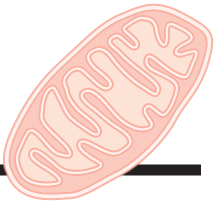
Sharing data by design *p. 1312*

Vitamin C and cancer *p. 1317* ▸



PERSPECTIVES

EVOLUTION

Dissecting diversity in the social brain

Male prairie voles with poor memory skills are less faithful to their partners

By **Gene E. Robinson**

Soon after launching an ambitious 25-year study of the population cycles of rodents in the fields and prairies near the University of Illinois at Urbana-Champaign in 1971, Lowell Getz saw something strange. Adult male and female prairie voles (*Microtus ochrogaster*) often appeared in the same live trap, unlike the meadow vole, whose sexes were more segregated. Moreover, the same pairs were often retrapped months later. Using radio tracking, Getz and his co-workers found that most trapped pairs were long-term partners living together in underground nests and sharing common home ranges (*1*). So began almost 50 years of pathbreaking research into the biology of prairie vole monogamy, in one of fewer than 5% of mammalian species with a monogamous lifestyle (*2*, *3*). On page 1371 of this issue, Okhovat *et al.* (*4*) use the prairie vole model system to investigate individual differences in this social behavior. Differences in social behavior are widely observed but poorly understood in most species.

A hallmark of the prairie vole model is its strong multidisciplinarity, from the field to the lab, and perhaps eventually to the clinic (*3*). Soon after his initial findings, Getz

---

Carl R. Woese Institute for Genomic Biology, Department of Entomology, Neuroscience Program, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA. E-mail: generobi@illinois.edu

