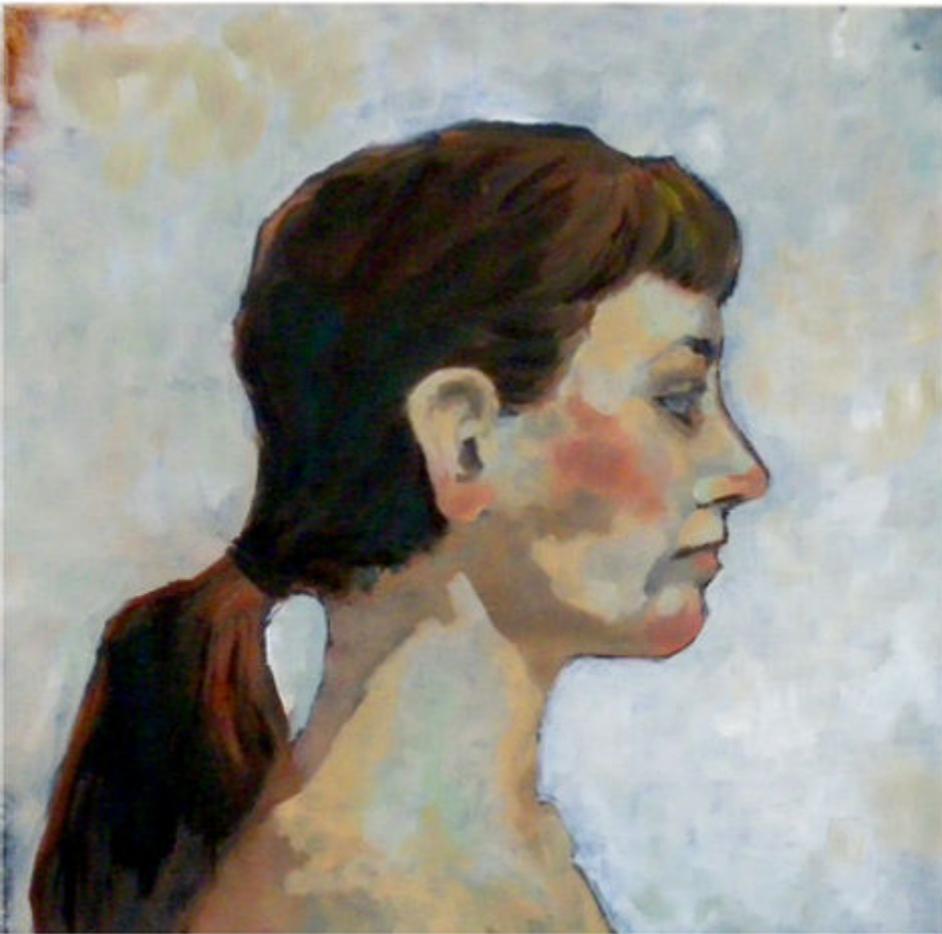


THE HUMAN HOLOGENOME

THE HOLOGENOME

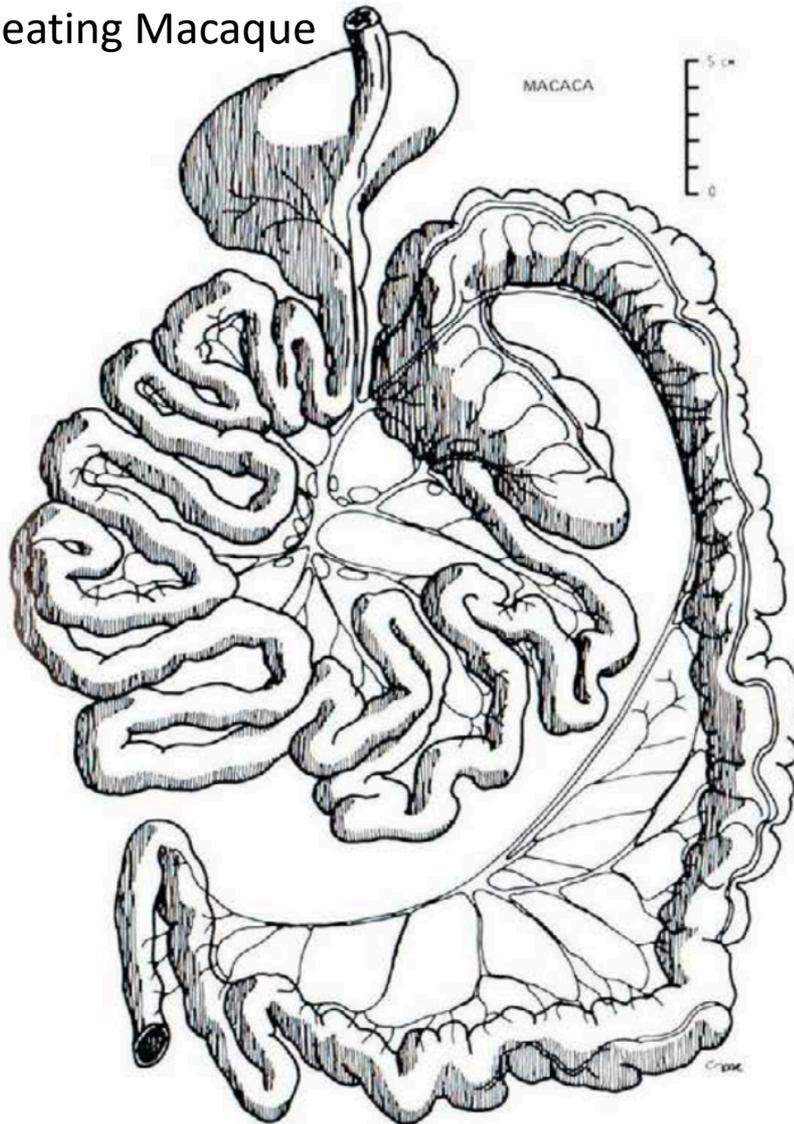


Me and My Other Self, Joana Ricou

EVOLUTION OF THE HUMAN HOLOGENOME

1. STOMACH (ACIDITY)

Crab-eating Macaque



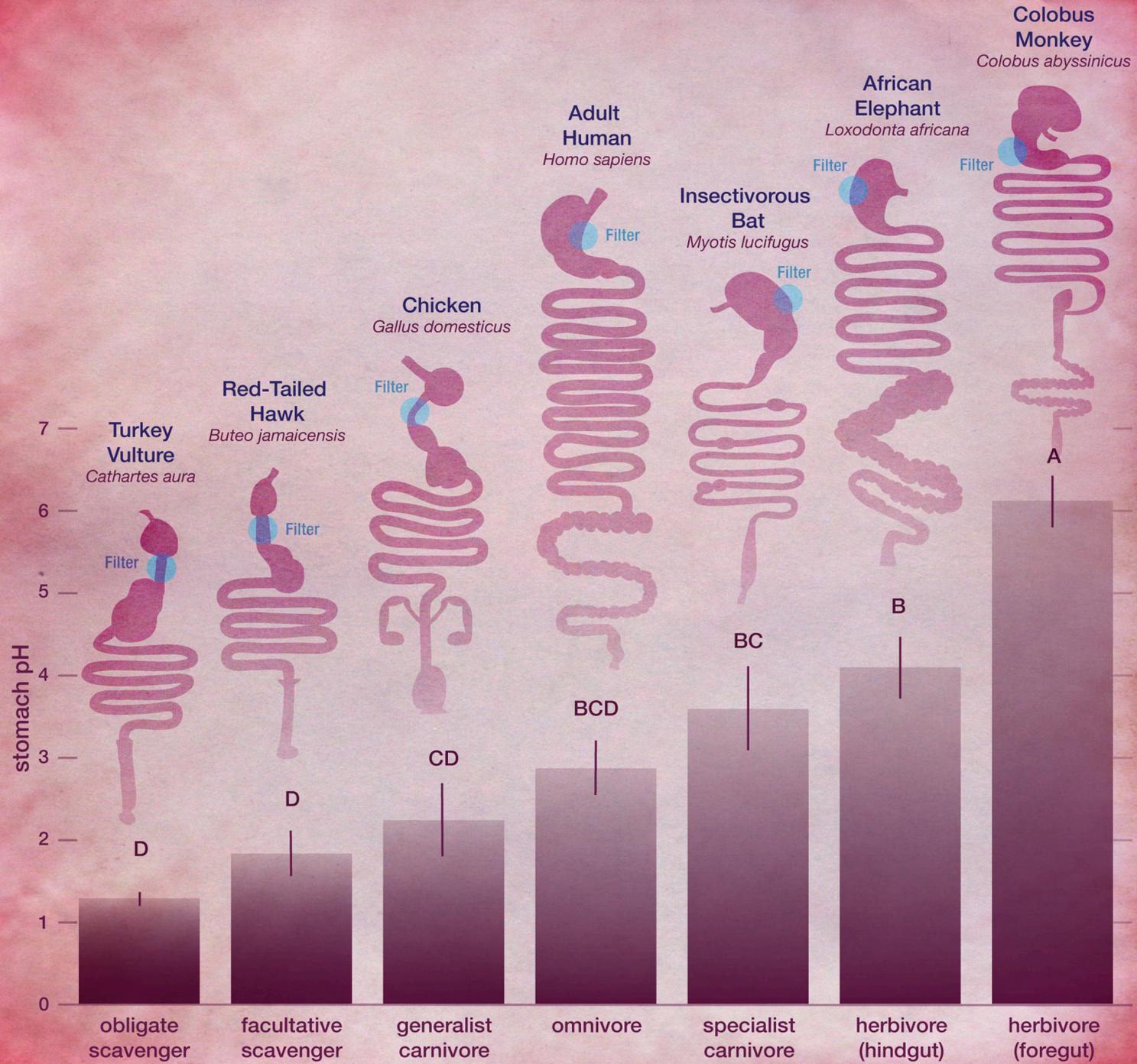


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Beasley, DeAnna E.,
Amanda M. Koltz, Joanna
E. Lambert, Noah Fierer,
and Rob R. Dunn. "The
evolution of stomach
acidity and its relevance to
the human microbiome."
PloS one 10, no. 7 (2015):
e0134116.

Dr. DeAnna Beasley, U. of Tennessee, Chattanooga

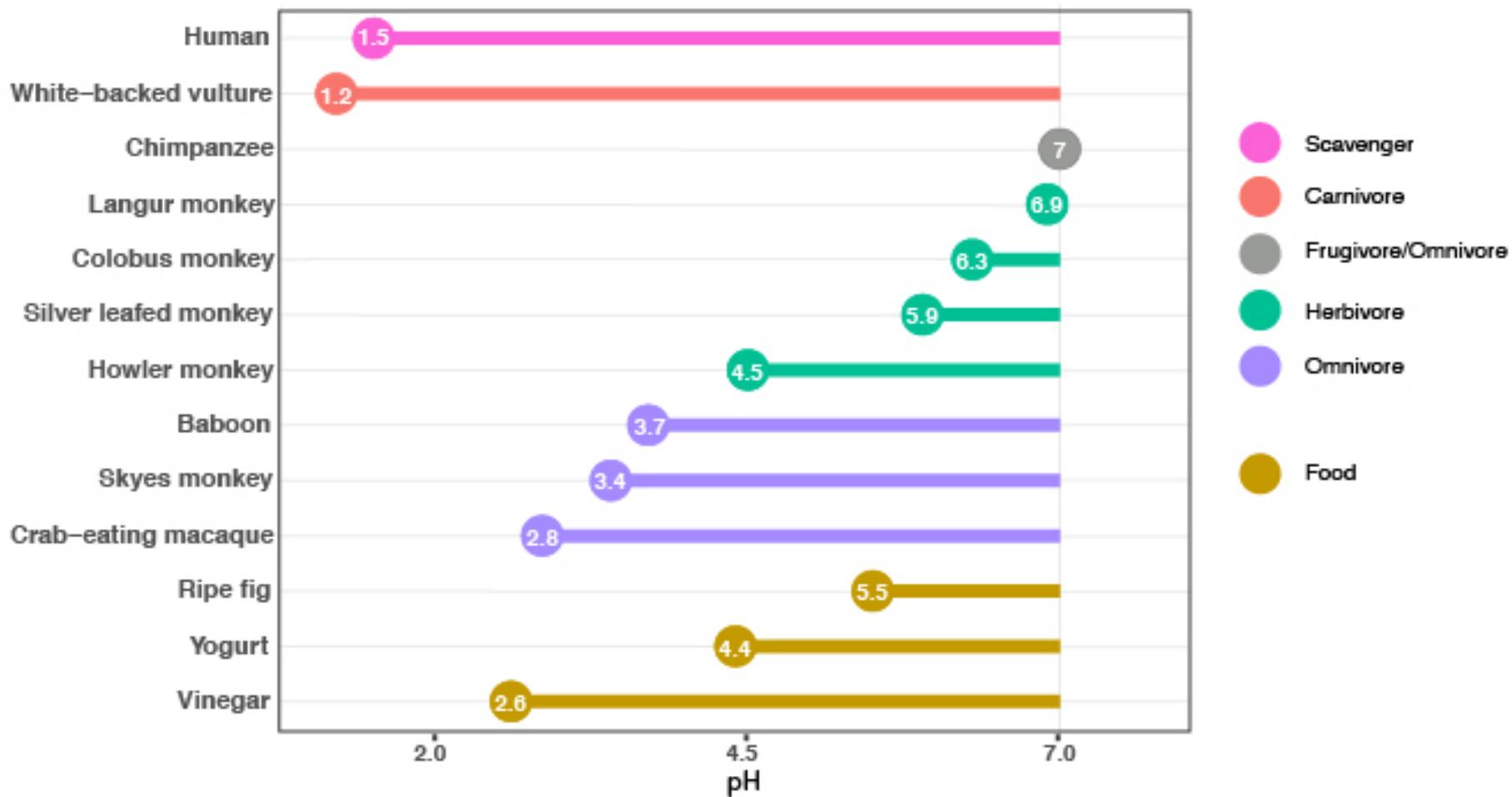




ZOO



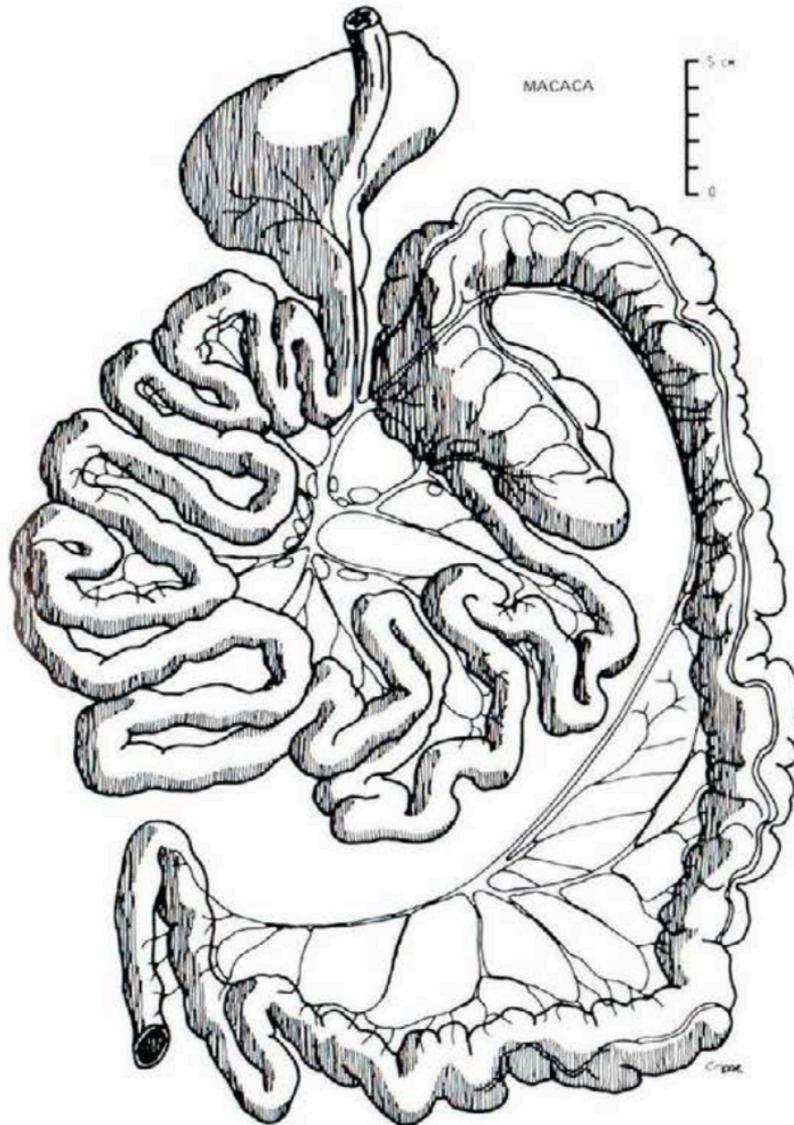
Dr. Sandra Andersen, Center for Evolutionary Hologenomics

