, Häuser C, Hickler T, Hölker F, Jähnig SC, Jeschke J, Kasen R, Kastner T, Kramer-Schadt S, Krug C, Lakner S, Loft L, Matzdorf B, Meakins F, De Meester L, Monaghan MT, Müller D, Overmann J, Quaas M, Radchuk V, Reyer C, Roos C, Scholz I, Schroer S, Sioen GB, **Sommer S**, Sommerwerk N, Tockner K, Turk Z, Warner B, Wätzold F, Wende W, Veenstra T, van der Voort H. Potsdam, Deutschland. 60 Seiten. doi: 10.5281/zenodo.6257476.
- 123b. Leibniz Research Network Biodiversity (2022) engl version available: 10 Must Knows from Biodiversity Science 2022. Thonicke K, Rahner E, Arneth A, Bartkowski B, Bonn A, Döhler C, Finger R, Freitag J, Grosch R, Grossart H.-P, Grützmaker K, Hartman Scholz A, Häuser C, Hickler T, Hölker F, Jähnig SC, Jeschke J, Kasen R, Kastner T, Kramer-Schadt S, Krug C, Lakner S, Loft L, Matzdorf B, Meakins F, De Meester L, Monaghan MT, Müller D, Overmann J, Quaas M, Radchuk V, Reyer C, Roos C, Scholz I, Schroer S, Sioen GB, **Sommer S**, Sommerwerk N, Tockner K, Turk Z, Warner B, Wätzold F, Wende W, Veenstra T, van der Voort H. Potsdam, Deutschland. 60 pages.
122. Müller-Klein N, Risely A, Schmid DW, Manser MB, Clutton-Brock T, **Sommer S** (2022) Two decades of tuberculosis surveillance reveal disease spread, high levels of exposure and mortality, and marked variation in disease progression in wild meerkats. *Transboundary and Emerging Diseases*. doi:10.1111/tbed.14679.
121. Risely A, Schmid DW, Müller-Klein N, Wilhelm K, Clutton-Brock T, Manser MB, **Sommer S** (2022) Gut microbiota individuality is contingent on temporal scale and age in wild meerkats. *Proceedings of the Royal Society B*, 289, 20220609. <https://doi.org/10.1098/rspb.2022.0609>.
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host gut microbiomes. *Animal Microbiome*, 4:48. <https://doi.org/10.1186/s42523-022-00198-5>.

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118. Wasimuddin, Malik H, Ratovonamana YR, Rakotondranary SJ, Ganzhorn JU, **Sommer S** (2022) Anthropogenic disturbance impacts gut microbiome homeostasis in a Malagasy primate. *Frontiers Microbiology, Community Series in the Wildlife Gut Microbiome and Its Implication for Conservation Biology, Volume II*, 13, 911275. doi: 10.1101/2022.04.02.486803.

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117. Alpízar P, Risely A, Tschapka M, **Sommer S** (2021) Agricultural fast food: Bats feeding in banana monocultures are heavier but have less diverse gut microbiomes. *Frontiers in Ecology and Evolution*, 9, 746783. <https://doi.org/10.3389/fevo.2021.746783>.
116. Fackelmann F, Gillingham MAF, Schmid J, Heni AC, Wilhelm K, **Sommer S** (2021) Human encroachment into wildlife gut microbiomes. *Communications Biology*, 4, 800. doi.org/10.1038/s42003-021-02315-7.
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114. Gillingham MAF, Montero BK, Wilhelm K, Grudzus K, **Sommer S**, Santos PSC (2021) A novel workflow to improve genotyping of multigene families in wildlife species: an experimental set-up with a known model system. *Molecular Ecology Resources*, 21, 982-998. <https://doi.org/10.1111/1755-0998.13290>.
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112. Montero BK, Wasimuddin, Schwensow N, Gillingham MAF, Ratovonamana YR, Rakotondranary SJ, Corman V, Drost C, Ganzhorn JU, **Sommer S** (2021) Evidence for MHC class I and II influencing viral and helminth infection via the microbiome in a non-human primate. *PLOS Pathogens*, 17(11): e1009675. <https://doi.org/10.1371/journal.ppat.1009675>.
111. Risely A, Gillingham MAF, Béchet A, Brändel S, Heni A, Heurich M, Menke S, Manser M, Schmid J, Tschapka M, Wasimuddin, **Sommer S** (2021) Phylogeny- and abundance-based

metrics allows for consistent comparison of core gut microbiome diversity indices across host species. *Frontiers in Microbiology*, 12, 659918. doi: 10.3389/fmicb.2021.659918.

110. Risely A, Wilhelm K, Clutton-Brock T, Manser MB, **Sommer S** (2021) Diurnal oscillations in gut bacterial load and composition eclipse seasonal and lifetime dynamics in wild meerkats, *Suricata suricatta*. *Nature Communications*, 12, 6017. <https://doi.org/10.1038/s41467-021-26298-5>.
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103. Viquez-R L, Fleischer R, Wilhelm K, Tschapka M, **Sommer S** (2020) Jumping the green wall: the use of PNA-DNA clamps to enhance microbiome sampling depth in wildlife microbiome research. *Ecology and Evolution*, 10, 11779-11786. DOI: 10.1002/ece3.6814.
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99. Jiménez RR, Alvarado G, Estrella J, **Sommer S** (2019) Moving beyond the host: unravelling the skin microbiome of endangered Costa Rican amphibians. *Frontiers in Microbiology*, 10, 2060.
98. Menke S, Heurich M, Henrich M, Wilhelm K, **Sommer S** (2019) Impact of winter enclosures on the gut bacterial microbiota of red deer in the Bavarian Forest National Park. *Wildlife Biology*, 2019(1). DOI: 10.2981/wlb.00503.
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on Major Histocompatibility Complex (MHC) genes in invasive wild rabbits in Australia. *Biological Invasions*, 19(4), 1255-1271.

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