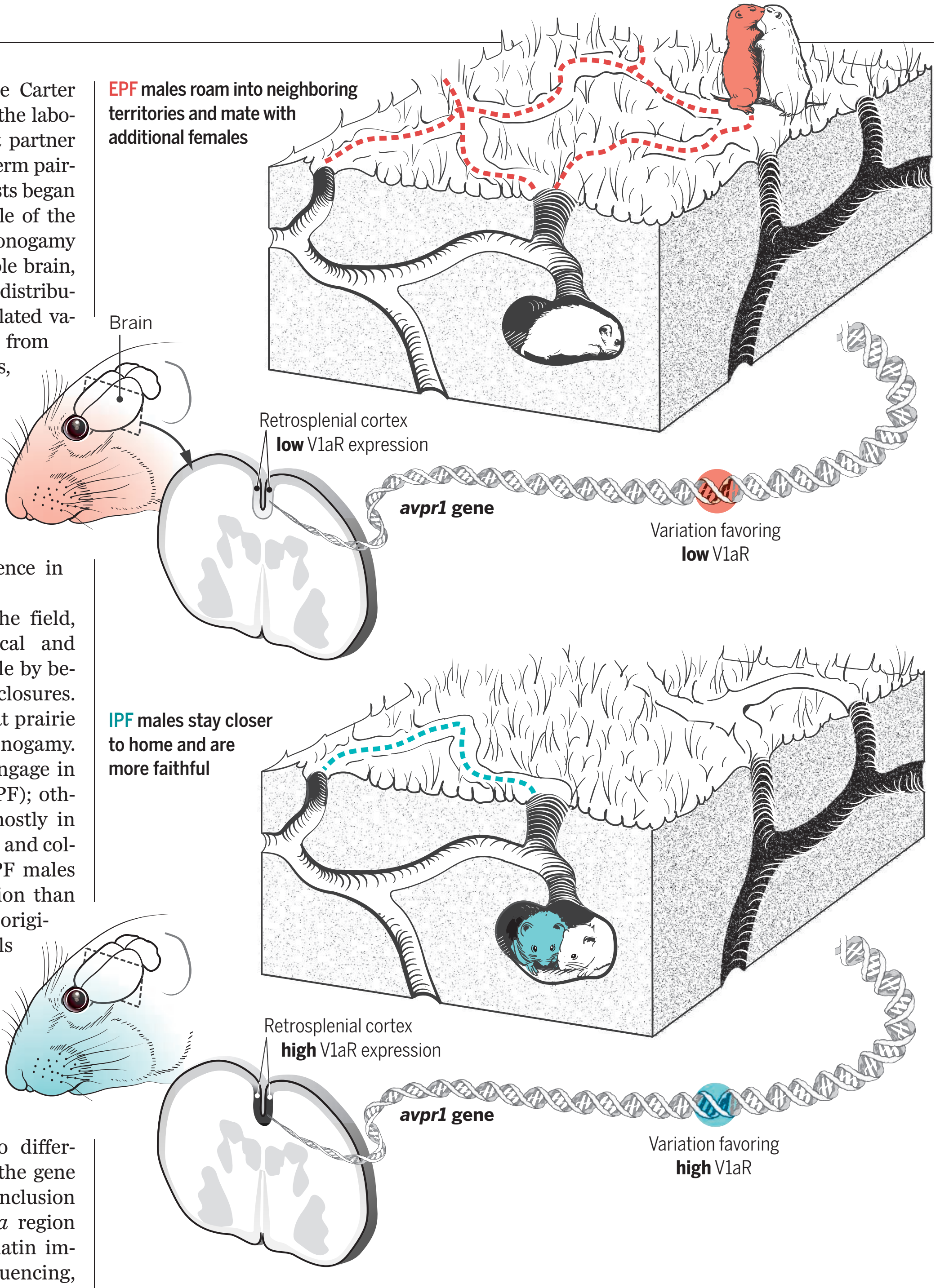
PHOTO: YVA MOMATIUK & JOHN EASTCOTT/MINDEN PICTURES/NEWSCO

Published by AAAS

teamed up with neurobiologist Sue Carter to show that prairie vole mating in the laboratory results in the kind of robust partner preference that would lead to long-term pairbonding in nature (*2*). Neurobiologists began to use prairie voles to study the role of the neuropeptide oxytocin in female monogamy (*5*). Focusing on the male prairie vole brain, Insel and Shapiro showed that the distribution of a receptor for the closely related vasopressin, V1aR, differed strikingly from closely related polygynous species, with a hot spot of expression in the ventral pallidum, a part of the basal ganglia known to mediate reward and motivation (*3*). Insel, Young, and their co-workers demonstrated that increased V1aR expression in the ventral pallidum increased partner preference in transgenic voles and mice (*3*).

Okhovat *et al.* now return to the field, blending genomics with ecological and evolutionary analyses made possible by behavioral studies in seminatural enclosures. They take advantage of the fact that prairie voles differ in their degree of monogamy. Some stray from their mate and engage in frequent extra-pair fertilization (EPF); others are more faithful, engaging mostly in intra-pair fertilization (IPF). Phelps and colleagues (*6*) showed earlier that EPF males have lower levels of V1aR expression than IPF males, but with a twist on the original V1aR findings: The lower levels of V1aR expression are not seen in the ventral pallidum but rather in parts of the brain involved in spatial learning, including the retrosplenial cortex.

Phelps and colleagues (*4*) confirm these findings and conclude that they are likely due to differences in the regulation of *avpr1a*, the gene encoding V1aR. They base this conclusion on DNA sequencing of the *avpr1a* region of the prairie vole genome, chromatin immunoprecipitation, bisulfite sequencing, and bioinformatic analysis. In the course of these experiments, the authors discovered four genetically linked single-nucleotide polymorphisms (SNPs) in putative enhancer regions for *avpr1a*, which puts them in the right places to influence *avpr1a* expression. They also found behaviorally related differences in methylation in various parts of the *avpr1a* gene, with enhancer methylation correlated with retrosplenial cortex *avpr1a* expression.



Degrees of faithfulness. Okhovat *et al.* report behavioral, neurobiological, genomic, and evolutionary analyses that explain individual differences in male prairie vole monogamy. They attribute the finding that less faithful (EPF) males range more widely than more faithful (IPF) males to poorer spatial memory skills, which are related to striking differences in the regulation of *avpr1a* and the expression of V1aR in the brain.

ILLUSTRATION: K. SUTLIFF/*SCIENCE*

Consistent with best practices in behavioral genetics, the authors replicated the behavior-SNP associations with animals from a different population. Nonetheless, it will be important to further examine the causal relationship between genetic and behavioral variation. Surely CRISPR/Cas9 prairie voles will not be long in coming.