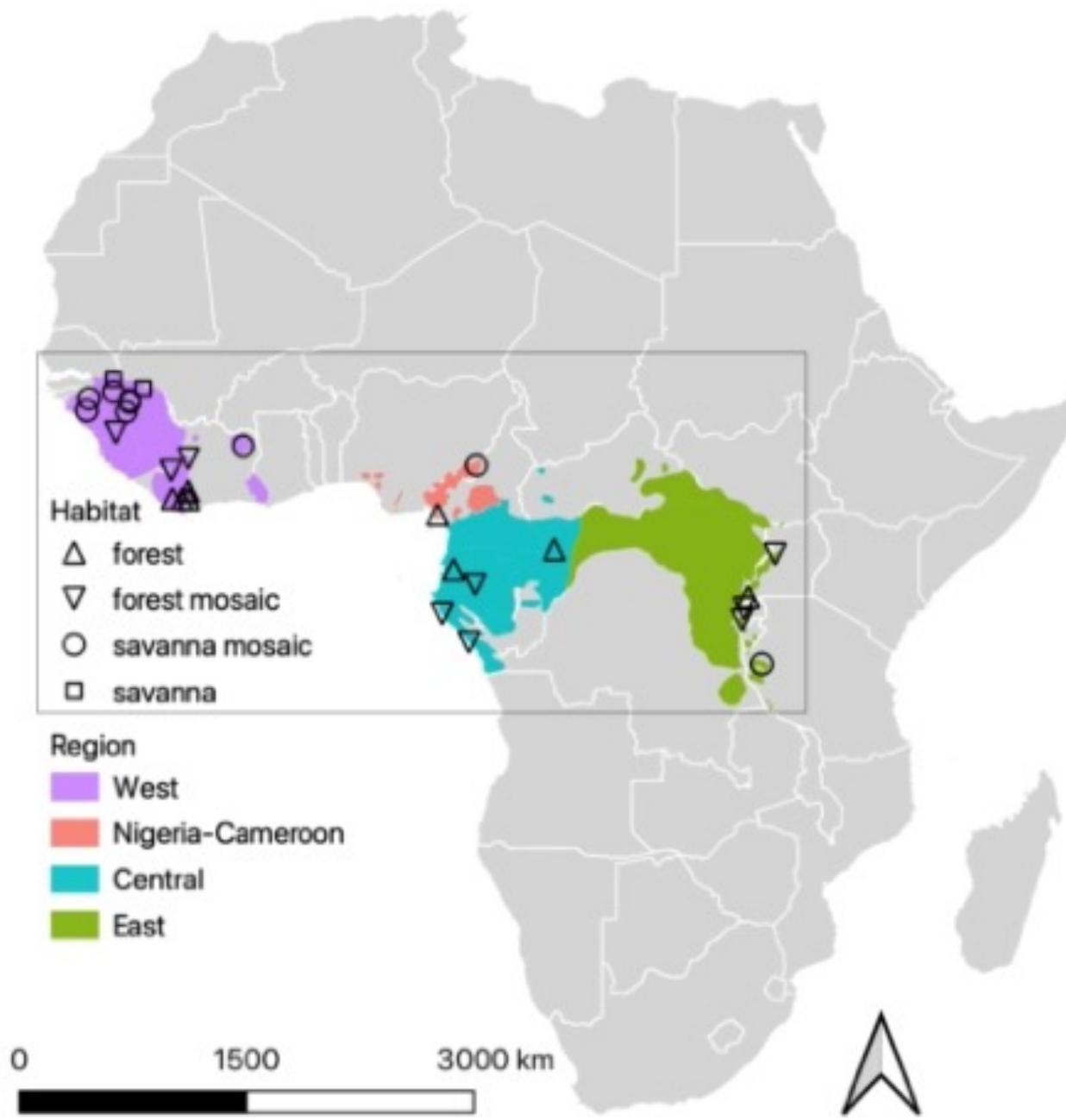


IMPORTANCE

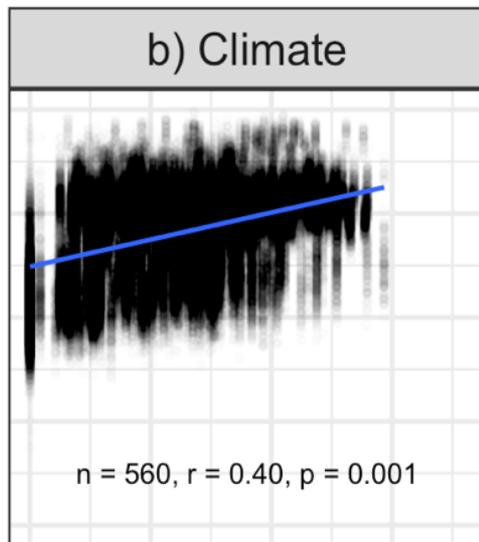
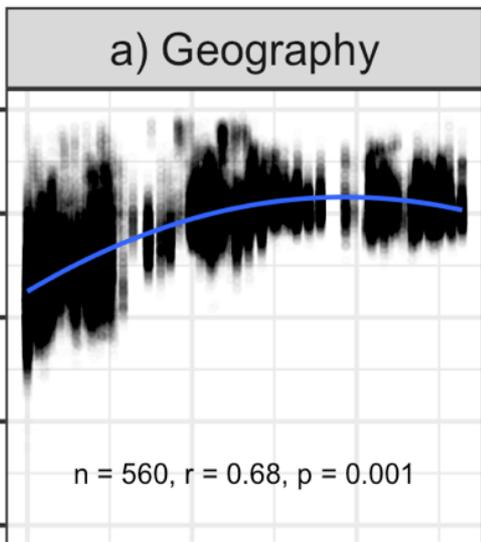
- Hard(er) for adult humans to acquire new microbes (e.g., from fermented foods)
- Any procedure or medicine that raises the pH of the stomach (makes it more neutral) increases risk of pathogens surviving to reach the intestines

2A. INTESTINES (GEOGRAPHY)

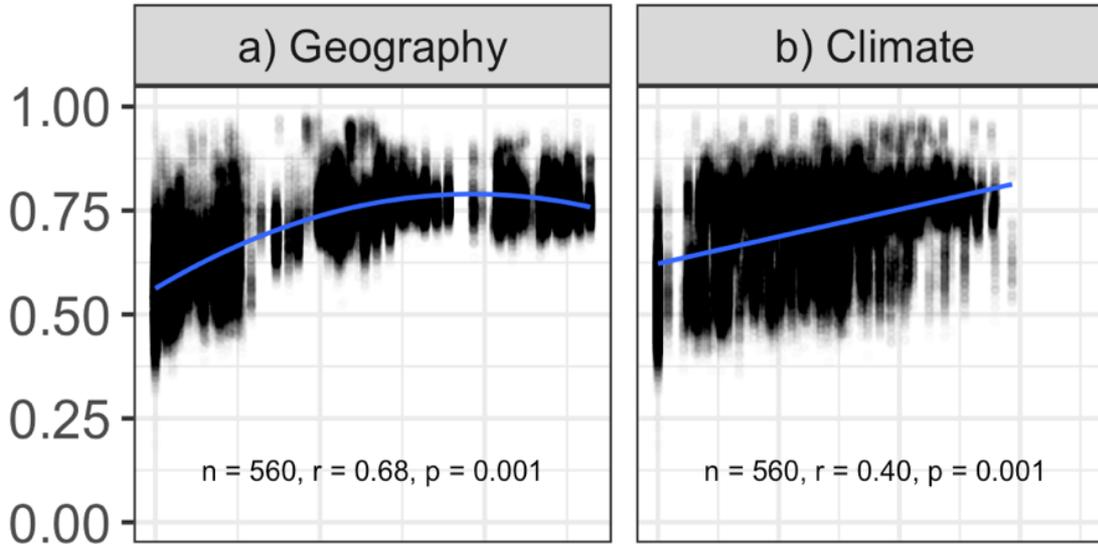




Bray-Curtis Dissimilarity



Bray-Curtis Dissimilarity

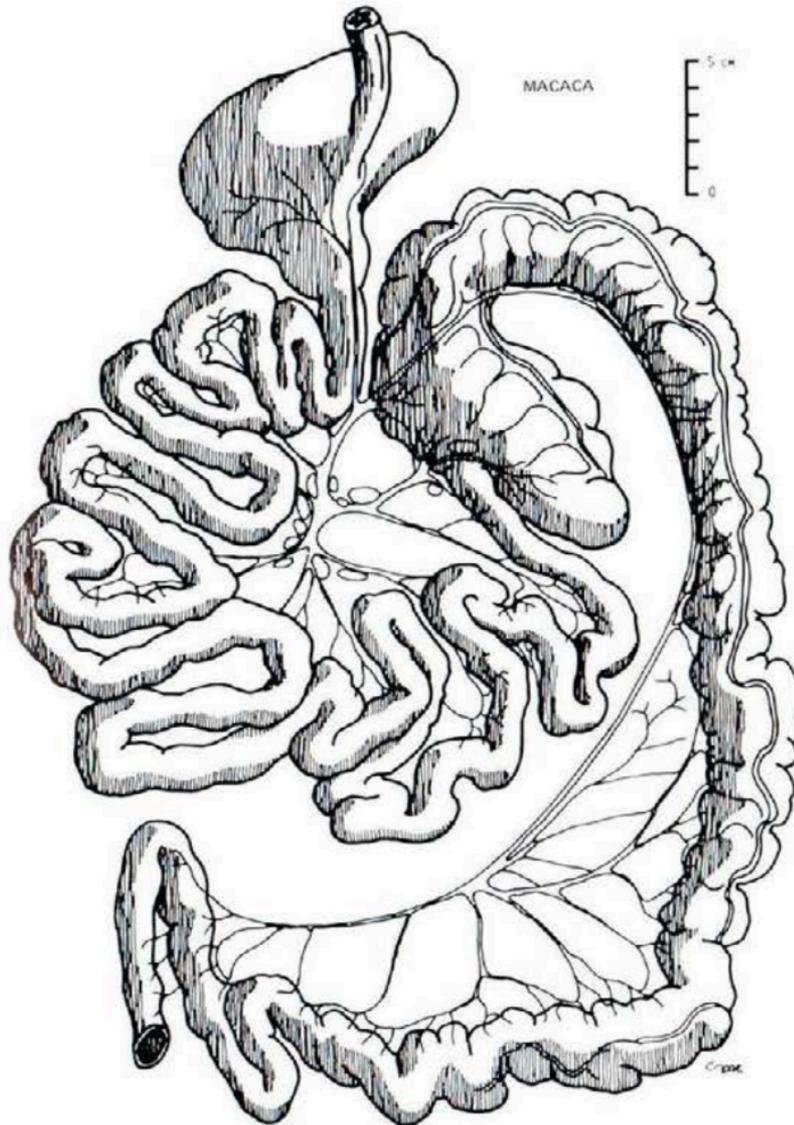


Due to a mixture of vertical inheritance of microbes from mom (during birth), environmental acquisition and diet.

Importance

- Has the effect of engendering microbiomes that reflect local conditions

2B. INTESTINES (CULTURE)



CHIMPANZEES HAVE GASTRONOMIC CULTURE







Democratic
Republic of
the Congo

Kenya

Rwanda

Burundi

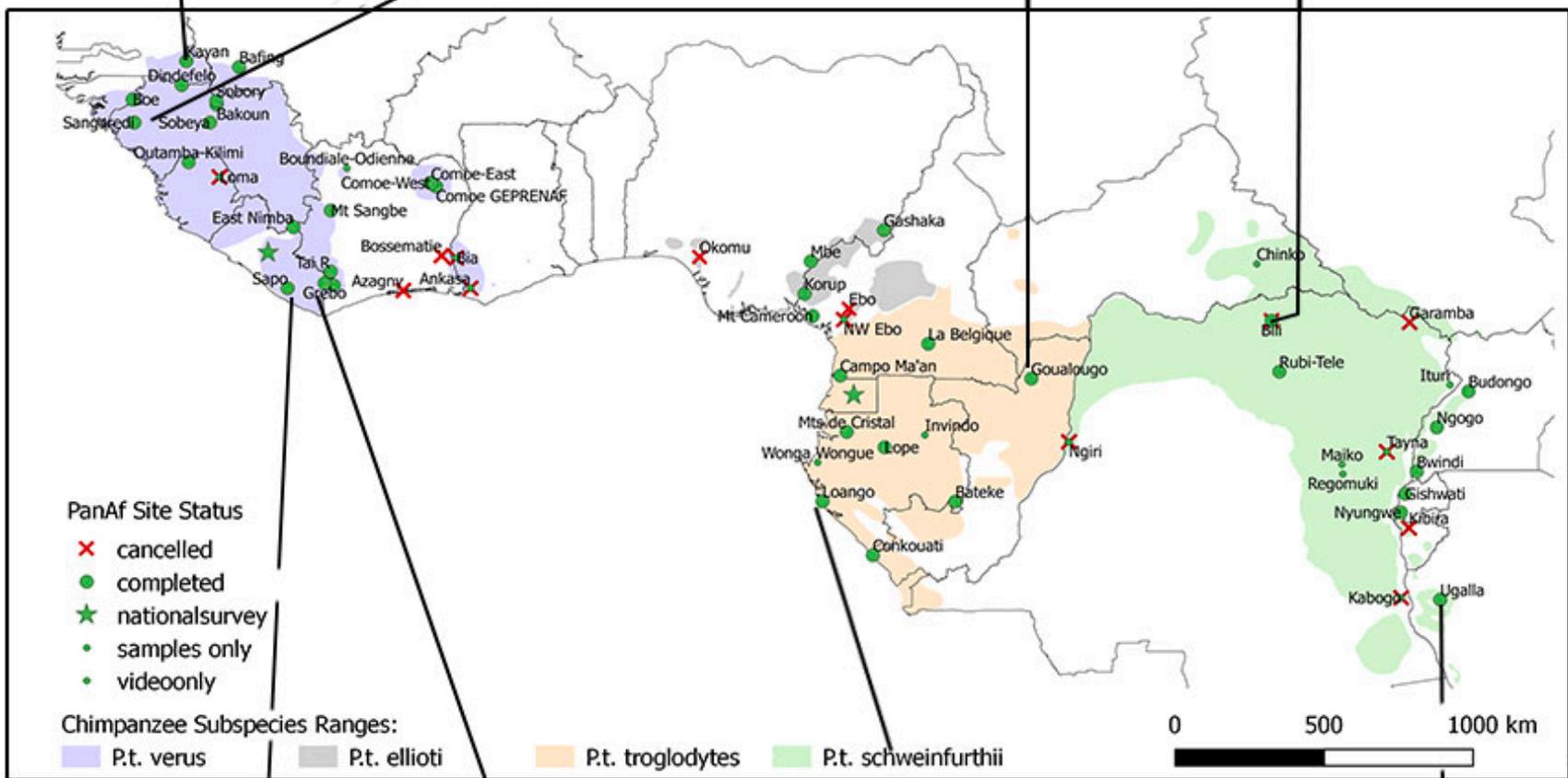
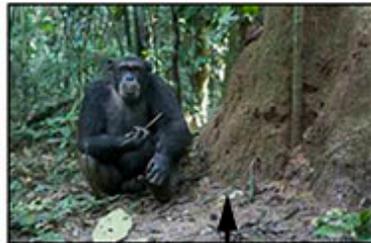
● Gombe National Park

📍 Mahale Mountain
National Park



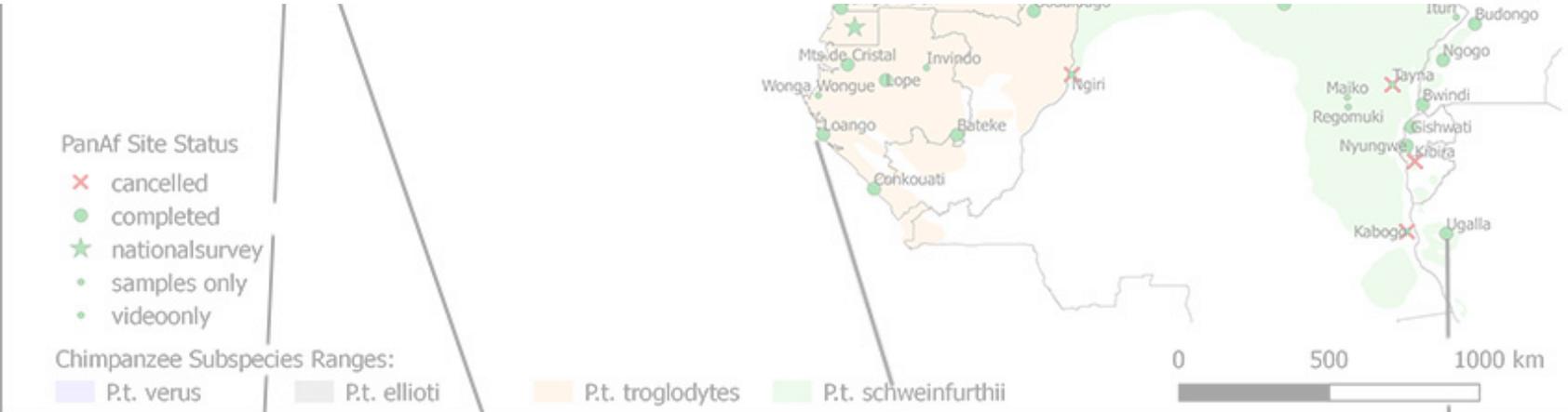


Zero calorie *Camponotus*





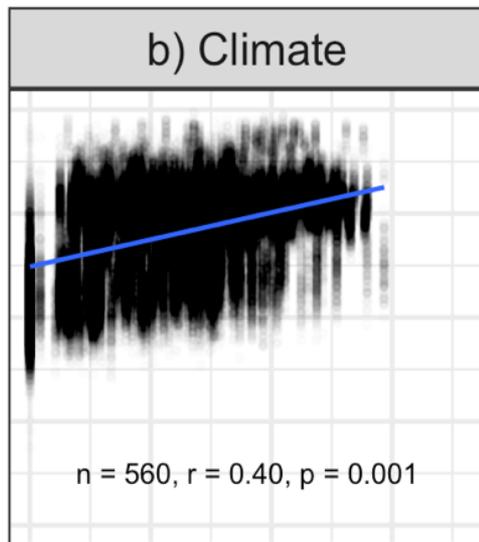
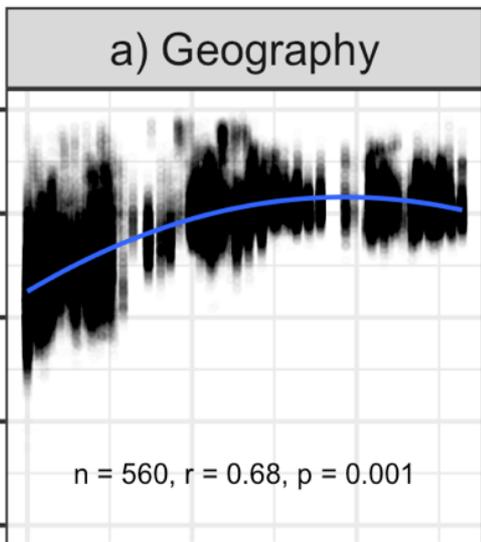
Different cultures have different microbiomes

