
Commentary | Cognition and Behavior

Of Mice and Men: Empirical Support for the Population-Based Social Epistasis Amplification Model (A Comment on Kalbassi et al., 2017)

Of Mice and Men

Matthew Alexander Sarraf¹ and Michael Anthony Woodley^{2,3}

¹*University of Rochester, Rochester, NY 14627, USA*

²*Center Leo Apostel for Interdisciplinary Studies, Vrije Universiteit Brussel, Krijgskundestraat 33, Brussels, B-1160, Belgium*

³*Unz Foundation, Palo Alto, California*

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Correspondence should be addressed to Michael A. Woodley of Menie, email: michael.woodley@vub.ac.be

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5 Matthew Alexandar Sarraf, University of Rochester, Rochester, NY, 14627

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7 Michael Anthony Woodley of Menie, Center Leo Apostel for Interdisciplinary Studies, Vrije
8 Universiteit Brussel, Krijgskundestraat 33, B-1160 Brussels, Belgium; and Unz Foundation, Palo
9 Alto, California. michael.woodley@vub.ac.be

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29 Significance Statement:

30 This commentary article offers new perspective on recent research investigating the behavioral
31 and social ecological effects of a mutation related to autism spectrum disorders in mice. The
32 authors explain the consistency of this research on mice with predictions advanced by a theory of
33 the role of interorganismal gene-gene interactions (social epistasis) in social species including
34 humans, known as the social epistasis amplification model. The potential significance of the
35 mouse research for understanding contemporary human behavioral trends is explored.

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38 Kalbassi et al. (2017) examined whether and how mice carrying a behavior-altering mutation
39 change their social ecologies. Specifically, the authors investigated the effect of deletion of the
40 gene *Nlgn3*, which is related to autism spectrum disorders, on the phenotypes of both “*Nlgn3*
41 knockout mice” and their “wild-type littermates” (i.e. mice without the deletion of *Nlgn3*) with
42 which they were raised (p. 1). The authors determined that litters containing male mice both with
43 (*Nlgn3*^{−/−}) and without (*Nlgn3*^{+/+}) deletion of *Nlgn3* were substantially different from litters
44 containing only *Nlgn3*^{+/+} mice (the authors also examined litters containing only *Nlgn3*^{−/−} mice
45 and various litters of female mice, but this comment does not focus on these cases). Among the
46 more striking findings are that the genotypically mixed compared to homogeneous litters lacked
47 “a structured social hierarchy” (p. 9) and had lower levels of testosterone (in both *Nlgn3*^{−/−} and
48 *Nlgn3*^{+/+} mice); additionally, *Nlgn3*^{+/+} mice from genotypically homogeneous litters showed more
49 interest in “social” as opposed to “non-social cues” (p. 9) than *Nlgn3*^{+/+} mice from genotypically
50 mixed litters (the latter did not show a preference for one type of cue over the other, “showing an
51 absence of interest for social cues” [p. 9]). However, “re-expression of *Nlgn3* in parvalbumin-

52 expressing interneurons in *Nlgn3*^{y/-} mice rescues their social submission phenotype and the
53 corresponding effect on the wild-type littermates” (p. 2). The authors infer that their findings,
54 taken collectively, indicate not only an effect of deletion of *Nlgn3* on the phenotypes of mice
55 carrying the mutation, but also on *Nlgn3*^{y/+} mice with which the carriers are raised. (Kalbassi et
56 al. [2017] also note that it appears not only that *Nlgn3*^{y/-} mice affect the phenotypes of *Nlgn3*^{y/+}
57 mice, but that the latter affect the phenotypes of the former.)

58

59 These results should be considered in the context of the broader body of theoretical and
60 empirical work with which they are consistent. Most saliently, a paper published earlier this year
61 integrated a great deal of research on social epistasis, i.e. interorganismal gene-gene interactions,
62 and mutation load in humans, mice, and other organisms to develop the novel thesis that the
63 fitness costs of the accumulation of certain kinds of deleterious mutations under conditions of
64 relaxed negative selection in humans are externalized onto non-carrier individuals and thereby
65 amplified via the damage that these mutations do to populations’ “group-level extended
66 phenotype[s]” (Woodley of Menie, Sarraf, Pestow & Fernandes, 2017). This theory, which was
67 termed the *social epistasis amplification model*, is based partly on the biological literature
68 concerning eusocial insects, in which the term “social epistasis” was coined (Linksvayer, 2007).
69 Research on such insects has found that the adaptively optimal development of members of
70 different castes in insect societies depends on certain inter-caste genotypic interactions, or social
71 epistases. Thus both the individual- and group-level fitness of eusocial insects, insofar as both
72 are contingent on (inter- and intra-) caste structure and cooperation, depend upon the existence of
73 particular social distributions of genotypes and epistatic interactions among them. This fact
74 suggests the possibility that, as a general rule, social species, including humans, require certain

75 patterns of interorganismal genetic interaction to achieve and maintain adaptive optima at the
76 individual and group levels.