Okhovat *et al.* also use radio-tracking data to show that EPF males have relatively larger home ranges, which overlap with the territories of other males. Are EPF males more amorous, gregarious, or novelty-seeking? We do not know yet, but the authors use their neuroanatomical data to argue for a more prosaic explanation: poor spatial memory.

The idea builds on an earlier suggestion (*7*) that IPF males might remember painfully well the locations of rough encounters with other males and thus stay closer to home, whereas EPF males are less inhibited by unpleasant spatial memories and continue to roam (see the figure). This speculation provided the basis for Okhovat *et al.*'s hypothesis that the well-known behavioral ecological trade-off between siring additional offspring and being cuckolded while out and about operates for prairie voles. They report a positive correlation between how often a male intrudes on a neighboring male's territory and how often his own territory is intruded upon by another wandering male. An EPF male encounters more females than IPF males and thus more opportunities for mating, but so does his partner back home. This trade-off is etched in the genome, with evidence of balancing selection for the above-mentioned *avpr1a* SNPs, but no such evidence at several other locations in the prairie vole genome.

Okhovat *et al.* propose that high population densities favor genetic variants resulting in lower V1aR expression, poorer spatial memory, and more expansive home ranges to capitalize on enhanced possibilities of extra-pair matings. Low population densities would favor the inverse of these traits. In other words, the evolutionary explanation for the persistence of both EPF and IPF males points to the very same cycles of population density that originally motivated Getz's field studies.

The study by Okhovat *et al.* impressively bridges mechanistic and evolutionary analyses to provide a detailed picture of individual differences in social behavior. Future studies should try to integrate the spatial learning and partner preference narratives for both males and females; the joint evolutionary dynamics of male and female traits must be considered to fully understand a mating system (*8*). With the availability of the prairie vole genome, future analyses also will no doubt include efforts to identify other genes that interact with *avpr1a*, in both mechanistic and evolutionary contexts (*9*). Measuring the effects of changes in population density on gene expression throughout the brain will help us better understand how nature and nurture shape social life (*10*). *M. ochrogaster* has come a long way from the traps on the prairie and clearly has much more to teach us. ■

REFERENCES AND NOTES

1. J. E. Hofmann, L. L. Getz, L. Gavish, *Am. Midland Nat.* **112**, 314 (1984).
2. C. S. Carter, L. L. Getz, *Sci. Am.* **268** (6), 100 (1993).
3. Z. R. Donaldson, L. J. Young, *Science* **322**, 900 (2008).
4. M. Okhovat *et al.*, *Science* **350**, 1371 (2015).
5. D. M. Witt *et al.*, *J. Neuroendocrinol.* **3**, 155 (1991).
6. A. G. Ophir, J. O. Wolff, S. M. Phelps, *Proc. Natl. Acad. Sci. U.S.A.* **105**, 1249 (2008).
7. S. M. Phelps, A. G. Ophir, in *Cognitive Ecology II*, R. Dukas, J. M. Ratcliffe, Eds. (Univ. of Chicago Press, Chicago, 2009), chap. 9.
8. S. Gavrilets, *Proc. Natl. Acad. Sci. U.S.A.* **109**, 9923 (2012).
9. C. C. Rittschof, G. E. Robinson, *Anim. Behav.* **192**, 263 (2014).
10. G. E. Robinson *et al.*, *Science* **322**, 896 (2008).

ACKNOWLEDGMENTS

I thank C. S. Carter, Z. R. Donaldson, L. L. Getz, and T. R. Insel for historical information, C. C. Lutz for comments that improved the manuscript, and M. Lee for expert assistance with the graphics.

10.1126/science.aad8071

DATA ACCESS

Sharing by design: Data and decentralized commons

Overcoming legal and policy obstacles

By **Jorge L. Contreras**[1]* and **Jerome H. Reichman**[2]

POLICY

Ambitious international data-sharing initiatives have existed for years in fields such as genomics, earth science, and astronomy. But to realize the promise of widespread sharing of scientific data, intellectual property, data privacy, national security, and other legal and policy obstacles must be overcome (*1*). Although these issues have attracted much attention in some circles, they have often taken a back seat to addressing technical challenges. Yet failure to account for legal and policy issues at the outset of a large transborder data-sharing project can lead to undue resource expenditures and data-sharing structures that may offer fewer benefits than hoped. Drawing on our experience with the Belmont Forum, a multinational earth change–research program, we propose a framework to help plan data-sharing arrangements with a focus on early-stage decisions including options for legal interoperability.