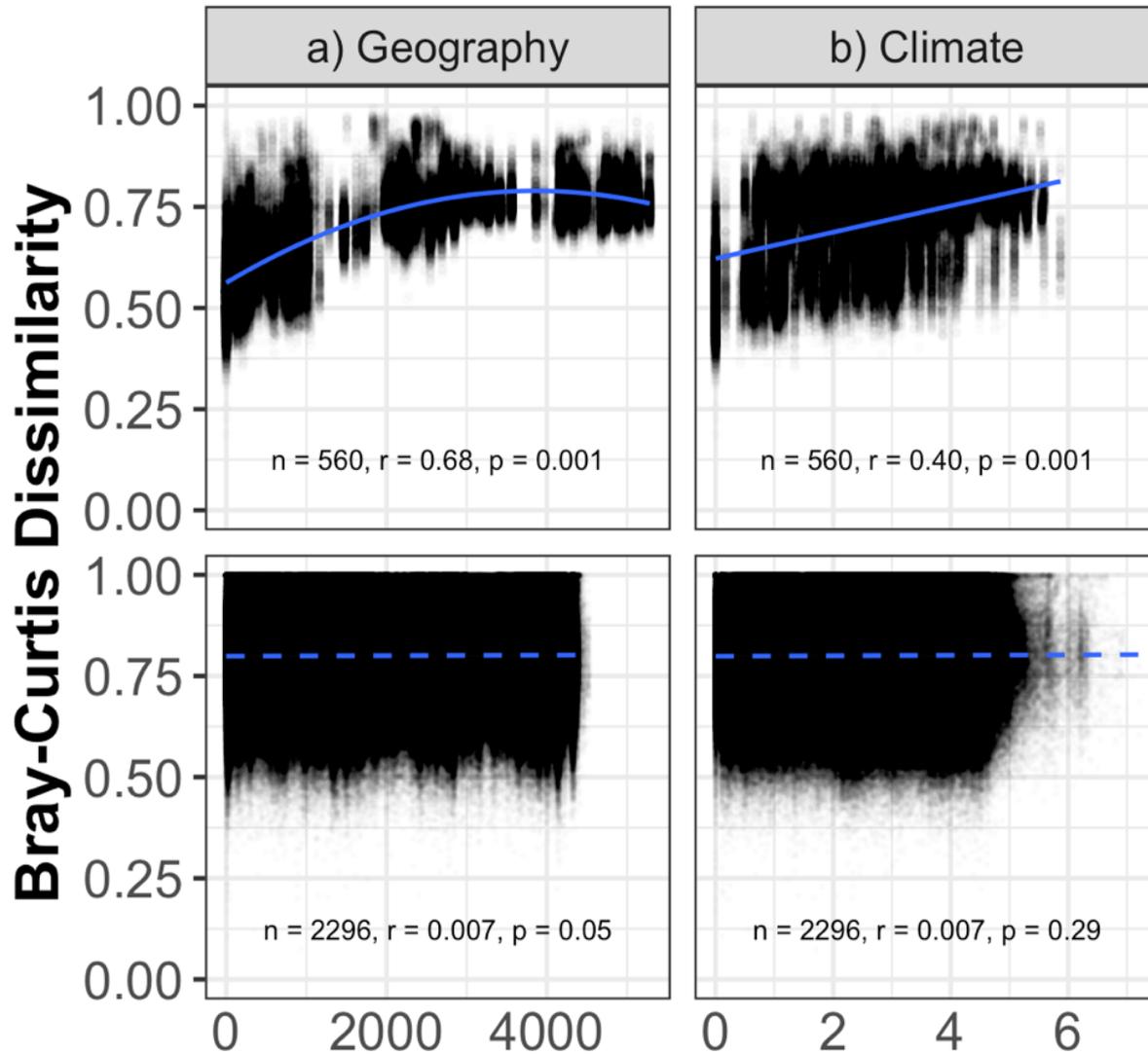


Importance (geography + culture)

- Has the effect of engendering microbiomes that reflect local conditions
- This becomes decoupled, however, when acquisition is interrupted (e.g., C-sections) or disconnects between ancestral and modern diets

Bray-Curtis Dissimilarity





C-sections + diet changes disconnect local context and microbiomes

Importance

- Has the effect of engendering microbiomes that reflect local conditions
- This becomes decoupled, however, when acquisition is interrupted (e.g., C-sections). This includes the loss of species.
- The species being lost are not only locally adapted, they are also key functional species.

Diet-induced extinctions in the gut microbiota compound over generations

Erica D. Sonnenburg^{1*}, Samuel A. Smits^{1*}, Mikhail Tikhonov^{2,3}, Steven K. Higginbottom¹, Ned S. Wingreen^{4,5} & Justin L. Sonnenburg¹

The gut is home to trillions of microorganisms that have fundamental roles in many aspects of human biology, including immune function and metabolism^{1,2}. The reduced diversity of the gut microbiota in Western populations compared to that in populations living traditional lifestyles presents the question of which factors have driven microbiota change during modernization. Microbiota-accessible carbohydrates (MACs) found in dietary fibre have a crucial involvement in shaping this microbial ecosystem, and are notably reduced in the Western diet (high in fat and simple carbohydrates, low in fibre) compared with a more traditional diet³. Here we show that changes in the microbiota of mice consuming a low-MAC diet and harbouring a human microbiota are largely reversible within a single generation. However, over several generations, a low-MAC diet results in a progressive loss of diversity, which is not recoverable after the reintroduction of dietary MACs. To restore the microbiota to its original state requires the administration of missing taxa in combination with dietary MAC consumption. Our data illustrate that taxa driven to low abundance when dietary MACs are scarce are inefficiently transferred to the next generation, and are at increased risk of becoming extinct within an isolated population. As more diseases are linked to the Western microbiota and the microbiota is targeted therapeutically, microbiota reprogramming may need to involve strategies that

distinct from controls ($P=3 \times 10^{-8}$, Student's *t*-test; UniFrac distance at 15 weeks) (Fig. 1b). To determine whether taxa had been lost over the course of the experiment, we compared the OTUs in the low-MAC diet group to those in the high-MAC diet group. We found that 50% of the OTUs in the low-MAC diet group were not found in the high-MAC diet group. In addition, 33% of the OTUs in the low-MAC diet group were not found in the high-MAC diet group. This indicates that the low-MAC diet perturbation induced 'scars' on the microbiota.

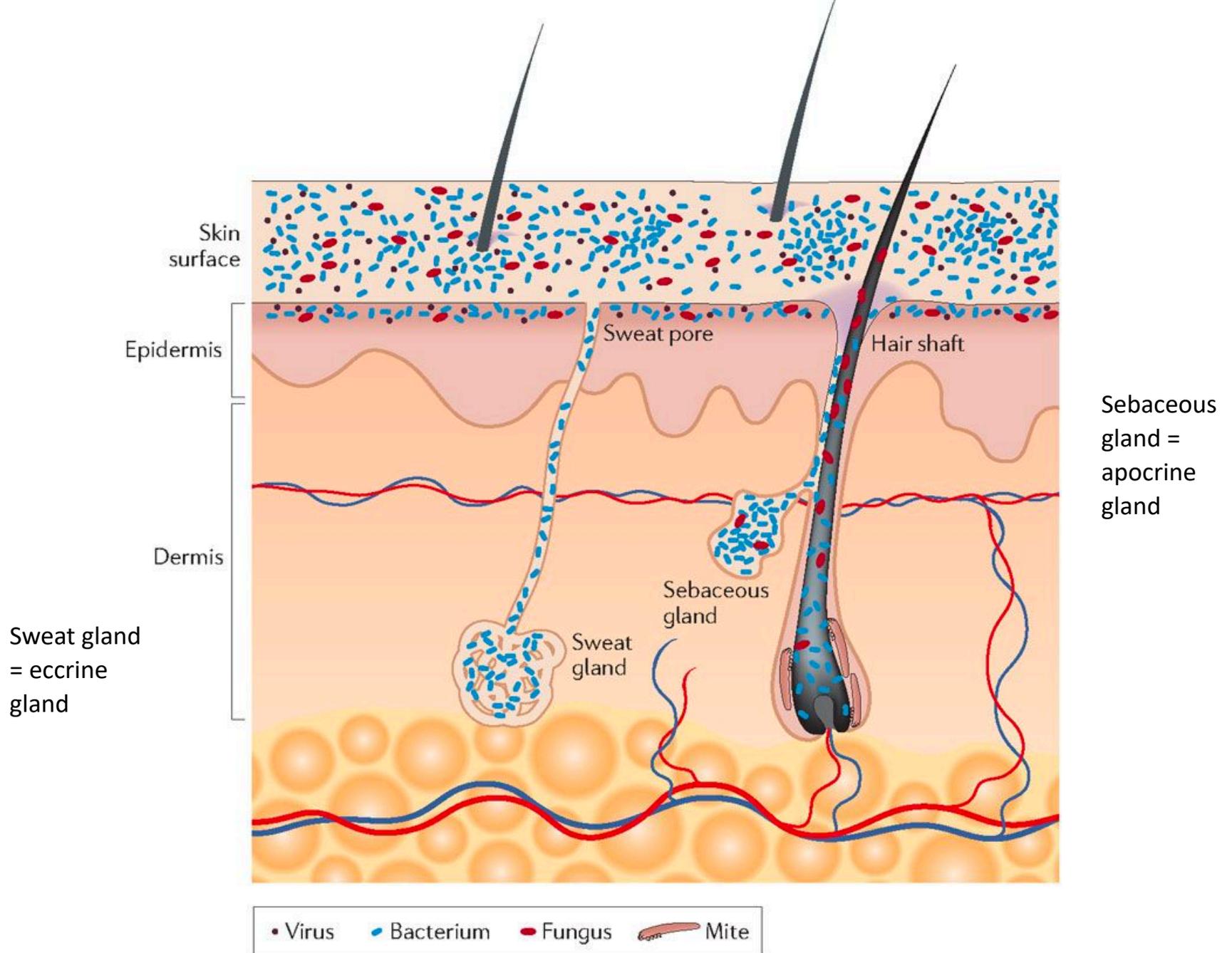
We proposed that diet-induced microbiota diversity loss would be magnified over generations. Mice from the previous experiment consuming the low-MAC diet or the high-MAC diet were used to generate



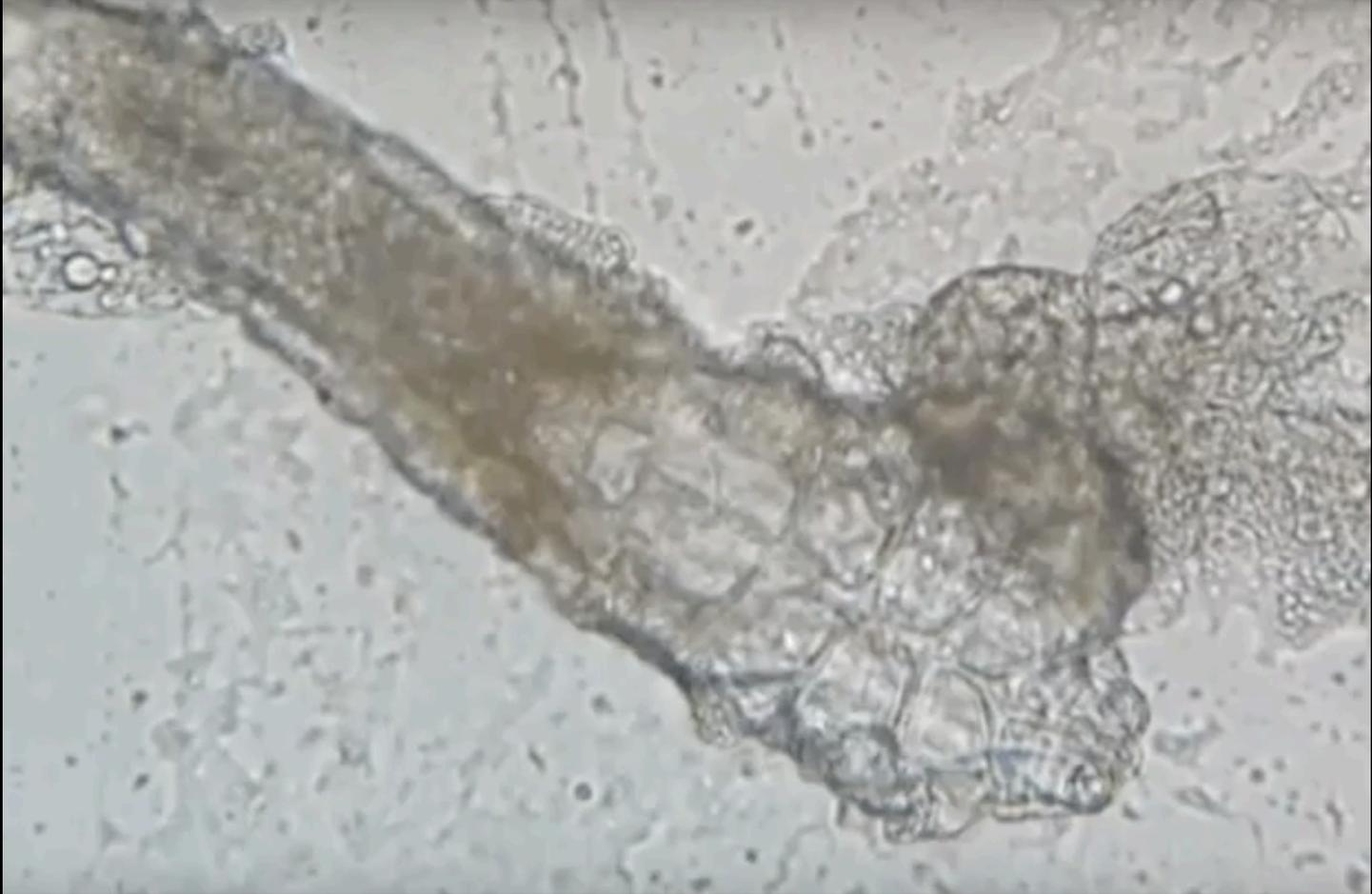
3. SKIN

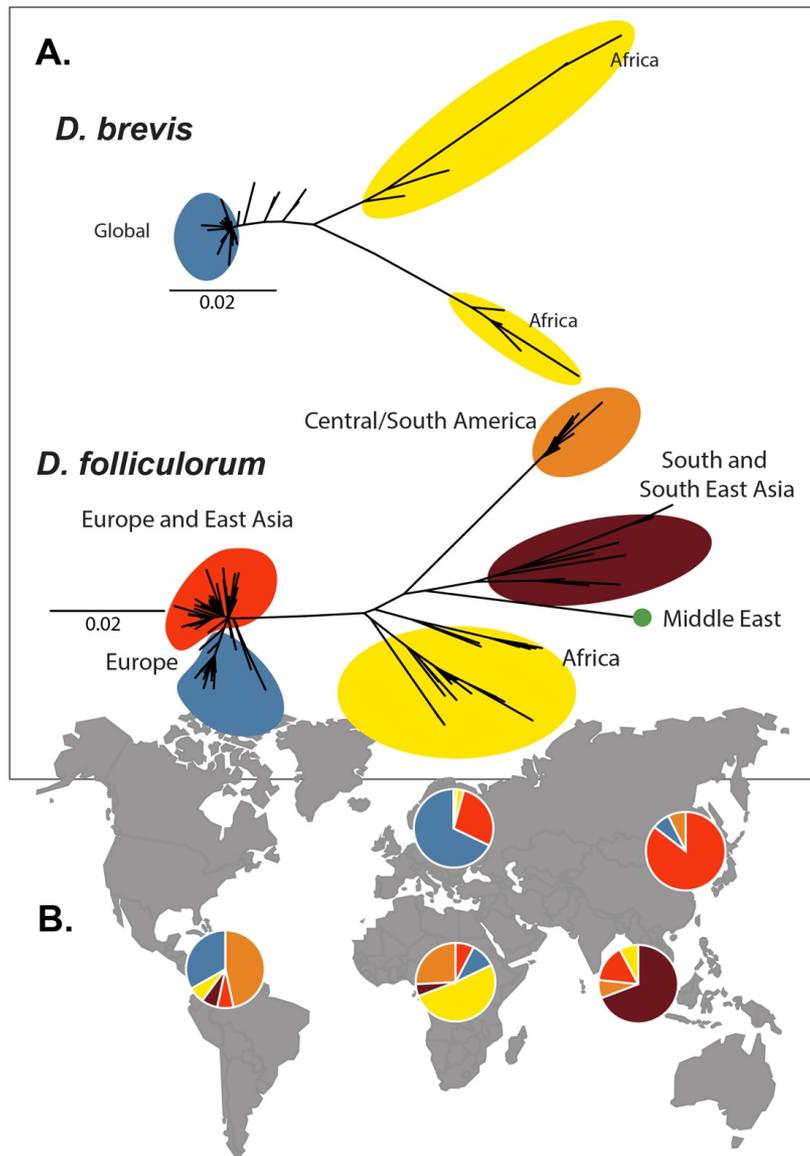
Sculpture by Ron Mueck





DEMODEX MITES





Global divergence of the human follicle mite *Demodex folliculorum*: Persistent associations between host ancestry and mite lineages