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78 In the same way that the *Nlgn3*^{+/−} mice damaged their immediate community ecology, e.g. by
79 inhibiting the development of normal social hierarchies and driving down the testosterone levels
80 of their *wild-type* litter-mates, it is possible that the carriers of behavior-altering mutations in
81 contemporary human populations reduce the fitness of their non-carrier counterparts and depress
82 group-level fitness overall in a similar fashion. The mutations characterized by Kalbassi et al.
83 (2017) were hypothesized to exist in Woodley of Menie et al. (2017), where they were described
84 with the term *spiteful mutations*. Such mutations degrade the fitness of their carriers, but also
85 incur opportunity costs on the fitness of conspecifics with whom they enter into social epistatic
86 transaction, e.g. by imposing sociocultural conditions that disincentivize procreation (note,
87 Kalbassi et al. [2017] found that the “courtship behavior” [p. 9] of *Nlgn3*^{+/+} mice was not
88 suppressed by exposure to *Nlgn3*^{+/−} mice, indicating that deletion of *Nlgn3* reduces fitness, to the
89 extent that it does, mostly via interference with social dominance behavior). Woodley of Menie
90 et al. (2017) ran population-based models to explore the effects of spiteful mutations, which
91 found that under relaxed negative selection, these mutations reach fixation because population
92 growth offsets their individual-level fitness costs. But once a critical prevalence of mutations is
93 present, their negative impact on the fitness of non-carriers causes rapid population decline. With
94 negative selection against the carriers of these spiteful mutations restored, population growth
95 continues until a stable equilibrium is established. Thus Kalbassi et al. (2017) found, as Woodley
96 of Menie et al.’s (2017) model predicts, that restoration of adaptive behavior occurred in mouse

97 communities when *Nlgn3* was re-expressed in *Nlgn3*^{+/−} mice (this restoration simulates the
98 effects of negative selection as reflected in Woodley of Menie et al.'s [2017] model).

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100 Further, there is much empirical evidence that some human populations are experiencing
101 increasing loads of behavior-altering, and fitness-reducing, mutations. In Western populations,
102 the prevalence of a number of mental disorders associated with advanced paternal age (because
103 older fathers bequeath more mutations to their offspring than younger ones [Rahbari et al.,
104 2016]), most notably unipolar depression (Laursen et al., 2007) and autism (Kong et al., 2012),
105 has substantially increased from the 20th to 21st centuries (Twenge et al., 2010; Demeneix, 2017,
106 p. 97). Furthermore, schizophrenia, another disorder associated with paternally acquired *de novo*
107 mutations (Malaspina, 2002), may have been extremely rare prior to AD 1800 (Hare, 1988), but
108 became more common thereafter, possibly because 19th century industrialization lowered the
109 fitness costs associated with the disease. These secular trends, and others suggesting a rising rate
110 of sub-clinical behavioral abnormalities also (e.g. Greenfeld, 2013, pp. 621-622), could indicate
111 a growing prevalence of spiteful mutations in these populations. Additionally, Kalbassi et al.'s
112 (2017) linking of the presence of *Nlgn3*^{+/−} mice to testosterone decline across the board in their
113 communities yields a compelling potential explanation for the observation of significantly
114 declining testosterone levels in Western males (Travison et al., 2007) and, perhaps resultantly,
115 diminished sperm quality, which has been falling precipitously for at least the past few decades
116 (Levine et al., 2017). Certain cultural changes, such as secularization, have also been connected
117 to fertility decline at the group and individual levels (Meisenberg, 2011), and there is also
118 evidence that irreligiosity is associated with behavioral and physical abnormalities indicative of
119 higher relative burdens of deleterious mutations (E.C. Dutton, personal communication).

120 Religion is a group-level adaptation in humans (Wilson, 2002), as is social hierarchy in mice
121 (van den Berg, Lamballais & Kushner, 2015). Thus the carriers of spiteful mutations may disrupt
122 the patterns of social epistasis that sustain religiosity and other group-level adaptations, and
123 consequently lower fitness.

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125 Woodley of Menie et al. (2017) predicted that results similar to Kalbassi et al.'s (2017) would be
126 found in mice subjected to the proper experimental design. Kalbassi et al. (2017) are to be
127 commended for devising a better procedure than that contained in the provisional experiment
128 offered by Woodley of Menie et al. (2017) — which was based on a variant of the “mouse
129 utopia” experiments of Calhoun (1973) — wherein two mice colonies were to be bred under
130 cornucopian conditions. The colony serving as a control would be an effective replication of
131 Calhoun's own “mouse utopia,” where, like Calhoun's colony, the mouse population would
132 presumably cycle through to collapse. However, the experimental colony would be treated with
133 *CRISPR* (a gene-editing technology) to remove deleterious mutations. If the experimental colony
134 could be indefinitely sustained and avoid the population collapse of the control colony, this
135 would strongly evidence that deleterious mutation accumulation, permitted by conditions of
136 minimized morbidity and mortality, is the cause of the control colony's breakdown. Since
137 Kalbassi et al. (2017) observed that adaptive behavior was restored in communities with both
138 *Nlgn3^{y/-}* and *Nlgn3^{y/+}*, and that restoration occurred in both types of mice, when *Nlgn3* was re-
139 expressed in *Nlgn3^{y/-}* mice, they have effectively demonstrated what Woodley of Menie et al.'s
140 (2017) proposed experiment was predicted to show.

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142 Finally, an interesting extension of the experiments of Kalbassi et al. (2017) would be to set up
143 competition over limited resources (such as restricted access to food, territory, etc.) between
144 differentially tagged groups of male mice (one group genotypically heterogeneous [containing
145 $Nlgn3^{y/+}$ and $Nlgn3^{y/-}$ mice] and the other homogeneous [containing only $Nlgn3^{y/+}$ mice]). Given
146 the suppressing effect of the presence of $Nlgn3^{y/-}$ mice on the testosterone levels of their *wild-*
147 *type* littermates, and given the hierarchy avoidant behaviors that result, it is predicted that the
148 homogeneous colony should outcompete the heterogeneous one indicating greater group-level
149 fitness. Competing differentially tagged groups of mice that are composed only of $Nlgn3^{y/+}$ mice
150 could serve as a control for such an experiment, as the outcome of the latter competition in terms
151 of which group gains the upper-hand should be due to contingent factors and would therefore
152 essentially be random.

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