Wakefield (1999a; 2005) has argued that mental disorders can only be classified as such when they are harmful dysfunctions. A *dysfunction* is a failure of a mechanism to perform as it was designed by natural selection. According to this definition, the disorder cannot be the function of a naturally selected mechanism. Therefore, a dysfunction of jealousy mechanisms would occur when they failed to motivate behaviors designed to prevent a partner's infidelity. Individuals diagnosed with morbid jealousy do deploy behaviors that function to prevent partner infidelity, even if the cues that activate the jealousy mechanisms are imagined by the individual. Perhaps morbid jealousy does not meet the dysfunction criterion and therefore should not be considered a mental disorder.

Wakefield's (1999a; 2005) harmful dysfunction analysis specifies a second criterion that must be met for a mental disorder to be considered as such. The disorder must generate harm, as defined by society. To conclude that morbid jealousy is not a disorder without assessing the associated harm would be a mistake, according to the harmful dysfunction analysis. Lives are disrupted, including the lives of the morbidly jealous individuals themselves as they constantly monitor their partner's behavior (e.g., Seeman 1979). Substantial stress is added to the relationship as morbidly jealous individuals constantly accuse their partner of infidelity (e.g., Vauhkonen 1968). Potential rivals may be derogated or attacked, partners of the morbidly jealous may be psychologically and physically abused, and sometimes this assault escalates to murder (e.g., Kingham & Gordon 2004; Mowat 1966; Shepherd 1961). Although morbid jealousy is harmful, is it more harmful than normal sexual jealousy? In fact, the greatest predictor of intimate partner homicide is sexual jealousy (Daly & Wilson 1988). It is possible that morbidly jealous individuals are more abusive toward their partners or are more likely to murder them than are individuals who experience normal sexual jealousy, but research has not investigated this possibility.

Morbid jealousy may be explained best not as a discrete categorical mental disorder, but as a continuation of normal sexual jealousy. Before this determination can be made, however, several factors must be examined (J. C. Wakefield, personal communication, March 20, 2006). First, we need to determine whether the morbid jealousy tail of a normal curve hides discrete points of jealousy disorders. For example, there are many causes of low intelligence. However, a smooth normal curve of intelligence would group these distinct causes together and would hide the individual causes of low intelligence. The same might be true of a normal sexual jealousy curve. Examining individual cases of morbid jealousy and comparing the symptoms and behaviors could help determine whether a normal sexual jealousy curve is grouping together distinct causes of morbid jealousy. If there are not multiple, distinct cases of morbid jealousy, then it could be argued that morbid jealousy is a continuation of normal sexual jealousy.

Second, we need to determine whether the morbid jealousy end of a sexual jealousy curve is fitness enhancing. Previous research has documented the adaptive benefits of normal sexual jealousy; notably, that it may prevent partner infidelity (e.g., Buss 2000). If morbid jealousy has similar adaptive benefits, this might provide further evidence that it should be viewed as part of a continuum of normal sexual jealousy.

Third, morbid jealousy may not be produced by a dysfunction of jealousy mechanisms, but instead by a dysfunction of related mechanisms. For example, individuals with morbid jealousy may have dysfunctions in mate-retention mechanisms. If this is the case, then morbid jealousy could not be considered continuous with normal sexual jealousy, as these related dysfunctions do not occur with sexual jealousy. This third issue could be investigated by examining individuals diagnosed with morbid jealousy to determine whether they have other, related dysfunctions.

Whether morbid jealousy is a discrete categorical mental illness or part of a continuum of normal sexual jealousy remains to be determined. We have discussed three research questions that could help address this question. Investigation of these questions through careful examination of individuals with morbid jealousy may lead to clarification of delusional disorder–jealous type, and may represent a model that could be used to clarify other mental disorders. Additionally, this clarification should lend support to continued use of the adaptationist approach and should provide a better understanding for the continued prevalence of disorders.

Mutations, developmental instability, and the Red Queen

Steven W. Gangestad and Ronald A. Yeo

Department of Psychology, University of New Mexico, Albuquerque, NM 87111.

sgangest@unm.edu **ryeo@unm.edu**

Abstract: We address two points. First, one must explain how different, rare mutations ultimately lead to common psychopathological conditions. The developmental instability model offers one solution. Second, Keller & Miller (K&M) perhaps miss the major processes other than variation fueled by rare deleterious mutations that account for interesting genetic variation in psychopathology, particularly when single alleles have non-negligible effects: Red Queen processes.