Michael F. Palopoli, Daniel J. Fergus, Samuel Minot, Dorothy T. Pei, W. Brian Simison, Iria Fernandez-Silva, Megan S. Thoenmes, Robert R. Dunn, and Michelle Trautwein

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^bNorth Carolina Museum of Natural Sciences, Raleigh, NC 27601;

^cDepartment of Applied Ecology, North Carolina State University, Raleigh, NC 27695;

^dCenter for Comparative Genomics, California Academy of Sciences, San Francisco, CA 94118;

^eDepartment of Biochemistry, Genetics and Immunology, University of Vigo, 36310 Vigo, Spain;

^fKeck Center for Behavioral Biology, North Carolina State University, Raleigh, NC 27695;

^gCenter for Macroecology, Evolution and Climate, Natural History Museum of Denmark, University of Copenhagen, 2100 Copenhagen Ø, Denmark

– Hide authors and affiliations

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<https://doi.org/10.1073/pnas.1512609112>

Edited by David M. Hillis, The University of Texas at Austin, Austin, TX, and approved November 12, 2015 (received for review June 26, 2015)

BACTERIA (AND FUNGI)

Photo by Martin Oegerli



The Bellybutton as seen by Martin Oegerli

MEDICALLY NORMAL = *Staphylococcus*

Photo by Martin Oegerli



The Bellybutton as seen by Martin Oegerli

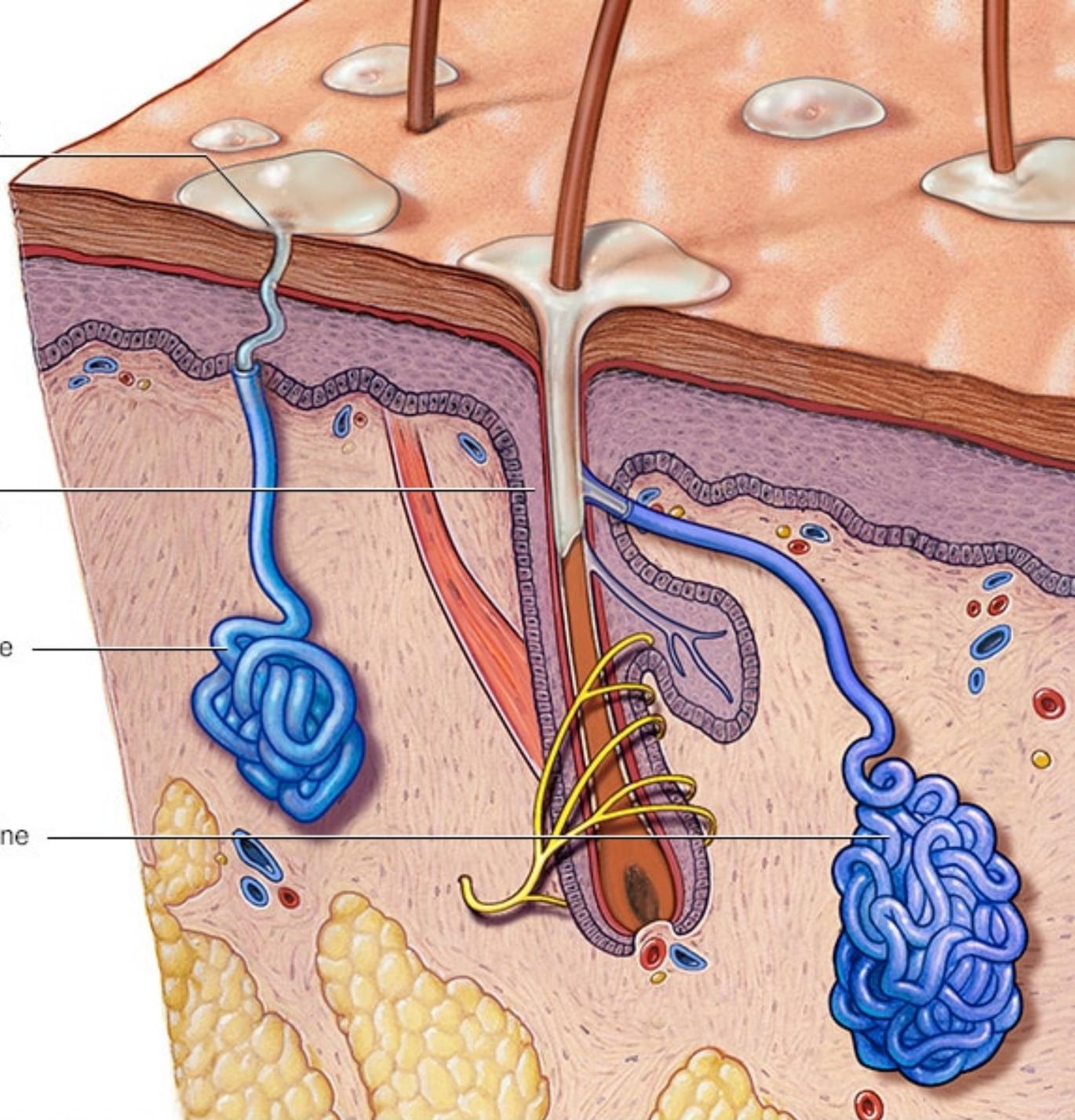


Sweat pore

Hair follicle

Eccrine sweat gland

Apocrine sweat gland





© Brian Lilly

POTENTIAL ORIGIN OF THE GLANDS

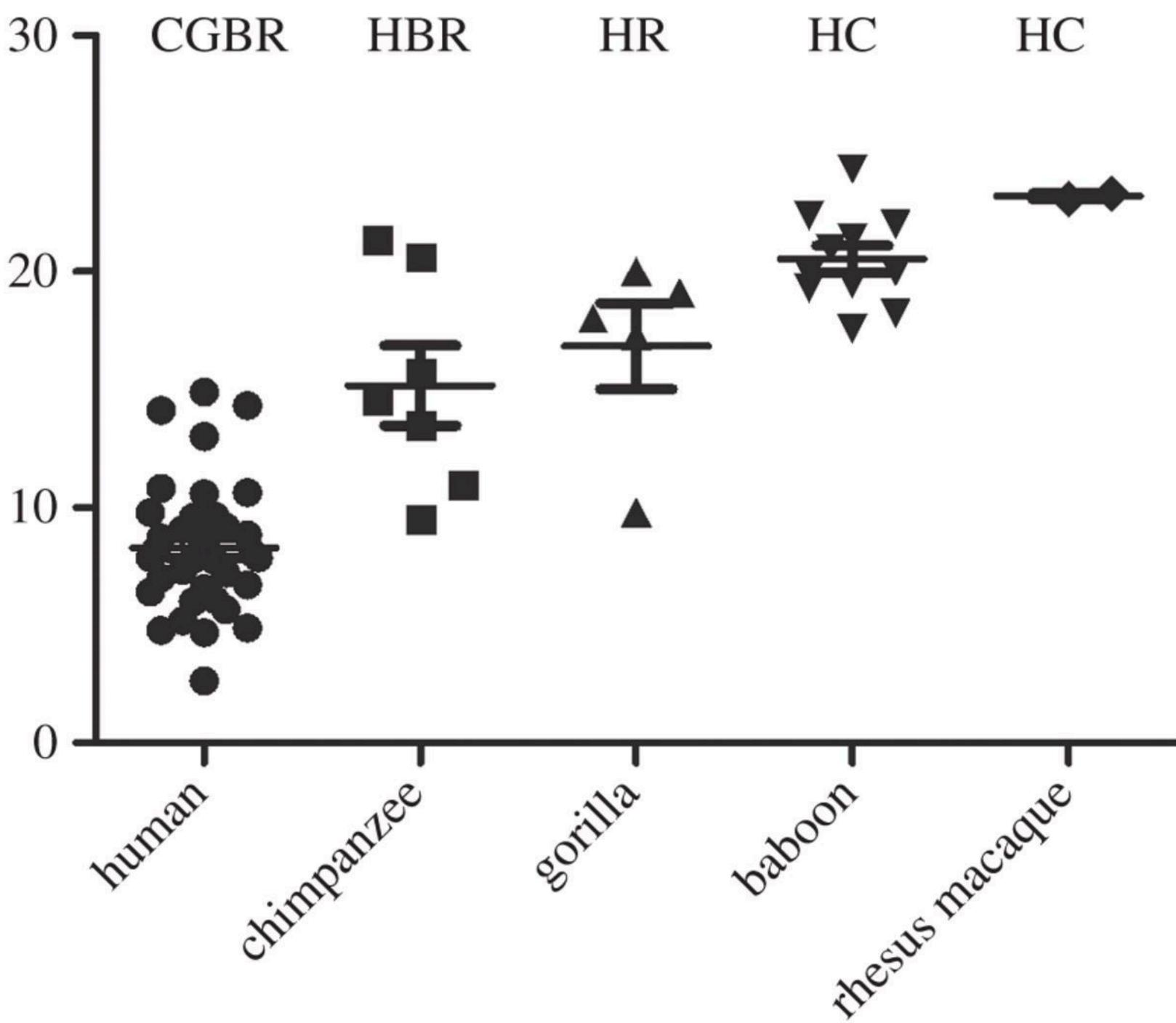
- Sexy (costly signal)
- Prevents pathogens (favors a good layer)
- Signals ill health (or good health)
- Other?
- Fun to develop theory here, but it hasn't been (not yet)

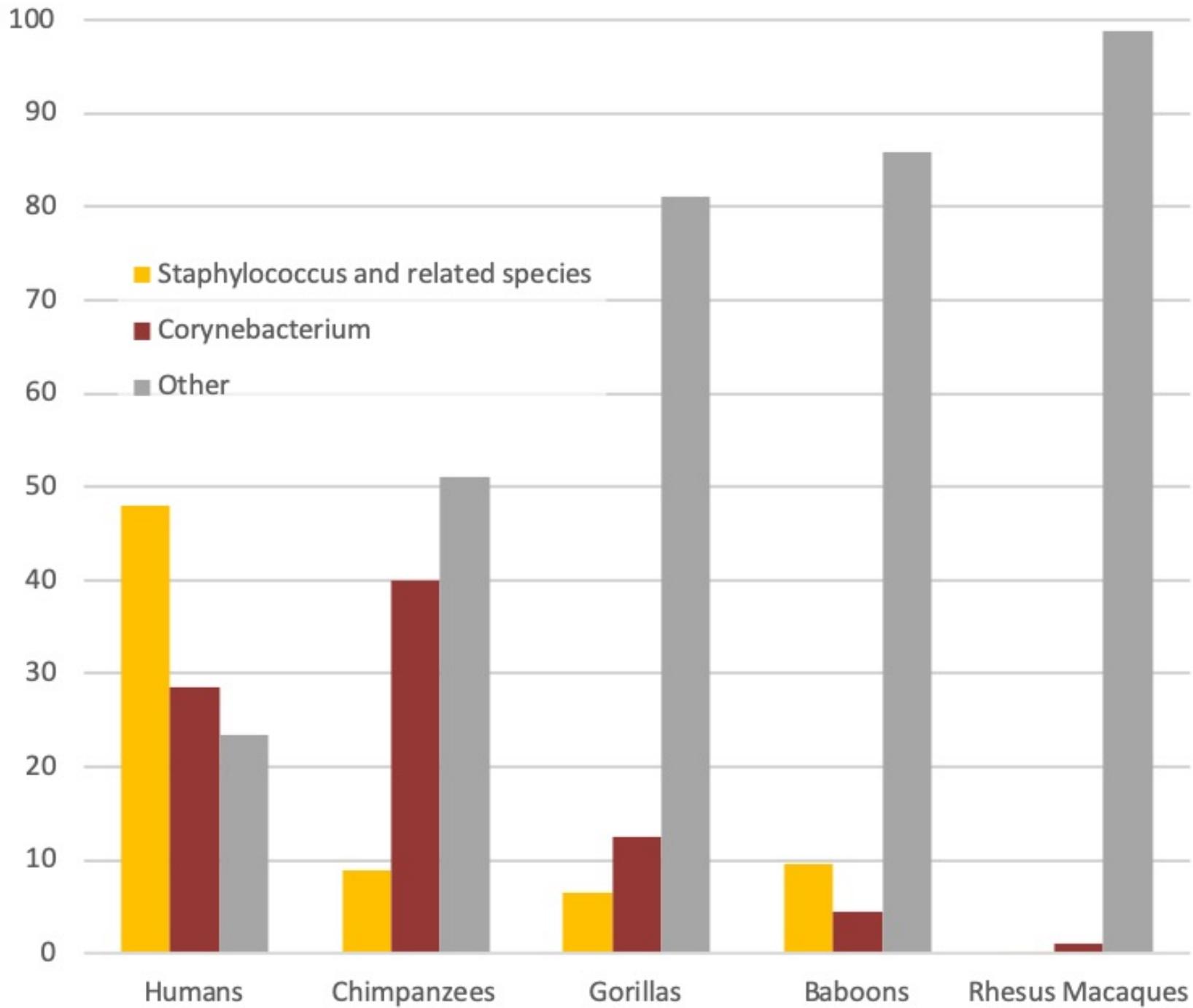


Dr. Julie Horvath Roth

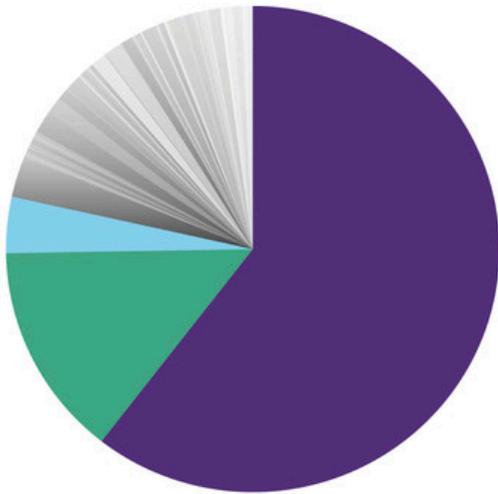


BACTERIAL DIVERSITY



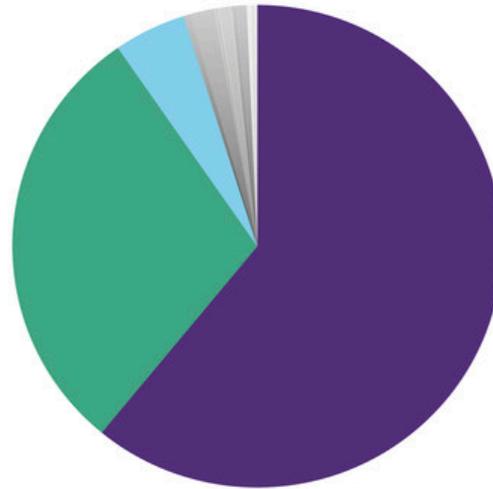


Variation among humans



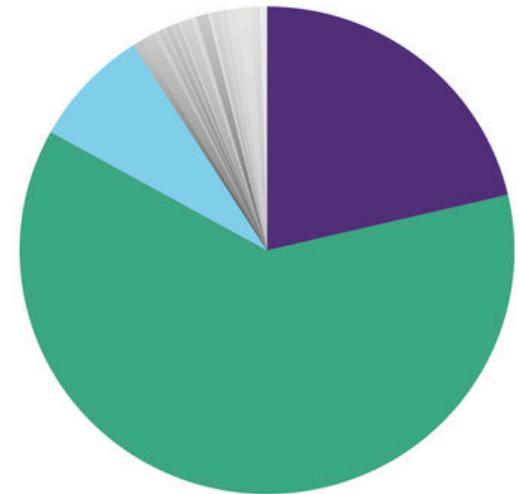
■ Staphylococcaceae 60%
■ *Corynebacterium* 14%
■ *Anaerococcus* 4%
■ Other 22%

Antiperspirant use



■ Staphylococcaceae 61%
■ *Corynebacterium* 29%
■ *Anaerococcus* 5%
■ Other 5%

Deodorant use



■ Staphylococcaceae 21%
■ *Corynebacterium* 62%
■ *Anaerococcus* 8%
■ Other 9%

No
Product use



Kate Coyle

Importance

- People with different skin microbiomes are differently susceptible to particular pathogens
- Skin microbiome composition influences attractiveness to mosquitoes (Staph = more attractive)
- Whatever the ancestral function of skin microbiomes, we have radically altered them

4. VAGINAL COMMUNITIES





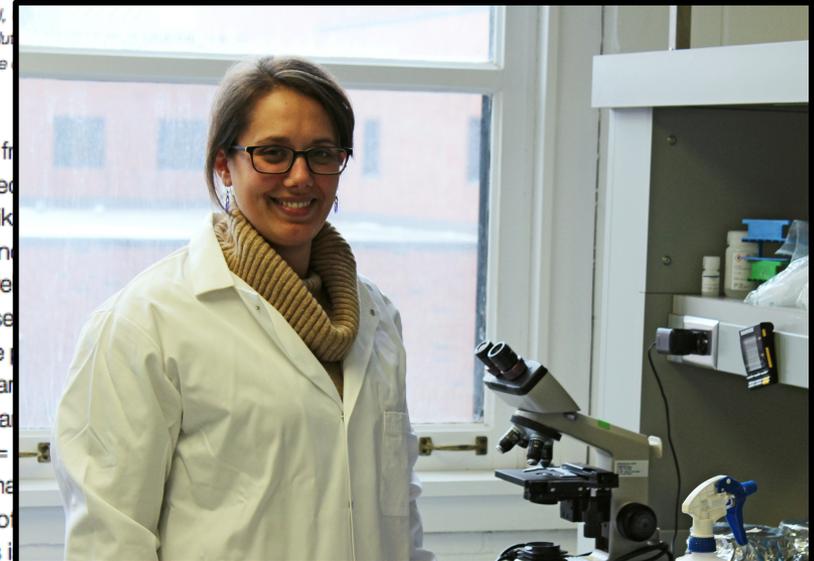
Lactobacilli Dominance and Vaginal pH: Why Is the Human Vaginal Microbiome Unique?