> *"Even if resources do not exist ... technically, there are advantages to fostering legal interoperability among distributed repositories."*

A rich literature beginning with the work of Ostrom (*2*) addresses the organization and governance of common pool resources shared by communities of users in contexts ranging from the global environment to communal living spaces. More recent work has expanded these principles to knowledge commons: collections of intangible resources, such as digital libraries, scholarly publications, and scientific data (*3*). Responding to calls for increased international scientific collaboration, several expert bodies have developed high-level principles for transborder data sharing (*4*–*6*). Although these efforts lay the groundwork for broad data-pooling initiatives, critical design decisions must be made before larger issues of governance and operation.

A SPECTRUM OF CENTRALIZATION. Although little empirical research exists on commons structures for data sharing and related costs, we have observed four basic structural models for scientific data pools along a continuum ranging from the most to the least centralized (see the table).

(i) *fully centralized*: all data are aggregated in a single, centrally managed repository;

(ii) *intermediate distributed*: repositories are distributed and separately maintained, but may be interconnected by a central access portal, share technical service components, and utilize a common data-exchange format [sometimes called a federated database system (*7*)];

(iii) *fully distributed*: repositories are maintained locally and are not technically integrated, but share a common legal and policy framework that allows access on uniform terms and conditions (legal interoperability);

(iv) *noncommons*: repositories are largely disaggregated and lack technical and legal interoperability and, at most, may share a common index.

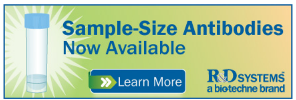
Centralized repositories with curation, analytics, and quality control can enhance the value of the data they contain [e.g., the GenBank repository of DNA and RNA sequence data (*8*)]. Centralized structures, however, come at a cost and may be impractical in many transborder collaborations because of political, legal, and organizational issues. But the alternative to a fully centralized commons need not be a noncommons. The shortfalls of noncommons models include incompatible data formats, inability to search across data sets, underutilization of data resources, individualized and inefficient access requirements, and difficulties moving data across national boundaries. Distributed commons structures, however, offer a meaningful subset of benefits with lower cost and resource commitments than fully centralized models.

For example, an online portal through which researchers can access multiple inde-

---

[1] S. J. Quinney College of Law and Department of Human Genetics, University of Utah, Salt Lake City, UT, USA.
[2] School of Law, Duke University, Durham, NC, USA.
*E-mail: jorge.contreras@law.utah.edu

EXTENDED PDF FORMAT
SPONSORED BY



Sample-Size Antibodies
Now Available
Learn More
R&D SYSTEMS
a biotechne brand
www.rndsystems.com

Dissecting diversity in the social brain

Gene E. Robinson

Science **350**, 1310 (2015);
DOI: 10.1126/science.aad8071

This copy is for your personal, non-commercial use only.

If you wish to distribute this article to others, you can order high-quality copies for your colleagues, clients, or customers by clicking here.

Permission to republish or repurpose articles or portions of articles can be obtained by following the guidelines here.

The following resources related to this article are available online at www.sciencemag.org (this information is current as of December 10, 2015):

Updated information and services, including high-resolution figures, can be found in the online version of this article at:
http://www.sciencemag.org/content/350/6266/1310.full.html

A list of selected additional articles on the Science Web sites **related to this article** can be found at:
http://www.sciencemag.org/content/350/6266/1310.full.html#related

This article **cites 9 articles**, 5 of which can be accessed free:
http://www.sciencemag.org/content/350/6266/1310.full.html#ref-list-1

This article appears in the following **subject collections:**
Evolution
http://www.sciencemag.org/cgi/collection/evolution

Downloaded from www.sciencemag.org on December 11, 2015

Science (print ISSN 0036-8075; online ISSN 1095-9203) is published weekly, except the last week in December, by the American Association for the Advancement of Science, 1200 New York Avenue NW, Washington, DC 20005. Copyright 2015 by the American Association for the Advancement of Science; all rights reserved. The title *Science* is a registered trademark of AAAS.