Keller & Miller (K&M) argue that much heritable variation in psychopathological conditions is fueled by deleterious mutation, rare at individual loci but ubiquitous in genomes. Ron Yeo, colleagues, and I offered a similar view a decade ago (Gangestad 1997; Gangestad & Yeo 1997; Thoma et al. 2002; Yeo & Gangestad 1993, 1998; Yeo et al. 1997, 1999), albeit less broadly applied to neurodevelopmental disorders (e.g., schizophrenia, dyslexia, attention deficit disorder). K&M do an excellent job of making this case.

Our quibbles pertain to details. We focus on two. First, mutations at many loci produce phenotypic variants much more common than individual mutations. Our model, curiously not mentioned by K&M, may explain how they do so. Second, K&M perhaps miss the most important alternative processes accounting for interesting genetic variation in psychopathology, particularly when single genes account for non-negligible ($>1\%$) variance.

The developmental instability model. Mutations at individual loci are rare. Neurodevelopmental disorders are much more common. A successful theory must explain how different mutations can produce similar outcomes. Though K&M discuss how different "upstream," specific defects can have common "downstream" effects (sect. 6.2), they do not present a particularly compelling, specific model for how this happens.

We have suggested one route: developmental imprecision. Microcircuitry of a computer chip must be manufactured in a dust-free environment, for only then can its design be actualized. Dust that inadvertently becomes part of the chip can affect the functioning of the circuitry in random ways, disrupting design. Similarly, mutations and other developmental stresses can act as "dust" in the environment in which epigenetic processes "manufacture" an organism's phenotype, introducing *developmental instability* and deviations from naturally selected design.

Neurodevelopmental errors may disrupt adaptive coordination of a broad array of processes within developmental systems, particularly as their frequency increases. As disrupted development may channel along particular paths, different perturbations (e.g., mutations) may ultimately have common outcomes. K&M argue that more than half of all human protein-coding genes are expressed in brain tissue and, hence, neural systems capture a large amount of mutational variation. As genes that affect

https://doi.org/10.1017/S0140525X06309090 Published online by Cambridge University Press

neural development need not be expressed in brain cells per se, however, mutations across an even larger proportion of the genome may affect neurodevelopmental disorders. As this theory expects, neurodevelopmental disorders covary with markers of developmental disruption or instability (e.g., minor physical anomalies and fluctuating asymmetry; see Yeo et al. 1999).

Disorder-specific features may arise because disruptions have different outcomes depending on their timing or differentially affect specific neural systems. Alternatively, disorders may be affected by specific factors in addition to developmental instability (see Yeo et al. 1999).

Antagonistic coevolutionary processes. K&M contrast three different kinds of evolutionary models of genetic variation: *mutation-selection balance*, *neutral variation*, and *balancing selection* – maintenance of variation because selection actually favors multiple alleles (e.g., through heterozygote superiority, spatiotemporal oscillations in selection, and frequency-dependent selection). But a fourth possibility they do not mention exists: rapid evolution at loci, particularly those involved in *antagonistic coevolutionary processes*.

Species may antagonistically coevolve with other species (e.g., in predator-prey or host-pathogen roles). New adaptations in one species evoke selection on the other to evolve counteradaptations. Antagonistic coevolution (or Red Queen processes; Van Valen 1973) may persist through evolutionary time, resulting in continual change in both species. Genetic conflicts of interest between males and females, mothers and fetuses, or pairs of cooperators may fuel persistent antagonistic coevolution of genes *within a species*, as well (Rice & Holland 1997).

Red Queen processes produce predictable evolutionary outcomes: (1) *Relatively rapid evolution*: Because new adaptations in a coevolving party change selection on the other party, alleles at coevolving loci should be subject to new positive selection relatively frequently (e.g., Swanson et al. 2001; Wyckoff et al. 2000). (2) *Interindividual variation*: More often than most loci, coevolving loci should be in states in which a new, favored allele has not yet become near-fixed in the population and coexist with alleles favored previously. (3) *A non-negligible level of maladaptation within populations*: Neither conflicting party is likely to adapt perfectly to the other party. The load of maladaptation will be carried disproportionately by individuals who lack newly favored alleles.

A Red Queen process that might explain some variation in psychopathological conditions is maternal-fetal coevolution (see also Gangestad & Yeo 1997). Fetal genes maximally benefit from a greater flow of nutrients from the mother than the level maximizing maternal fitness (Trivers 1974). Maladaptive outcomes of pregnancy (e.g., maternal hypertension, gestational diabetes) may be by-products of ensuing antagonistic coevolution (Haig 1993). Maladaptive by-products could include disruption of fetal epigenesis, resulting in neurodevelopmental disorder. In this model, some fetal genes associated with poor development (e.g., developmental instability) now once were not, for they once did not coexist with current maternal genes that promote counteradaptation. (The model is akin to spatially varying selection, but not as a form of balancing selection; cf. target article, sect. 5.3.)