Elizabeth A. Miller^{1*}, DeAnna E. Beasley², Robert R. Dunn^{3,4} and Elizabeth A. Archie^{1,5}

¹ Department of Biological Sciences, University of Notre Dame, Notre Dame, IN, USA, ² Department of Biology, Geology and Environmental Science, University of Tennessee at Chattanooga, Chattanooga, TN, North Carolina State University, Raleigh, NC, USA, ³ Center for Macroecology, Evolution and Microbiology, University of Copenhagen, Copenhagen, Denmark, ⁴ Institute of Microbiology, University of Nairobi, Nairobi, Kenya

The human vaginal microbiome is dominated by bacteria from the genus *Lactobacillus* which create an acidic environment thought to protect against transmitted pathogens and opportunistic infections. Strikingly, the human vaginal microbiome appears to be unique to humans; while the relative abundance of *Lactobacillus* in the human vagina is typically >70%, in other mammals lactobacilli are rare members of the vaginal microbiota. Several hypotheses have been proposed to explain the unique human vaginal microbiota, including humans' distinct reproductive anatomy and high risk of microbial complications linked to pregnancy. We tested these hypotheses using comparative data on vaginal pH and relative abundance of lactobacilli in 26 mammalian species and 50 studies ($N = 1,000$ mammals for lactobacilli relative abundance). We found that humans exhibit the lowest vaginal pH during the period of pregnancy, while the vaginal pH of non-human mammals is never as low as that of humans (vaginal pH in humans = 4.5; range of pH across all 21 non-human mammals = 5.4–7.8). Contrary to disease and obstetric risk hypotheses, we found no significant relationship between vaginal pH or lactobacilli relative abundance and multiple metrics of STD or birth injury risk (P -values ranged from 0.13 to 0.99). Given the lack of evidence for these hypotheses, we discuss two alternative explanations: the common function hypothesis

Dr. Elizabeth Miller,
Now at U. of Minnesota



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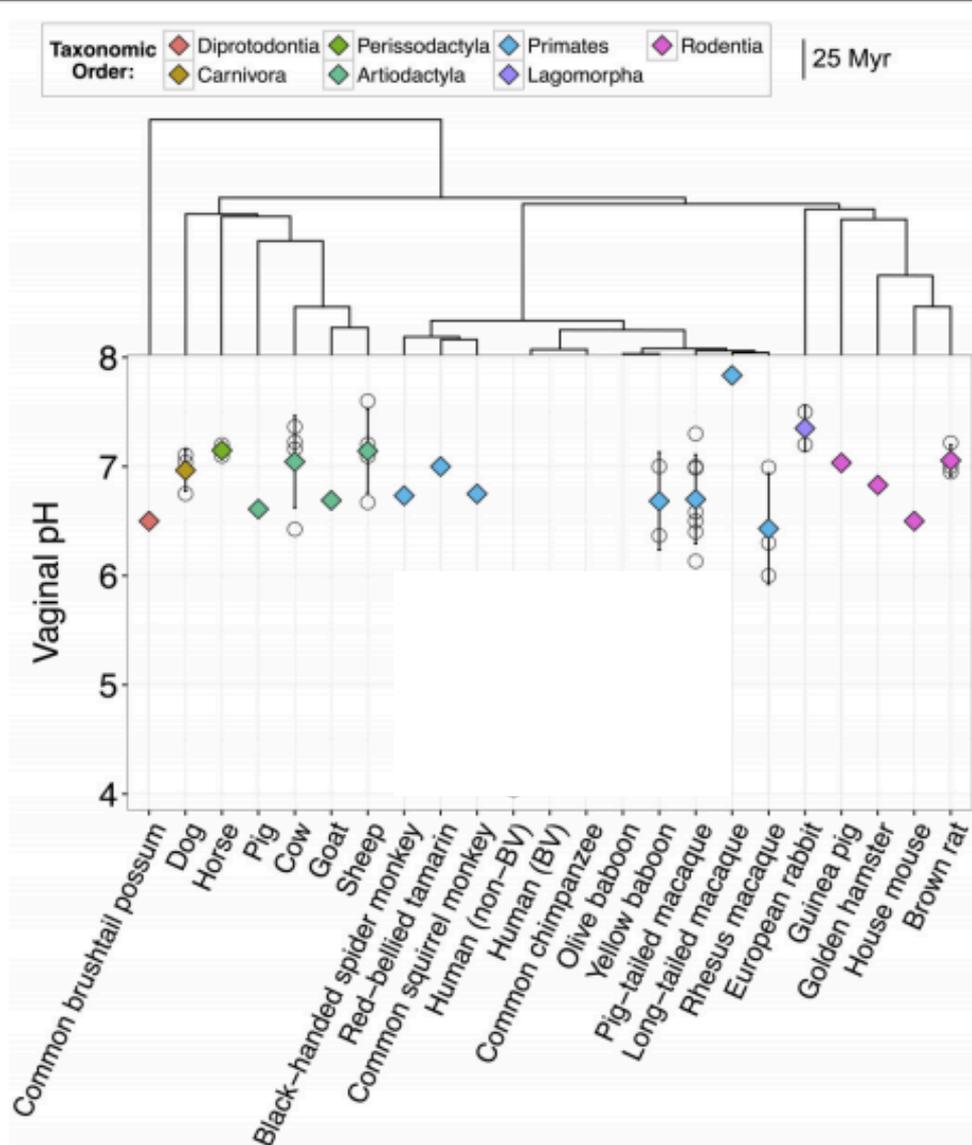


FIGURE 1 | Vaginal pH across 22 species of mammals including humans. Open circles represent mean pH from individual studies and diamonds represent the overall mean for that species. Diamonds are color-coded based on taxonomic order. Error bars represent the standard

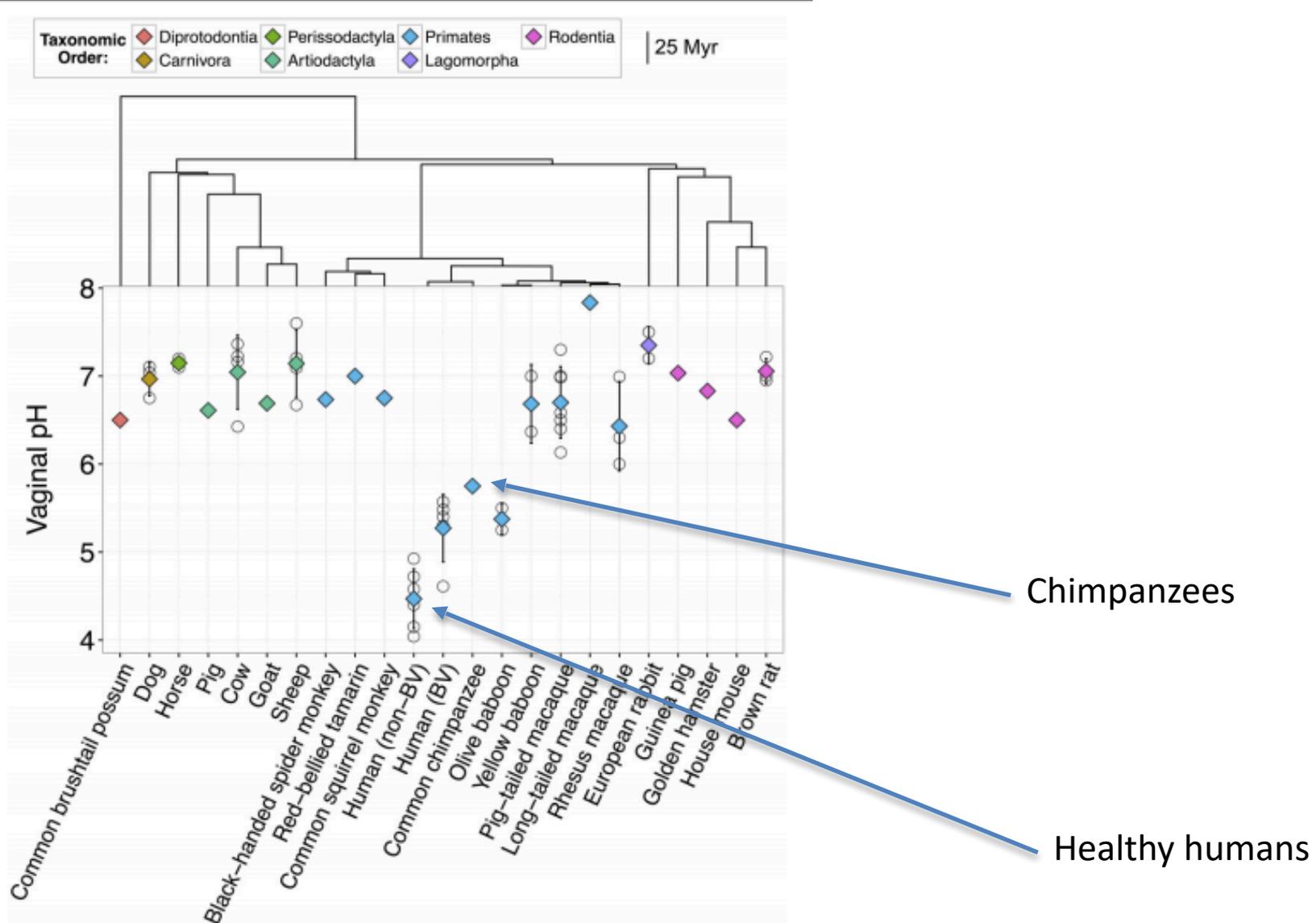


FIGURE 1 | Vaginal pH across 22 species of mammals including humans. Open circles represent mean pH from individual studies and diamonds represent the overall mean for that species. Diamonds are color-coded based on taxonomic order. Error bars represent the standard

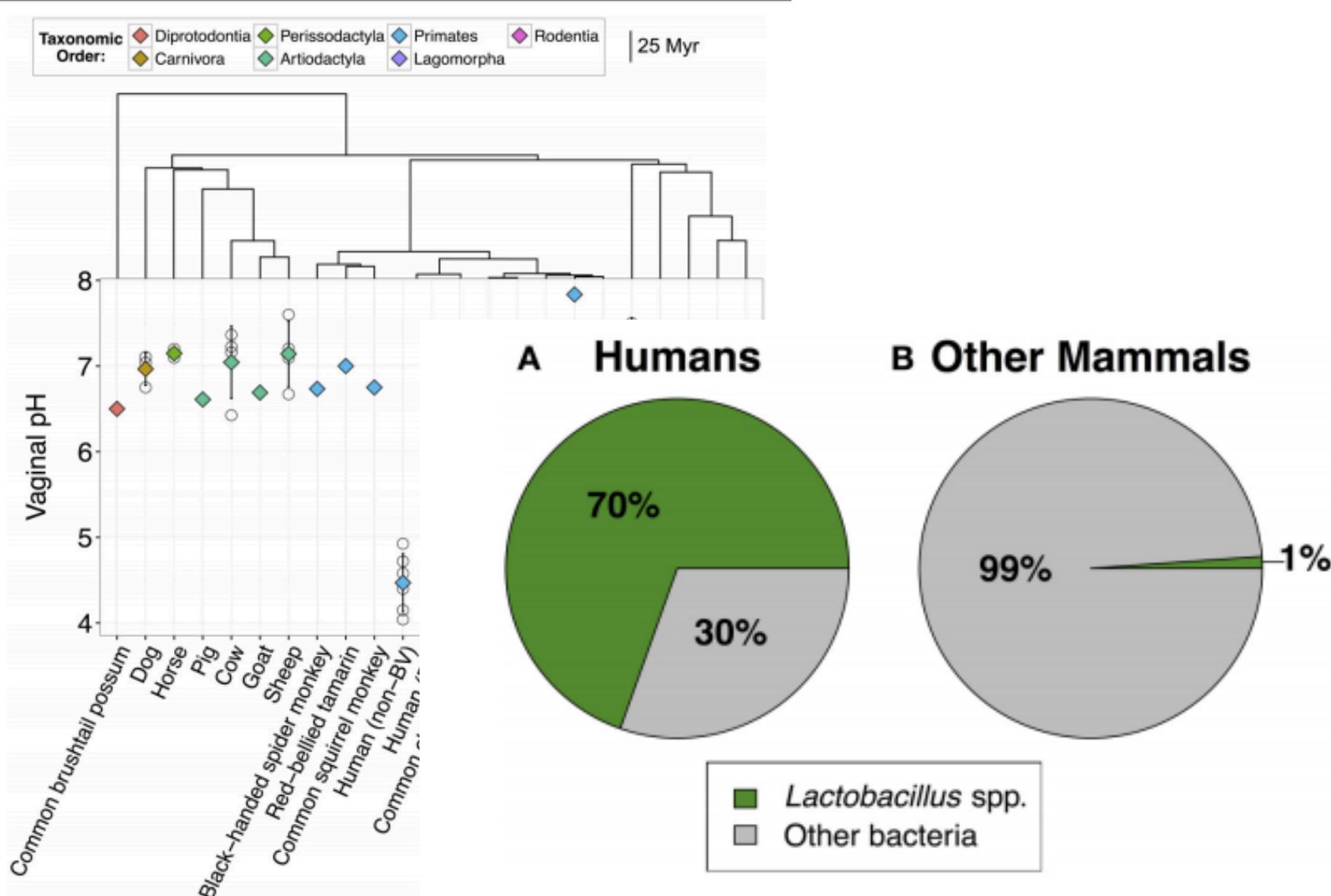
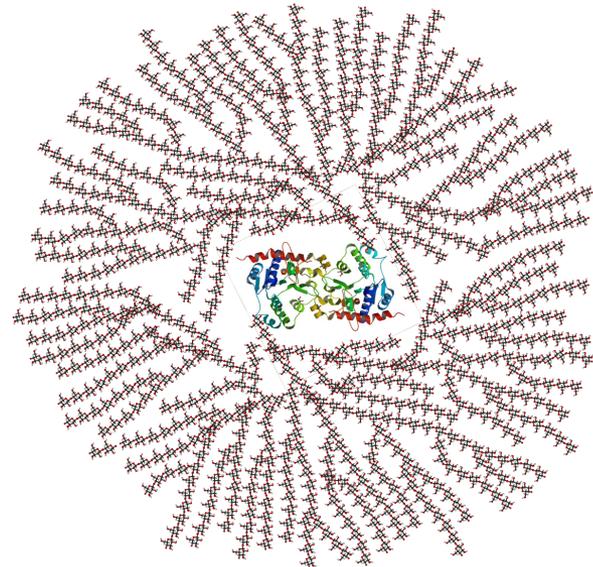


FIGURE 1 | Vaginal pH across 22 species of mammals including humans. Open circles represent mean pH from individual studies and diamonds represent the overall mean for that species. Diamonds are color-coded based on taxonomic order. Error bars represent the standard

TABLE 3 | Concentration of glycogen in the vaginal tract across mammalian species.

