de-ubiquitinated for recycling to the plasma membrane or sent to a degradation pathway?

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Department of Biological Chemistry, Molecular Biology Institute and Jonsson Comprehensive Cancer Center, David Geffen School of Medicine at UCLA, Los Angeles, CA 90095, USA.
E-mail: colicelli@mednet.ucla.edu

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Primatology: "A Faithful Friend Is the Medicine of Life"

Close, stable social bonds enhance longevity in wild baboons, providing clues about the importance of social bonds in our own evolutionary history.

Susan C. Alberts

One of the mysteries of social evolution is the emergence, in evolutionary history, of close, enduring social bonds in animal groups. Neither of the two main proposed functions of group living — the protection from predation that comes with increased numbers, or the increased access to food that comes with shared defense and knowledge of resources [1–3] — obviously requires the well-differentiated social bonds that animals of many species, notably primates, develop. Anyone who has watched a group of primates for any length of time has surely been struck by the attention that animals in these groups pay to distinguishing their close associates — their 'friends' — from others, and to nurturing their close bonds. What evolutionary forces have shaped the pursuit of these bonds?

Joan Silk and her colleagues have been digging into this question for several years. In earlier work they demonstrated, in two different populations of baboons, that females with stronger social bonds experience higher survival of their infants [4,5]. Writing in this issue of *Current Biology*, they have extended these results to show that females with stronger and more stable social bonds also experience greater longevity themselves (Figure 1) [6]. Moreover, the effect of close, stable bonds is independent of the effect of dominance rank, which also contributed to longevity in the study. Survival and longevity are a major component of Darwinian fitness — all else being equal, individuals that live longer will produce more offspring and have higher fitness that those that die young. Thus, this new study provides a strong basis for inferring natural selection on the development and maintenance of close social bonds.

This is a remarkable result, which has some interesting and important parallels in human biomedical research. Research in the past several decades has revealed striking associations between loneliness and social isolation on the one hand, and health and wellness on the other. Among the most robust of these is a link between loneliness and survival after heart attacks [7], but data on a number of other health indicators and physiological measures show that people who experience social isolation have poor health outcomes in a number of contexts, as well as elevated physiological indicators of stress [6,8–10]. Social contact has also been shown to have an ameliorating effect on physiology in a number of animals, including laboratory rodents, monkeys, and domestic companion animals [11,12].

An effect of social isolation on longevity (as opposed to an effect on health, or on survival after trauma or illness) in a healthy cohort has not been frequently documented (but see [13]). This current study [6] not only calls for more such analyses, it points to deep evolutionary roots for the functional consequences of social connectedness in our species.

What is the mechanism by which social bonds function to enhance the survival of individual baboons and their offspring, independent of the effect of dominance rank? Silk and colleagues [6] point to the ameliorating effects of social ties on stress and adrenocortical function as the likely mechanism that ties social bonds to longevity. But why should we have a built-in vulnerability of this sort, a predisposition towards social bonding that is so great that without strong and stable social bonds our physiological functioning is compromised to the point of reduced survival? Surely it would be better, from an evolutionary perspective, to build an organism that could suffer the slings and arrows of outrageous fortune without the need of a close friend to talk about it with — or, in the case of baboons, to groom with and be near afterwards?

The study by Silk and colleagues [6] cannot answer this question. It does not resolve the question posed at the beginning of this dispatch of why social bonds evolved in the first place. Identifying the current function for a trait does not necessarily provide information about how that trait arose. In the case of social bonds for human and non-human primates, one would have to hypothesize that not having them would make the animal so vulnerable to predation, disease or starvation that a physiological drive to form bonds would evolve. But it remains unclear just how strong, differentiated and stable social bonds would substantially reduce predation or disease risk or enhance food or resource acquisition, beyond what is accomplished simply by living with and staying near conspecifics in groups.

The possibility that such bonds enhance the development of cooperative alliances among animals, that this enhancement acts independently of dominance rank and that these alliances in turn increase an animal's ability to locate and defend resources, remains a live hypothesis for the origin of social bonds [14]. This hypothesis is more difficult to test than it seems: it would require identifying variation — preferably both within and between species — in the strength and stability of social bonds among individuals, and linking that variation to variation in the efficacy of resource acquisition, independent of dominance rank. The number of potential confounding variables, and the problem of identifying causation rather than simple correlation, present daunting hurdles for a biologist interested in this hypothesis, but it should be tested.

An alternative hypothesis is that the need for close social bonds is a by-product of the need for a close mother–offspring bond, the functional consequences of which are more obvious. Possibly, the mother–offspring bond is of such importance that it entrains a set of processes that persist throughout the lifetime, creating a physiological need for bonds to replace that original one, long after the function of the original bond has ceased. In any case, the maintenance of such bonds across a wide range of primate species with varying ecologies points to some crucial function of well-differentiated, close and stable social bonds — not just simple aggregations — in the evolutionary history of primates.