Some fetal genes involved in this conflict are imprinted – expressed differently depending on parent-of-origin. Imprinting is selected because fetal genes from fathers are also in conflict with those obtained from mothers (Haig 2000). Among genes that account for more than a negligible amount of variance in psychopathology, imprinted genes (or other genes involved in the imprinting process; e.g., genes that control imprinting; Burt & Trivers 2000) may be over-represented, for example, on schizophrenia, autism, or bipolar disorder (see Bah et al. 2004 [GRIK2]; Corradi et al. 2005 [GNAL]; DeLisi et al. 2002 [chromosome 22]; Francks et al. 2003 [chromosome 2]; Xu et al. 2001 [CHRNA7]); on attention-deficit hyperactivity disorder (ADHD) (see Borglum et al. 2003 [dopa decarboxylase]; Hawi et al. 2005 [9 genes putatively associated with ADHD]; Kirley et al. 2002 [TH]; Mill et al. 2004 [SNAP-25]). Only a few percent of genes are imprinted (on the mouse genome, see Luedi et al. 2005).

Findings in linkage studies have historically been fragile. Cautious interpretation is advised. Nonetheless, even if most variation in psychopathology is a result of rare mutation, some single genes probably do have non-negligible effects. One evolutionary theory K&M do not mention points toward genes involved in Red Queen processes.

Autism: Common, heritable, but not harmful

Morton Ann Gernsbacher,[a] Michelle Dawson,[b] and Laurent Mottron[b]

[a]*Department of Psychology, University of Wisconsin–Madison, Madison, WI 53706;* [b]*Pervasive Developmental Disorders Specialized Clinic, University of Montreal, Hôpital Rivière-des-Prairies, Montreal QC H1E 1A4, Canada.*

MAGernsb@wisc.edu **http://www.gernsbacherlab.org**
naamichelle@yahoo.ca **http://www.sentex.net/~nexus23/naa_02.html**
mottronl@istar.ca
http://www.psychia.umontreal.ca/recherche/chercheur/mottron.htm

Abstract: We assert that one of the examples used by Keller & Miller (K&M), namely, autism, is indeed common, and heritable, but we question whether it is harmful. We provide a brief review of cognitive science literature in which autistics perform superiorly to non-autistics in perceptual, reasoning, and comprehension tasks; however, these superiorities are often occluded and are instead described as dysfunctions.

We appreciate Keller & Miller (K&M) grappling with the age-old evolutionary paradox of why certain human phenotypes are so common, so heritable, but so harmful. In their treatise, K&M provide several examples of what they refer to as mental disorders, clumping together numerous phenomena, including schizophrenia, bipolar disorder, depression, phobias, panic disorders, Tourette's syndrome, obsessive-compulsive disorder, low intelligence, anorexia, and autism. We – a cognitive scientist, a research psychiatrist, and an autistic (who conducts cognitive science research) – are most interested in K&M's inclusion of autism. Therefore, we restrict ourselves to that exemplar, agreeing that autism is common and heritable but questioning whether autism is harmful.

Autism is definitely a common phenotype – even more common than K&M report. Current prevalence estimates are 200 per 100,000 for DSM-IV (American Psychiatric Association 1994) defined "autistic disorder" and around 600 per 100,000 for the entire autism "spectrum" (Chakrabarti & Fombonne 2005). A rash of public attention has spotlighted what are considered dramatic recent increases in autism prevalence, but our most reasoned logic suggests that the increases are due to purposely broadened diagnostic criteria, yoked with dramatically raised public awareness and conscientiously improved case finding (Gernsbacher et al. 2005). And when some lay spokespersons mistakenly suggest that autism first appeared in society only in the 1940s (Kennedy 2005), they are confusing the codification of the phenotype with its onset (see Frith [1989] for a convincing, albeit speculative, history of autism in society).

Autism is also a highly heritable phenotype, based on estimates from twin studies and sibling-recurrence rates. However, the existing heritability estimates warrant caution in interpretation. The twin-based estimates are derived from only a handful of studies, which are based on only a few handfuls of twins, and estimating sibling recurrence requires a reliable population prevalence rate.

But is autism a "harmful" phenotype? Primarily, K&M employ an evolutionary connotation of *harmful*, namely,

https://doi.org/10.1017/S0140525X06309090 Published online by Cambridge University Press