Order	Species	Common name	Vaginal glycogen content		References
			Tissue ($\mu\text{g}/100\text{ mg}$ of wet tissue)	Genital fluid (Glycogen:Protein [$\mu\text{g}/\mu\text{g}$])	
RODENTIA					
	<i>Mesocricetus auratus</i>	Golden Hamster	182.78	–	Gregoire and Guinness, 1968
	<i>Mus musculus</i>	House Mouse	68.98	–	Balmain et al., 1956
	<i>Oryctolagus cuniculus</i>	European Rabbit	44.00	–	Gregoire and Hafs, 1971
	<i>Rattus norvegicus</i>	Brown Rat	35.56	–	Shukla et al., 1989
PRIMATES					
	<i>Homo sapiens</i>	Human (non-BV)	1395.75	–	Gregoire et al., 1971
		Human (BV)	–	0.2	Mirmonsef et al., 2012
	<i>Macaca mulatta</i>	Rhesus Macaque	603.67	–	Gregoire and Parakkal, 1972
			–	0.004	Mirmonsef et al., 2012
	<i>Macaca nemestrina</i>	Pig-Tailed Macaque	–	<0.001	Mirmonsef et al., 2012



5A. THE EXTENDED HOLOGENOME

Toward a Global Ecology of Fermented Foods

Robert R. Dunn, John Wilson, Lauren M. Nichols, and Michael C. Gavin

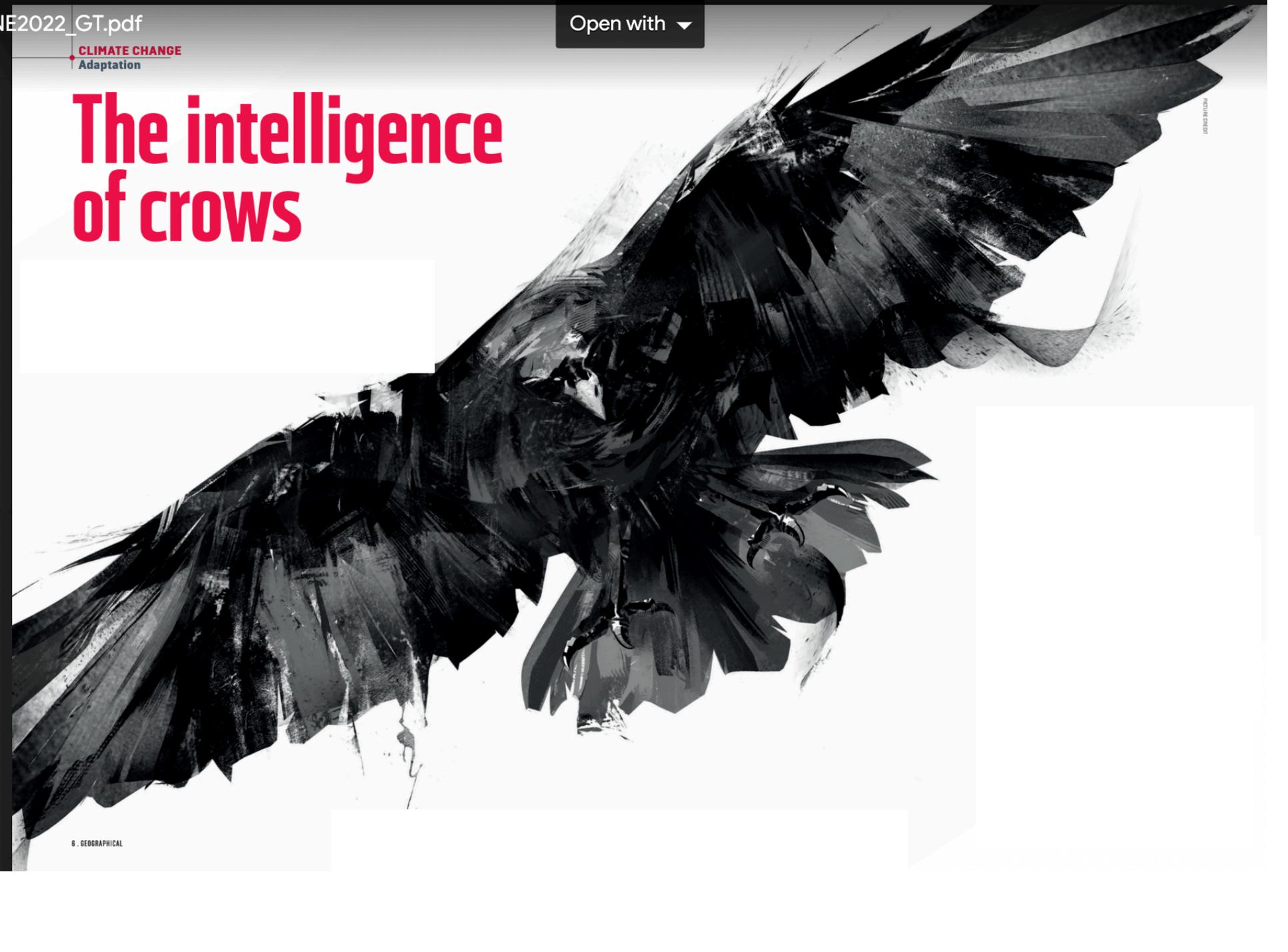
The control of microbes in food has been as important to human societies as the domestication of plants and animals. The direct or indirect management of microbes has been critical to food safety, ensuring nutrient availability, and developing desired sensory characteristics in food. Fermentation is more universal than is agriculture inasmuch as it is practiced by agricultural societies, pastoralists, and hunter-gatherers. In addition, fermentation likely predates agriculture, potentially by hundreds of thousands of years. However, we lack a general approach to understanding of (*a*) when and why technologies associated with fermentation emerged and (*b*) how those technologies and the microbes associated with them diverged once they emerged. Here we offer a framework for the study of the diversification of fermented foods in and among human societies. In developing this framework, we draw heavily from research on language and more generally cultural diversification.

Fermented foods and beverages have played a critical role in human history and prehistory and continue to be highly valued by human societies. Annual sales of fermented beverages alone exceed \$2 trillion (Allied Market Research 2018; Zion Market Research 2018*a*, 2018*b*). In addition, the human control of fermentation in order to produce and use what are, in essence, microbial farms, likely predates agriculture (Amato et al. 2021; Boethius 2016; Braidwood et al. 1953; Liu et al. 2018), potentially by hundreds of thousands of years (Speth 2017). Over the course of human history fermentation has helped ensure the safety of foods and beverages and has also shaped the sensory

producing bacteria and yield products that are both alcoholic and acidic. Alkaline ferments, on the other hand, include tempeh, a subset of mold-ripened cheeses, and lutefisk (a traditional Nordic dish of fish fermented in lye). Fermented foods and drinks can also be divided as a function of the substrate being fermented. Many fermentations rely on protein. Protein ferments include fermented meats, fish, legumes, and nuts. Other fermentations begin with carbohydrates. Carbohydrate ferments are represented by fermented cereals, tubers, vegetables, fruits, and dairy products. A third group of fermentations is based on animal fats; such fermentations are often used to add desired flavors to butter or

THE COGNITIVE BUFFERING HYPOTHESIS

The intelligence of crows

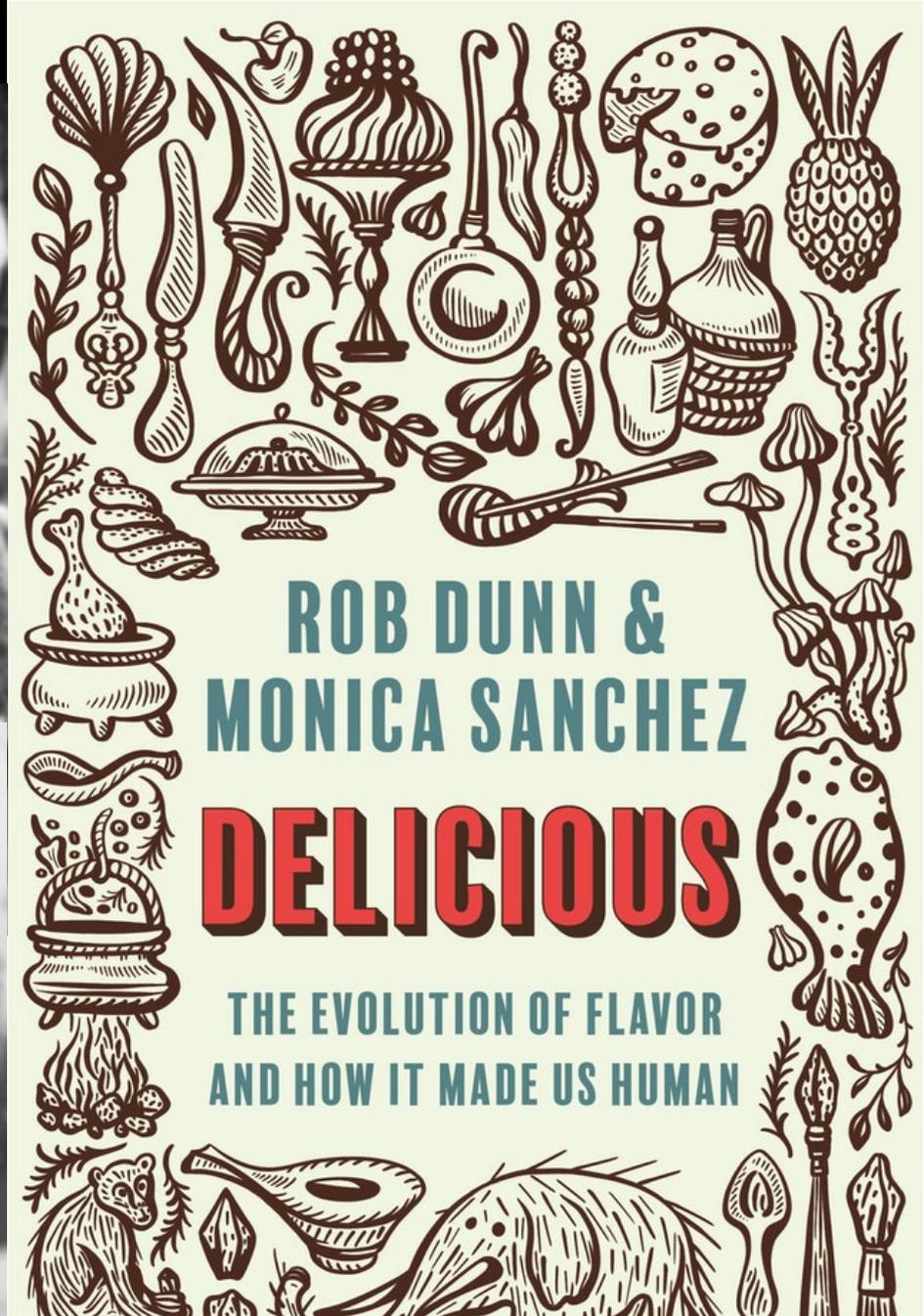


© 2013 PHOTON



EXTENDING THE HOLOGENOME...

- Makes inedible food edible (some roots/tubers)
- Allows foods to be stored
- Helps to transform what is edible in a landscape (transforms the edible landscape)
- May help kill foodborne pathogens
- **BUFFERS HARD TIMES**

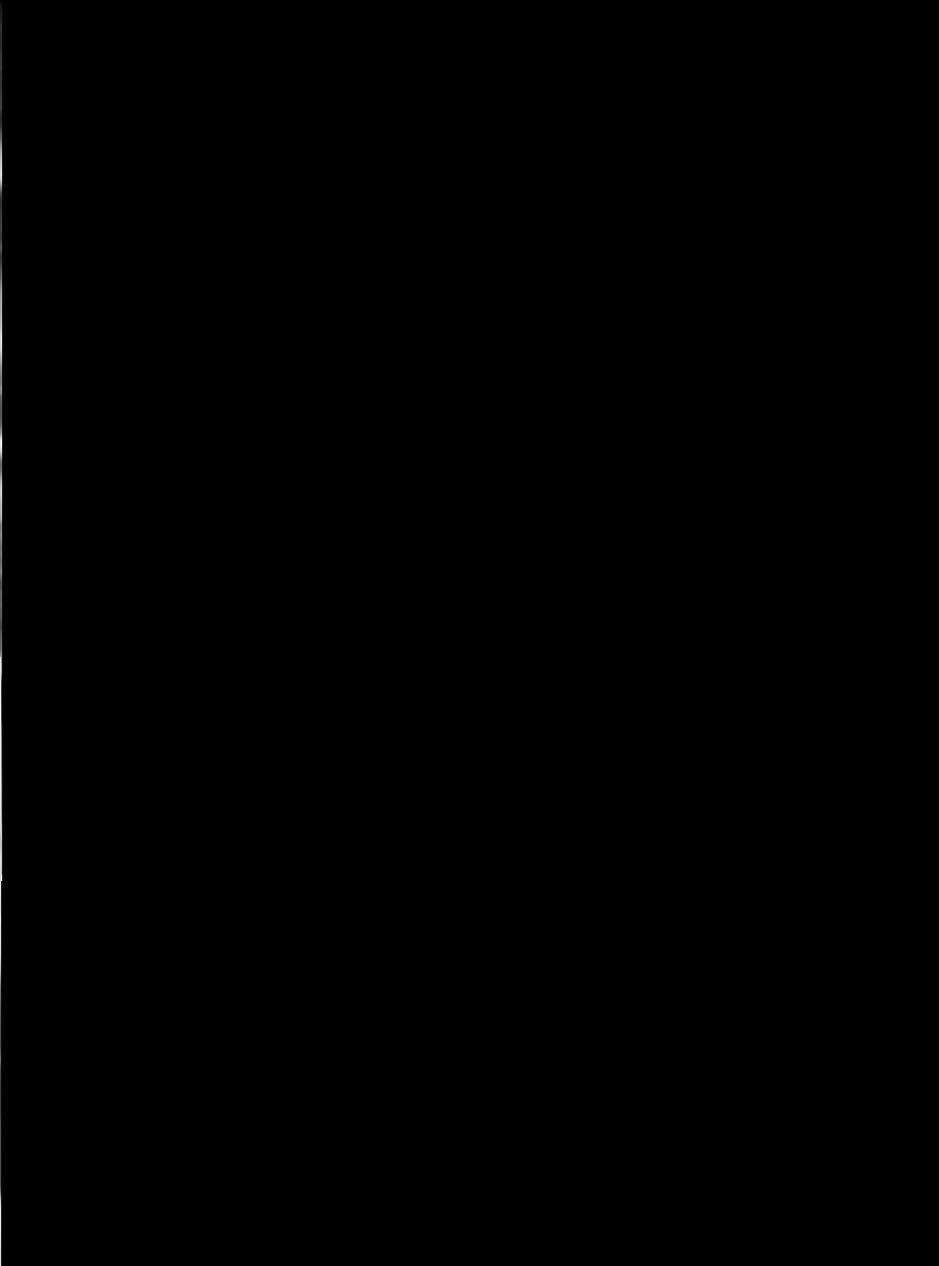


ROB DUNN &
MONICA SANCHEZ

DELICIOUS

THE EVOLUTION OF FLAVOR
AND HOW IT MADE US HUMAN

FERMENTATION APPEARS ANCIENT



Two Kinds of Rot

Rot by yeasts
and lactic acid
bacteria (safe
because of
acids and
alcohols)

Rot by molds (= typically not safe)



Alcohol



Hominids adapted to metabolize ethanol long before human-directed fermentation

Matthew A. Carrigan^{a,b,1}, Oleg Uryasev^b, Carole B. Frye^b, Blair L. Eckman^b, Candace R. Myers^c, Thomas D. Hurley^c, and Steven A. Benner^b

^aDepartment of Natural Sciences, Santa Fe College, Gainesville, FL 32606; ^bFoundation for Applied Molecular Evolution, Gainesville, FL 32604; and ^cDepartment of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, IN 46202

Edited by Robert Dudley, University of California, Berkeley, CA, and accepted by the Editorial Board October 28, 2014 (received for review March 4, 2014)

Paleogenetics is an emerging field that resurrects ancestral proteins from now-extinct organisms to test, in the laboratory, models of protein function based on natural history and Darwinian evolution. Here, we resurrect digestive alcohol dehydrogenases (ADH4) from our primate ancestors to explore the history of primate-ethanol interactions. The evolving catalytic properties of these resurrected enzymes show that our ape ancestors gained a digestive dehydrogenase enzyme capable of metabolizing ethanol near the time that they began using the forest floor, about 10 million y ago. The ADH4 enzyme in our more ancient and arboreal ancestors did not efficiently oxidize ethanol. This change suggests that exposure to dietary sources of ethanol increased in hominids during the early stages of our adaptation to a terrestrial lifestyle. Because fruit collected from the forest floor is expected to contain higher concentrations of fermenting yeast and ethanol than similar fruits hanging on trees, this transition may also be the first time our ancestors were exposed to (and adapted to) substantial amounts of dietary ethanol.

experimental paleogenetics | alcohol dehydrogenase | ethanol | primates | evolution

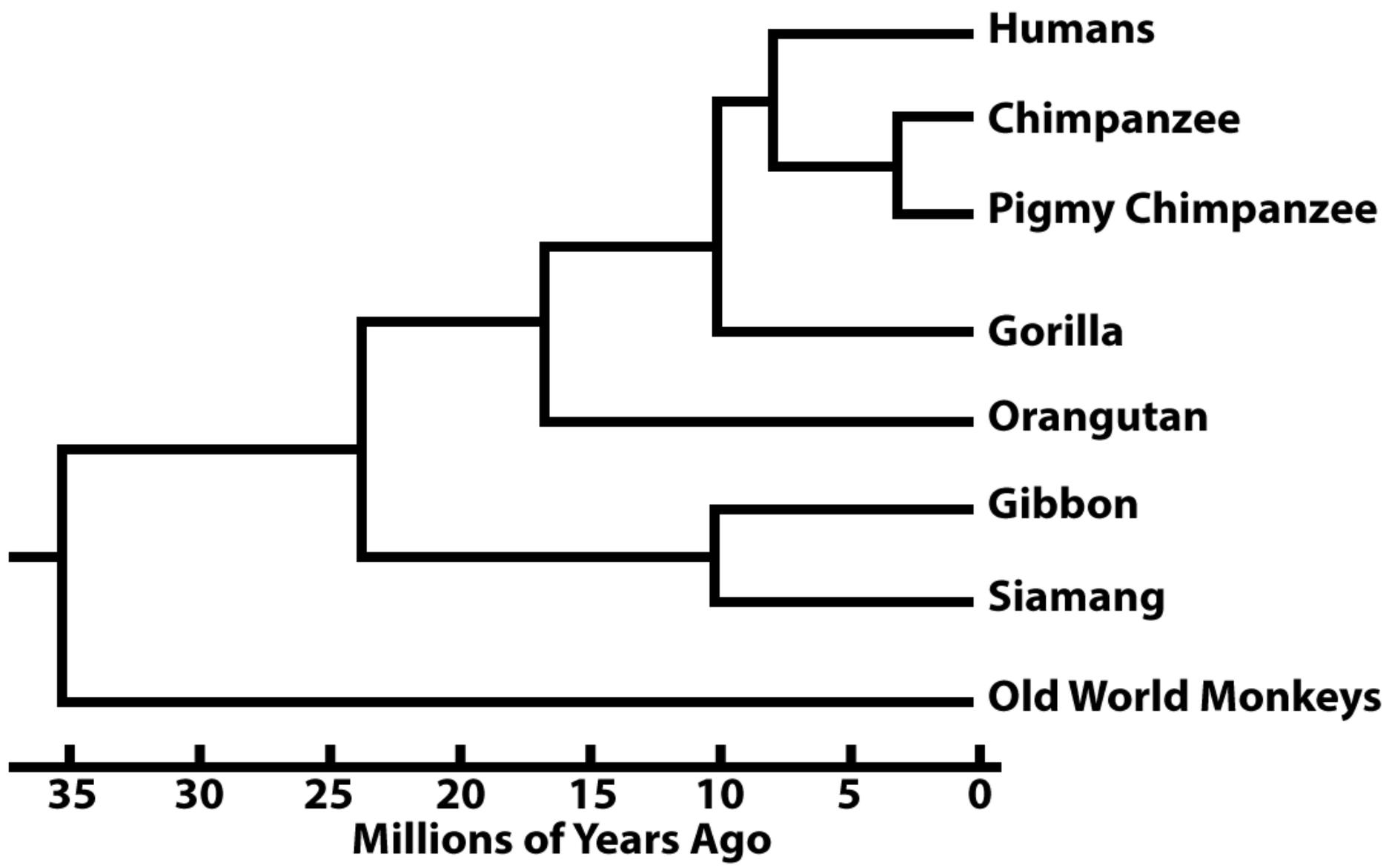
One trend in modern medicine attributes diseases in humans to an incomplete adaptation of the human genome to new challenges presented by our changing cultural and demographic environment (1). This attribution is especially convincing for some “lifestyle” diseases. For example, the recent increase in sugar consumption (including sucrose and fructose) is associated with the emergence of obesity, diabetes, and hypertension (2). Under an evolutionary paradigm, an organism fully adapted to a sugar-rich diet would not be expected to become diseased by