A final, critical point this paper [6] highlights is the value of long-term biological research on natural animal populations [15]. The Moremi baboon population, the subject of this study, was under continuous observation for 30 years; for the last 15 of these years the research was led by Dorothy Cheney and Robert Seyfarth at University of Pennsylvania [16]. Endeavors of this nature require sustained and patient effort and a strong, often life-long commitment on the part of the lead researchers. They are usually carried on in the face of daunting logistical and funding challenges. The odds are against their continuation, especially given the paucity of explicit mechanisms for long-term funding. Yet in an era where the quantity of genomic and genotypic data is increasing at a rapid rate, good phenotypic data, essential for making the most of the genotypic information, will be seen as more and more valuable. Long-term field studies are an unparalleled source of detailed phenotypic data and should be cultivated for that reason, and because they represent the best opportunity for a deep understanding of behavior in the context of ecology and life history.

Figure 1. Yellow baboon females and infant in Amboseli, Kenya.

Female baboons form strong, stable social bonds, which they express through affiliative interactions such as grooming, support during aggressive interactions, and maintaining proximity to each other. Silk and colleagues [6] found that such social bonds contribute to longevity in a different species, the chacma baboons of southern Africa.

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Department of Biology, Duke University, Box 90338, Durham NC 27708, USA.
E-mail: alberts@duke.edu

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Cell Cycle: Deconstructing Tension

Prior to anaphase, sister chromatids must be attached to microtubules and under tension, a condition that satisfies the spindle checkpoint. Removal of sister chromatid cohesion is predicted to cause a fall in tension. Two studies shed light on how cells avoid re-activation of the spindle checkpoint when cohesion is lost.

Andrea Musacchio

The early life of sister chromatids, in the aftermath of DNA replication, is spent in the reassuring embrace of cohesion. Being prevented from loosing sight of each other, the sisters align as a pair on the mitotic spindle (metaphase). At this point, cohesion is removed and the sisters are abruptly parted to opposite spindle poles. As shocking as it may be, the separation of sisters at the metaphase–anaphase transition is for good. Failing to part sisters creates imbalances in chromosome numbers that derange cell physiology and put the rest of the family in jeopardy. Thus, when it comes to separating sisters, cells are quite inflexible and want to do it properly.

Chromosomes attach to the mitotic spindle at kinetochores. These large protein scaffolds, built on centromeric DNA, promote the formation of load-bearing attachments to spindle microtubules [1]. They also regulate feedback control mechanisms required for errorless sister chromatid separation. The first mechanism, error correction, repairs erroneous connections of kinetochores with spindle poles, such as syntelic (both sisters bound to the same pole) or merotelic (one sister bound to both poles) attachment. Likely, correction implies severing the incorrect connections, thus transiently generating unattached kinetochores. This, in turn, provides chromosomes with a new chance to bi-orient, i.e., reaching the correct configuration in which the sisters are bound to opposite spindle poles [2]. The second mechanism, the spindle assembly checkpoint, acts to synchronize mitotic exit to the achievement of bi-orientation of chromosomes on the mitotic spindle. Under normal conditions, the checkpoint becomes satisfied when all chromosomes are bound to spindle microtubules and bi-oriented. Once cells have transited through this obligatory step, sister chromatid cohesion can be removed [2].

The relationship between tension-dependent error correction and the spindle checkpoint is conceptually challenging and controversial. Based on pioneering studies by Nicklas on meiosis I spindles (reviewed in [2]), it was realized that tension stabilizes kinetochore–microtubule attachments, and that lack of tension favors error correction. Thus, a fundamental distinction between correct and incorrect attachments is that the former generate tension in the kinetochore and centromere region and are selectively stabilized, whereas the latter fail to do so and will eventually fall off. Understanding the molecular basis of this process is one of the current challenges in kinetochore biology. It has also largely become accepted that lack of microtubule attachment activates the checkpoint. The dispute concerns the role of tension (or lack thereof) in the spindle checkpoint. Three main models are crossing horns (Figure 1A). In Model 1, lack of tension acts indirectly on the checkpoint by promoting an error correction activity that ultimately generates unattached kinetochores (i.e., kinetochores that are devoid of microtubules). The latter, in turn, signal to the checkpoint. This model pictures the checkpoint and error correction as completely distinct but interconnected devices, purely sensing attachment and tension, respectively [3]. In Model 2, lack of tension acts directly on the checkpoint and on error correction regardless of whether unattached kinetochores are present. The checkpoint is imagined as consisting of two pathways, one sensing tension and one sensing attachment, and both possibly converging on the creation of the same effector complex. Finally, Model 3 makes the same assumptions