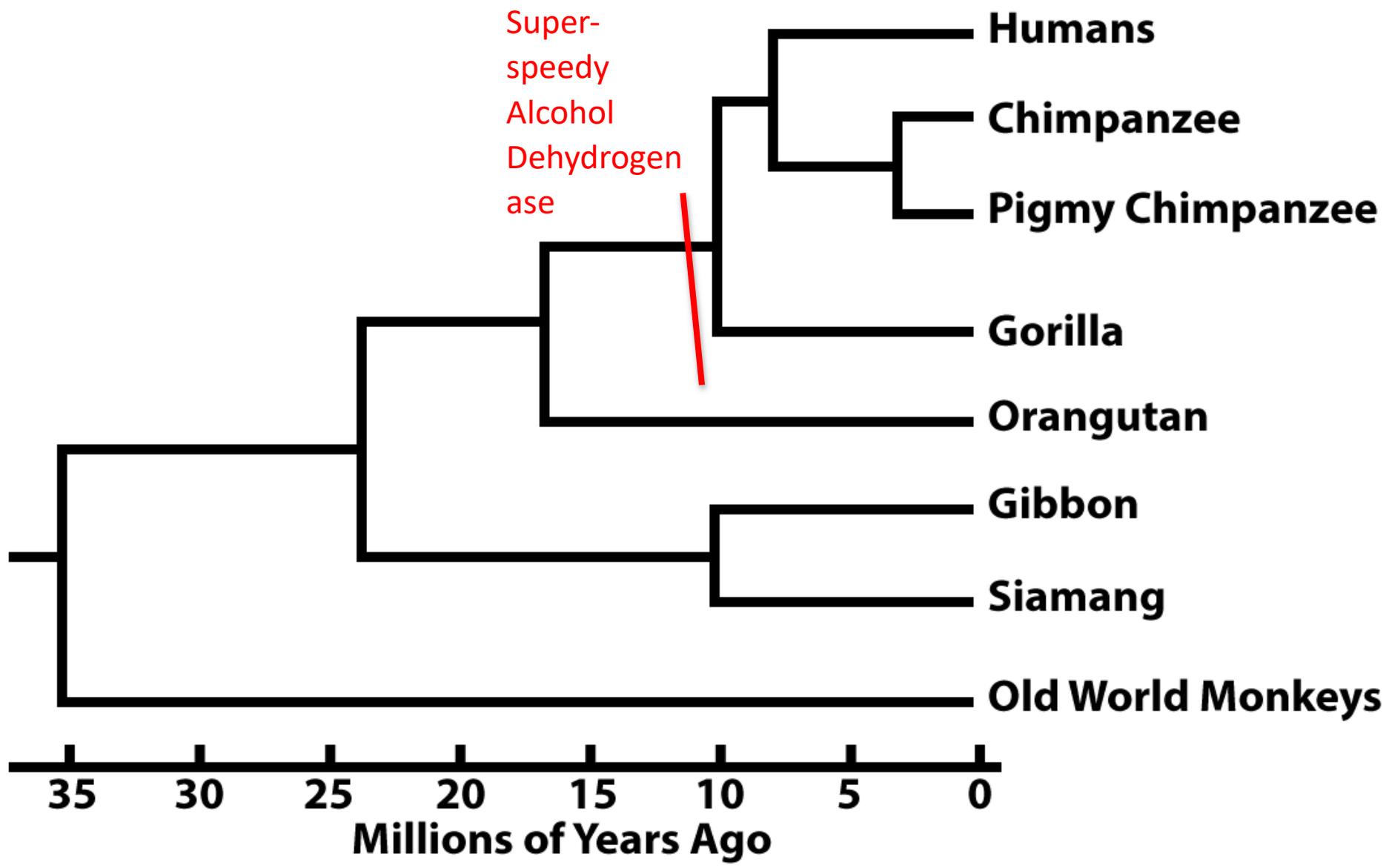
when angiosperm plants first produced fleshy fruits that can become infected by yeast capable of the accumulating ethanol via fermentation (12). In one version of this model, small amounts of ethanol present in slightly fermenting fruit attached to trees attracted arboreal primates foraging in the trees. In this version, our contemporary attraction to ethanol is an “evolutionary hang-over” that ceased to be beneficial once that attraction became redirected to beverages with high concentrations of ethanol (13), made possible only after humans developed the tools allowing them to intentionally direct fermentation (and enhanced with the advent of technology to distill ethanol to higher concentrations). Another version of the “ethanol early” model for ethanol exposure recognizes that ethanol itself, as well as the food naturally containing it, can be a significant source of nutrition. This model posits that any organism with metabolic adaptations that permit the exploitation of ethanolic food would have access to a specialized niche or important fallback foods unavailable to organisms without this metabolic capacity.

Paleogenetics is an emerging field designed to address such natural historical hypotheses and, in particular, to distinguish between competing historical models (14). Here, to gain a genetic perspective on the natural history of the interaction between our human ancestors and ethanol, we examined the evolution of Class IV alcohol dehydrogenases (ADH4) (see *SI Text* for a discussion of the various synonyms used within the ADH family). These digestive enzymes are abundant in the stomach, esophagus, and tongue of primates and are active against a wide range of alcohols. Thus, ADH4 is the first alcohol-metabolizing enzyme to

Significance

Many modern human diseases are attributed to incompatibility





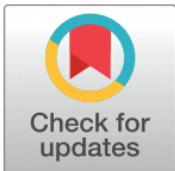
RESEARCH ARTICLE

Metabolites of lactic acid bacteria present in fermented foods are highly potent agonists of human hydroxycarboxylic acid receptor 3

Anna Peters¹, **Petra Krumbholz**¹, **Elisabeth Jäger**², **Anna Heintz-Buschart**^{3,4}, **Mehmet Volkan Çakir**¹, **Sven Rothemund**⁵, **Alexander Gaudl**⁶, **Uta Ceglarek**⁶, **Torsten Schöneberg**¹, **Claudia Stäubert**^{1*}

1 Rudolf Schönheimer Institute of Biochemistry, Faculty of Medicine, Leipzig University, Leipzig, Germany, **2** Department of Internal Medicine, Division of Rheumatology, Leipzig University, Leipzig, Germany, **3** German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany, **4** Helmholtz-Centre for Environmental Research GmbH - UFZ, Department of Soil Ecology, Halle (Saale), Germany, **5** Core Unit Peptide-Technologies, Leipzig University, Leipzig, Germany, **6** Institute for Laboratory Medicine, Clinical Chemistry and Molecular Diagnostics, University Hospital Leipzig, Leipzig, Germany

* claudia.staebert@medizin.uni-leipzig.de



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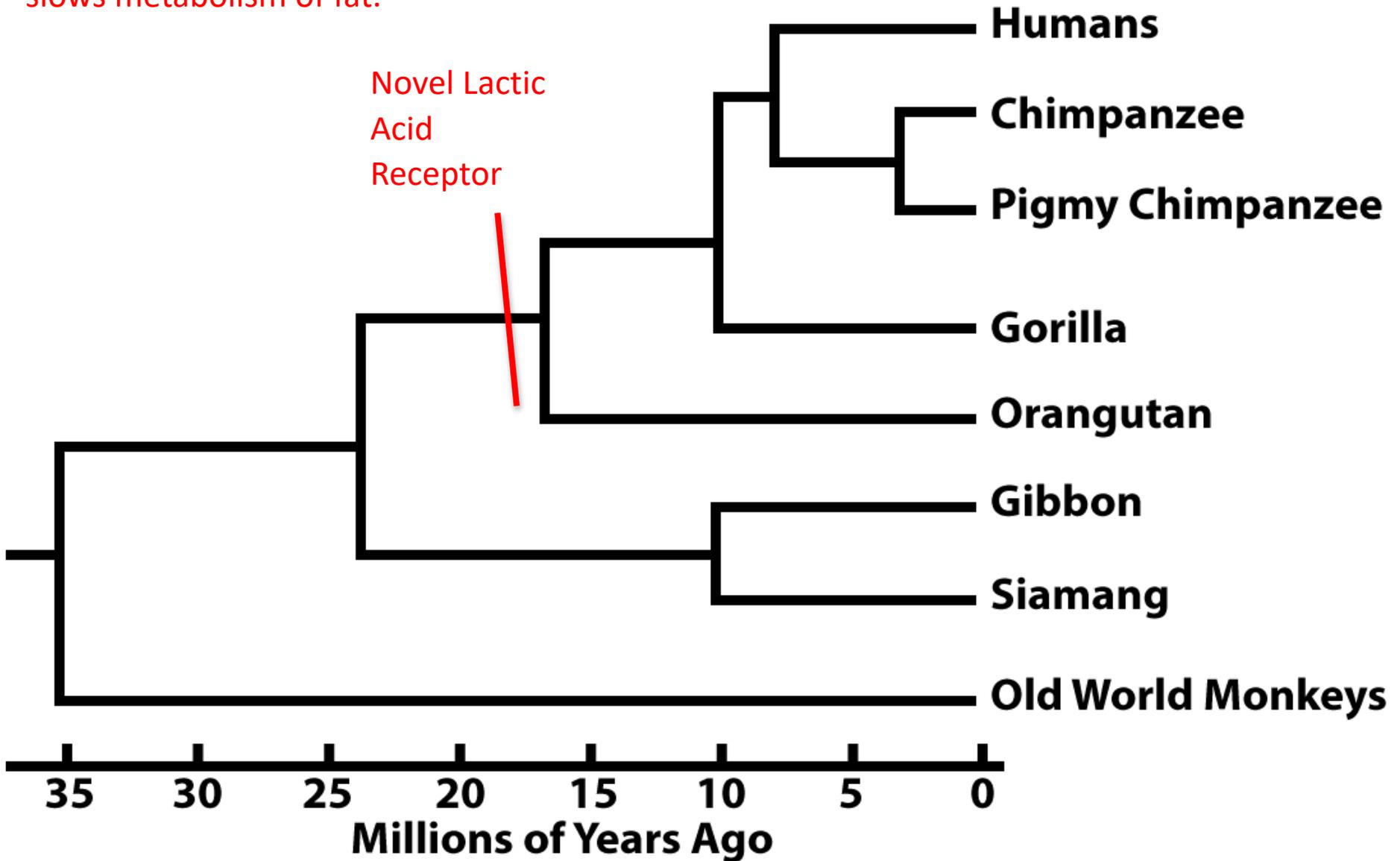
Citation: Peters A, Krumbholz P, Jäger E, Heintz-Buschart A, Çakir MV, Rothemund S, et al. (2019) Metabolites of lactic acid bacteria present in fermented foods are highly potent agonists of

Abstract

The interplay of microbiota and the human host is physiologically crucial in health and diseases. The beneficial effects of lactic acid bacteria (LAB), permanently colonizing the human intestine or transiently obtained from food, have been extensively reported. However, the molecular understanding of how LAB modulate human physiology is still limited

Suppresses immune response and slows metabolism of fat.

Novel Lactic Acid Receptor



Review



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Subject Category:

Ecology

Subject Areas:

behaviour, ecology, evolution

The evolution of sour taste

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The evolutionary history of sour taste has been little studied. Through a combination of literature review and trait mapping on the vertebrate phylogenetic tree, we consider the origin of sour taste, potential cases of the loss of sour taste, and those factors that might have favoured changes in the valence of sour taste—from aversive to appealing. We reconstruct sour taste as having evolved in ancient fish. By contrast to other tastes, sour taste does not appear to have been lost in any major vertebrate taxa. For most species, sour taste is aversive. Animals, including humans, that enjoy the sour taste triggered by acidic foods are exceptional. We conclude by considering why sour taste evolved, why it might have persisted as vertebrates made the transition to land and what factors might have favoured the preference for sour-tasting, acidic foods, particularly in hominins, such as humans.

A brief history of fermentation (beer, fruit, grain, honey)



A brief history of fermentation (meat)



Prof. Dan Fisher,
University of Michigan





A flavor “like Stilton cheese and steak all in one”



5B. THE ROLE OF THE BODY



Dr. Emily Meineke



Musician Joe Kwon



Chef
Mama
Kwon





Dr. Emily Meineke



Musician Joe Kwon



Chef
Mama
Kwon



Tson mat (Hand Flavor)



Soured with GI and sometimes vaginal *Lactobacillus*

SCIENCE

Using vaginal fluids to make yoghurt

Image: Fugt

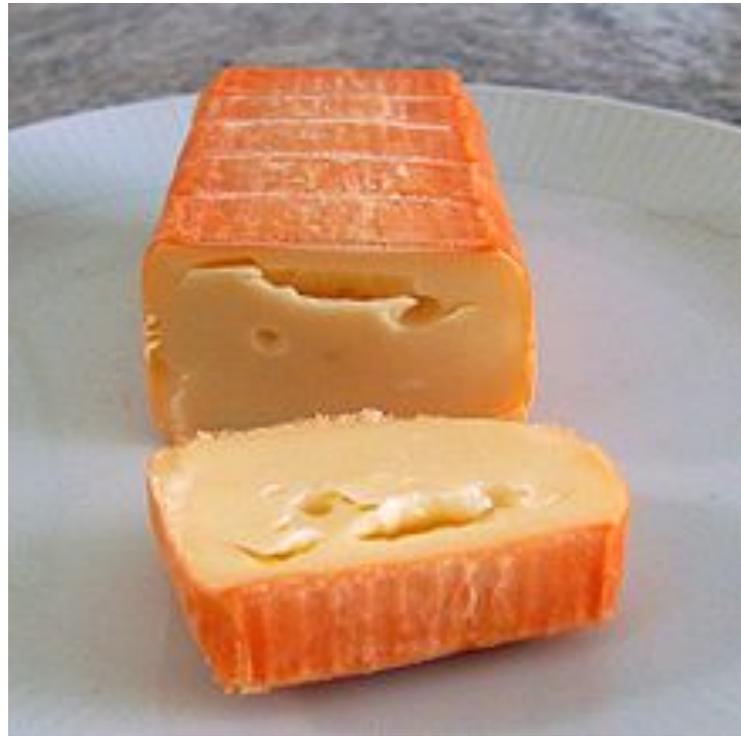
Not your average science workshop, participants are learning how to transform vaginal cultures into yoghurt - Vaghurt

Lena Rutkowski, additional reporting Mike Young





Sour with GI and sometimes vaginal *Lactobacillus*



Reddened by skin *Brevibacterium linens*



Sticky with foot *Bacillus subtilis*



Sour and punchy with oral *Streptococcus*

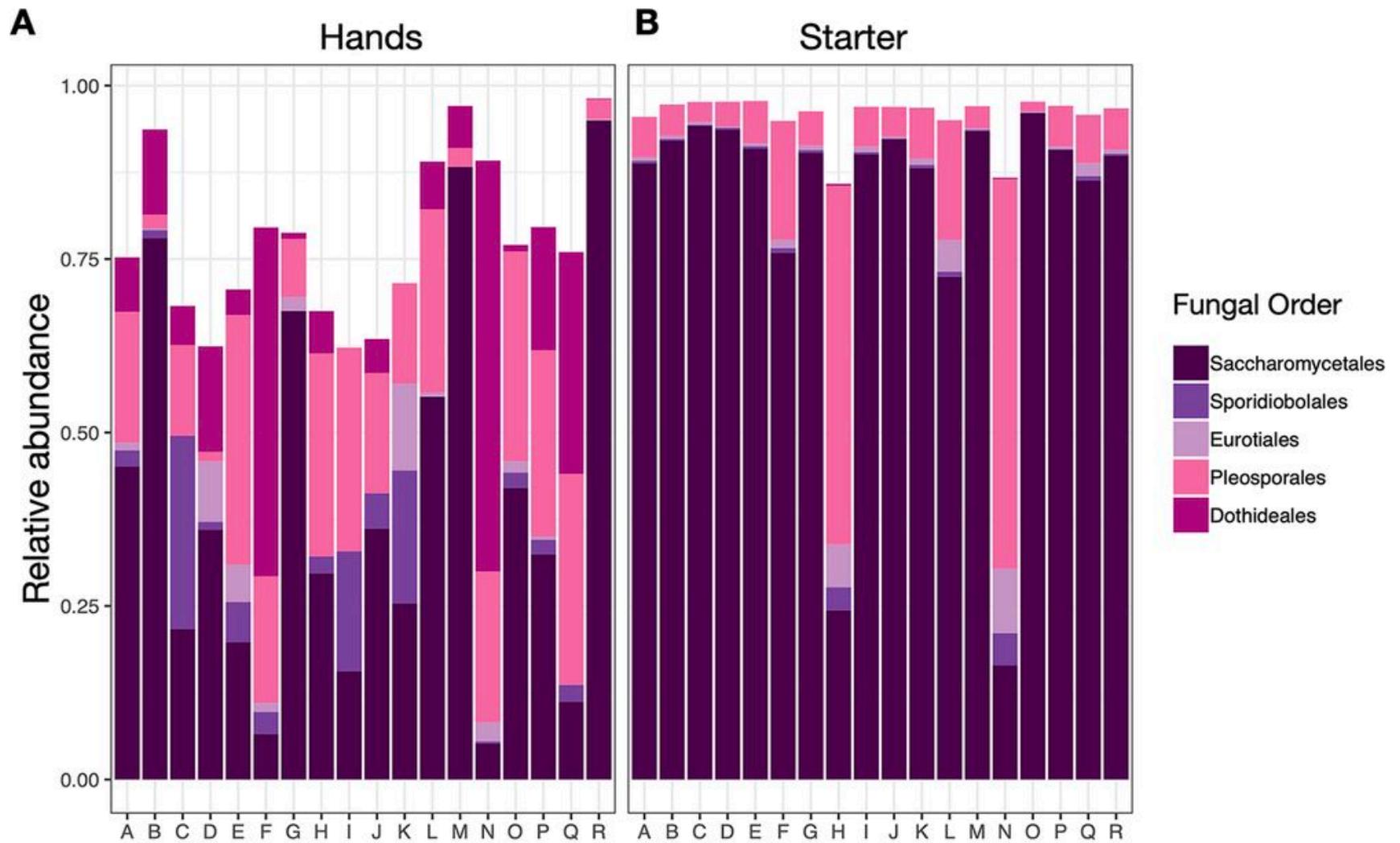


BODY FLAVOR

Big Man, Ron Mueck

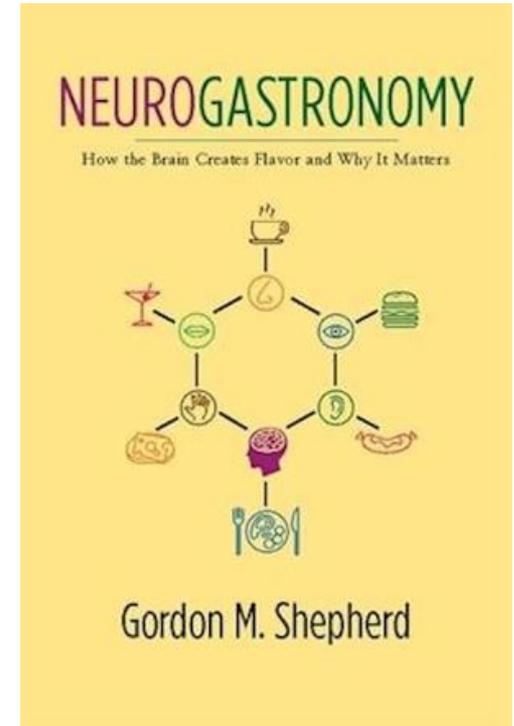
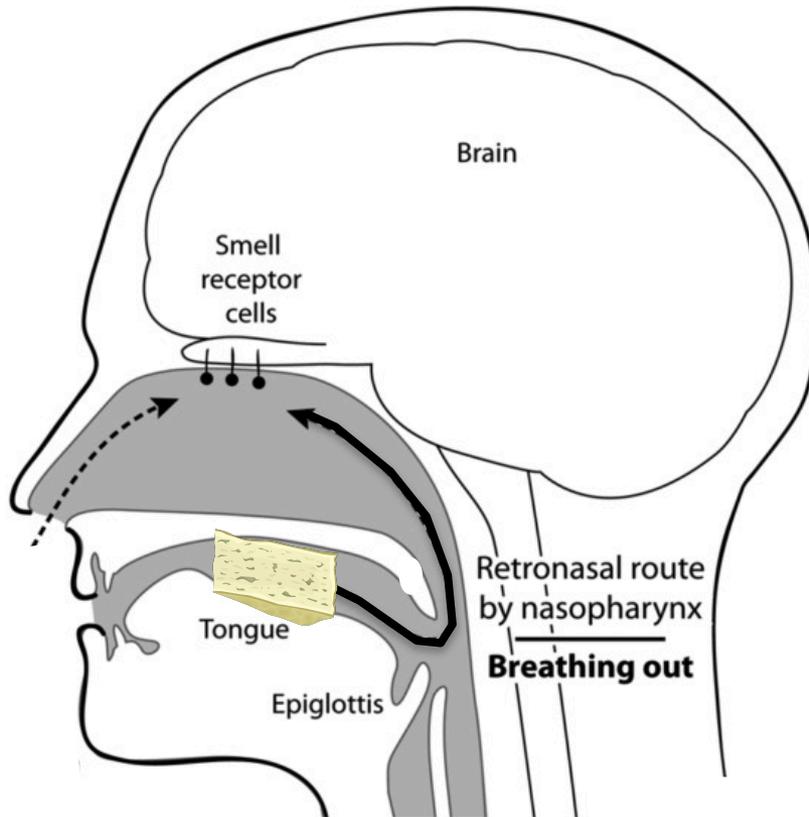






Reese, Aspen T., Anne A. Madden, Marie Joossens, Guylaine Lacaze, and Robert R. Dunn. "Influences of ingredients and bakers on the bacteria and fungi in sourdough starters and bread." *Msphere* 5, no. 1 (2020): e00950-19.

FOR MORE ON THE INTERSECTION OF ORTHONASAL OLFACTION AND THE BRAIN, SEE ALSO... SHEPHERD





ARAPESH

see

OCEANIA - MELANESIA - PAPUA NEW GUINEA -
EAST SEPIK DISTRICT - MOUNTAIN ARAPESH
OCEANIA - MELANESIA - PAPUA NEW GUINEA -
EAST SEPIK DISTRICT - SOUTHERN ARAPESH



THIS BEGINS EARLY IN LIFE

Sculpture by Ron Mueck





½ ate anise
½ did not



Scrunchy-faced
displeasure



Lick-lipping
pleasure





5C. IT IS NOT JUST HUMANS





- A. Banana
- B. Pineapple
- C. Mango
- D. Papaya
- E. Avocado
- F. Coffee
- G. Cocoa
- H. Rubber
- I. Cashew
- J. Peanut
- K. Sesame
- L. Soybean
- M. Corn
- N. Rice
- O. Wheat
- P. Barley
- Q. Oats
- R. Rye
- S. Sorghum
- T. Millet
- U. Buckwheat
- V. Amaranth
- W. Quinoa
- X. Chia
- Y. Flax
- Z. Hemp



ALEXIS ROCKMAN, THE ECOTOURIST



Stefanini, Irene, Leonardo Dapporto, Jean-Luc Legras, Antonio Calabretta, Monica Di Paola, Carlotta De Filippo, Roberto Viola et al. "Role of social wasps in *Saccharomyces cerevisiae* ecology and evolution." *Proceedings of the National Academy of Sciences* 109, no. 33 (2012): 13398-13403.

Illustration 14.1 Carl Bloch, *In a Roman Osteria* (detail), 1866. Photo by Robert Dunn.

The ecology of insect–yeast relationships and its relevance to human industry

Anne A. Madden, Mary Jane Epps, Tadashi Fukami, Rebecca E. Irwin, John Sheppard, D. Magdalena Sorger and Robert R. Dunn

Published: 21 March 2018 | <https://doi.org/10.1098/rspb.2017.2733>

Abstract

Many species of yeast are integral to human society. They produce many of our foods, beverages and industrial chemicals, challenge us as pathogens, and provide models for the study of our own biology. However, few species are regularly studied and much of their ecology remains unclear, hindering the development of knowledge that is needed to improve the relationships between humans and yeasts. There is increasing evidence that insects are an essential component of ascomycetous yeast ecology. We propose a 'dispersal–encounter hypothesis' whereby yeasts are dispersed by insects between ephemeral, spatially disparate sugar resources, and insects, in turn, obtain the benefits



INNOVATION: New Beers



The Innovation: Led to a patent and a start up (Lachancea LLC, John Sheppard). Dr. Anne Madden pictured (not here tonight).

RESEARCH ARTICLE

Sugar-seeking insects as a source of diverse bread-making yeasts with enhanced attributes

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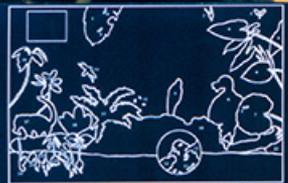
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Correspondence

Robert R. Dunn, Department of Applied Ecology, North Carolina State University,

Abstract

Insects represent a particularly interesting habitat in which to search for novel yeasts of value to industry. Insect-associated yeasts have the potential to have traits relevant to modern food and beverage production due to insect–yeast interactions, with such traits including diverse carbohydrate metabolisms, high sugar tolerance, and general stress tolerance. Here, we consider the potential value of insect-associated yeasts in the specific context of baking. We isolated 63 yeast strains from 13 species of hymenoptera from the United States, representing 37 yeast species from 14 genera. Screening for the ability to ferment maltose, a sugar important for bread production, resulted in the identification of 13 strains of *Candida*, *Lachancea*, and *Pichia* species. We assessed their ability to leaven dough. All strains produced baked loaves



- | | | |
|-----------|------------------|------------|
| 1. Root | 10. Petiole | 19. Flower |
| 2. Stem | 11. Node | 20. Fruit |
| 3. Leaf | 12. Internode | 21. Seed |
| 4. Vein | 13. Axillary bud | 22. Pollen |
| 5. Flower | 14. Terminal bud | 23. Fruit |
| 6. Fruit | 15. Node | 24. Seed |
| 7. Seed | 16. Internode | 25. Fruit |
| 8. Root | 17. Node | 26. Seed |
| 9. Stem | 18. Internode | 27. Fruit |



ALEXIS ROCKMAN, THE ECOTOURIST



5D. WHY SHOULD ONE CARE?



REVIEW SUMMARY

MICROBIOTA

Vulnerability of the industrialized mi

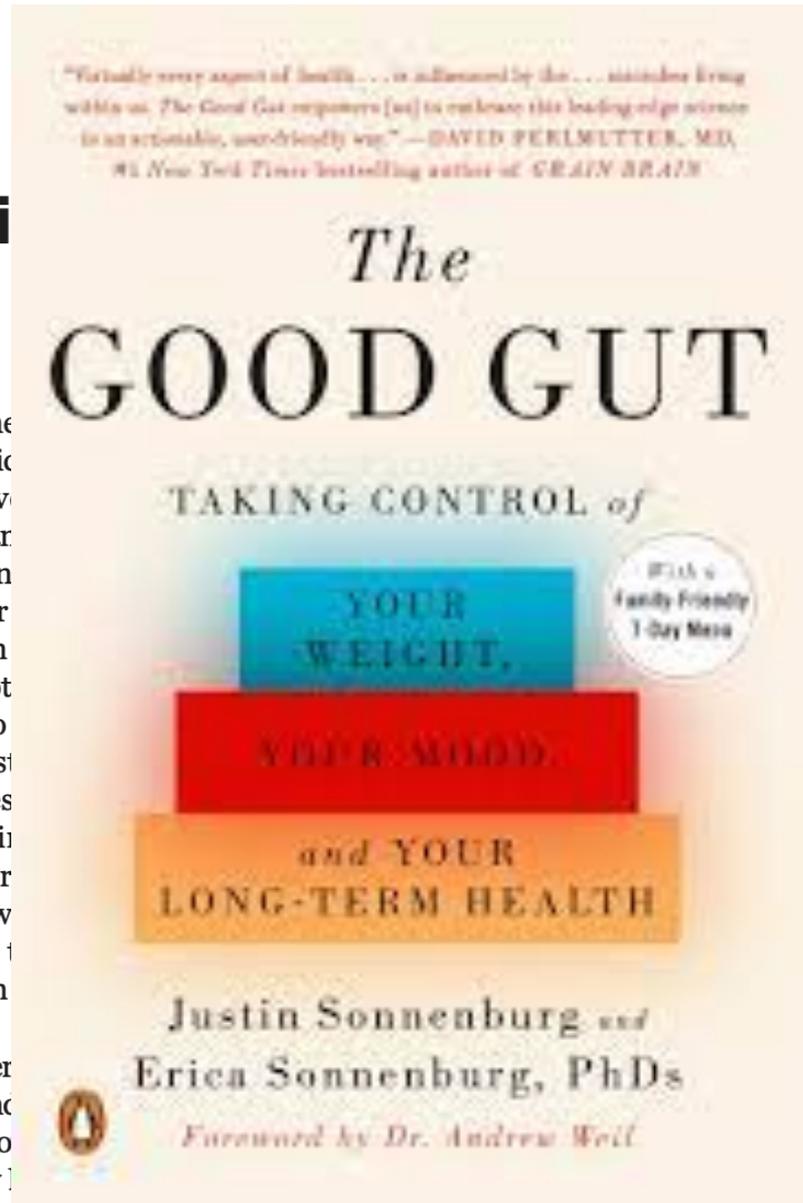
Justin L. Sonnenburg* and Erica D. Sonnenburg*

BACKGROUND: The collection of trillions of microbes inhabiting the human gut, called the microbiome or microbiota, has captivated the biomedical research community for the past decade. Intimate connections exist between the microbiota and the immune system, central nervous system, and metabolism. The growing realization of the fundamental role that the microbiota plays in human health has been accompanied by the challenge of trying to understand which features define a healthy gut community and how these may differ depending upon context. Such insight will lead to new routes of disease treatment and prevention and may illuminate how lifestyle-driven changes to the microbiota can impact health across populations. Individuals living traditional lifestyles around the world share a strikingly similar microbiota composition that is distinct from that found in industrialized populations. Indeed, lineages of gut microbes have cospeciated with humans over

Relative to the “industrial” microbial membership arising from nized settings or states between have microbiot correspond to change. Industrial biotics, processed sanitized environment influence microbial mission and wplemented in their effects on

ADVANCES: Her harbored by industrialized world is o experienced by industrial microbiota has been shaped by re-

microbiota to humans,



Fermented foods restructure gut microbiota and promote immune regulation via microbial metabolites

Authors:

Sean Paul Spencer^{1,2}, Evelyn Giselle Lemus Silva¹, Elisa Benedetti Caffery¹, Matthew Merrill Carter¹, Rebecca Neal Culver³, Min Wang^{4,5}, Rebecca Hope Gellman¹, Hannah Constance Wastyk⁴, Steven Kyle Higginbottom¹, and Justin Laine Sonnenburg^{1,6,7*}

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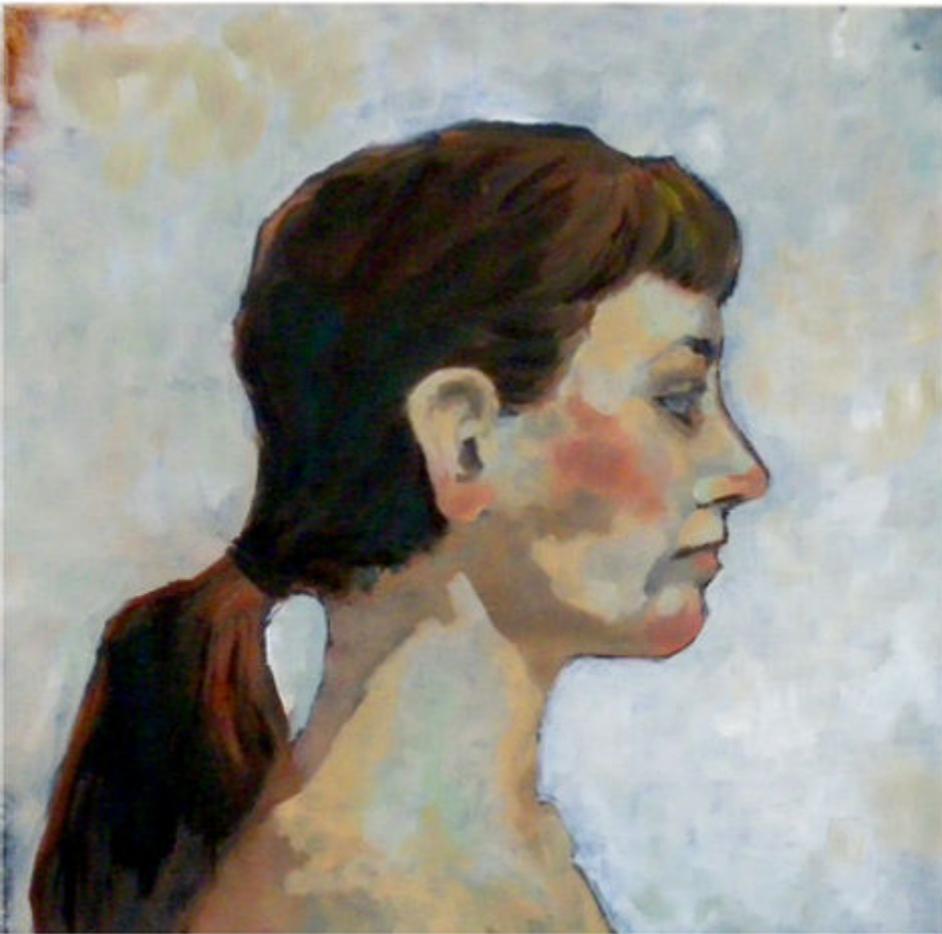
⁷ Chan Zuckerberg Biohub, San Francisco, CA, 94305, USA.

*Corresponding author. Email: jsonnenburg@stanford.edu

Abstract:

Fermented foods are ancient and ubiquitous, thought to be consumed in nearly every culture over

THE HOLOGENOME (Zooming back out)



Me and My Other Self, Joana Ricou

A FEW EXAMPLES OF MANY

