els. Indeed, a growing body of North American research shows that men involved in affiliative relationships with a female partner and direct paternal care tend to have lower testosterone levels. Here, we extend the cross-cultural scope of this research to Ariaal pastoralists of northern Kenya. The Ariaal present an interesting test case because marital relations tend to be aloof and direct paternal care minimal by cross-cultural standards, polygyny is prevalent and increases with age and the age set system highly structures the transition to marriage. To test predictions, we recruited 205 men aged 20 and older from both a settled agropastoral community and nomadic populations. Each participant provided morning and afternoon saliva samples in which testosterone levels were measured, provided demographic background during interviews and had anthropometrics taken. As predicted, during the dynamic ages (20-39) of transition from life as a bachelor and warrior to monogamous marriage, men with one wife had significantly lower testosterone levels than unmarried men. Contrary to prediction, however, polygynously married men did not have higher testosterone levels than their monogamously married counterparts. These results held after controlling for potentially confounding effects of age, body composition and residential status. These data lend further support to the framework that male testosterone levels reflect, in part, variation in male mating and parenting effort.

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Phylogenetic analysis of the *tprC, D, I, K, G*, and *J* genes in the genus *Treponema*.

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The pathogenic treponemes include three *Treponema pallidum* subspecies, *T. carateum* (pinta), *T. paraluiscuniculi* (rabbit syphilis), and an unclassified simian isolate. *T. pallidum* subsp. *pallidum* is the causative agent of human venereal syphilis and *T. pallidum* subsp. *pertenue* and *T. pallidum* subsp. *endemicum* cause yaws and bejel, respectively. Although these treponemes are highly related antigenically, they cause distinct clinical diseases, suggesting important genetic differences.

The *tpr* (*Treponema pallidum* repeat) gene family codes for antigens that play an important role in the immune response against *T. pallidum*. Three subfamilies can be identified in which the gene products from Subfamilies I (*tprC, D, F, I)* and II (*tprE, G, J*) have conserved amino and carboxyl terminal sequences with unique central regions, while Subfamily III (*tprA, B, H, K, L)* has scattered conserved and variable regions.

In order to investigate the evolution of this gene family and the treponemes themselves, we constructed phylogenies based on maximum likelihood methods using PAUP*. We used *tprC, D, I, K, G,* and *J* sequences from several strains of the three *T. pallidum* subspecies as well as from the rabbit and simian treponemes. The evolution of these genes appears to be largely due to multiple gene conversion events that occurred after the gene duplications that created the gene family. We were able to determine directionality of three gene conversion events between *tprC* and *D* and to tentatively identify five gene conversions at *tprG* and *J*. Sequences from *tprC*, *I* and *K* support the following order for evolution of the human treponemes: subsp *endemicum*, followed by *pertenue* and *pallidum*.

Mixed longitudinal growth of agropastoral children in northern Uganda.

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From August thru mid-December, 2004, dietary observations, nutritional and health assessments, and anthropometric examinations were carried out monthly among a sample of 28 Karimojong women and 105 of their children. The children were born between 1990 and 2004, and birth dates could be firmly established for the entire sample. Additionally, thirty-six of the children and their mothers were measured in a previous cross-sectional study, carried out in this population in 1998-99.

With the exception of breastfed infants (N=27) younger than age 6 months, all children in the sample exhibited slow physical growth and development. The sample fell at or below the third percentile of NCHS growth standards in length or height, and most also were thin for their stature. Little gain in either length or weight was observed among infants and toddlers during the 4.5 months of the study. Some infants lost weight, and cases of acute malnutrition in the form of kwashiorkor and marasmus were diagnosed among children younger than age 5 years. In young children, delays were observed in key developmental landmarks, including crawling and walking, whereas none of the children aged between 13-to-14 years exhibited any signs of pubertal onset.

Slow and stunted growth in this sample is an effect of mild-to-moderate protein malnutrition compounded by recurring diarrheal and respiratory infections and multiple infestations by intestinal worms, scabies, fleas ("jiggers"), and other parasites. In older children, particularly girls, effects of chronic low-level infections and nutrient deficiencies are likely exacerbated by heavy work demands.

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Limb joint size proportions in *Australopithecus afarensis* and *Australopithecus africanus.*

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Based on their analyses of body proportions, McHenry and Berger (1998) argued that *Australopithecus afarensis* possessed more human-like limb proportions than *Australopithecus africanus*. Due to the error involved in estimating limb length and body size, however, support for these conclusions has been limited. For this study we used resampling methods to test their hypothesis and assess the statistical strength of the species differences.

We used bootstrap analyses to impose sampling constraints that artificially reduced extant ape and human distributions of joint measurements to sample sizes comparable to the fossil samples. Composite ratios of fore and hindlimb geometric means were built by resampling elements from the reduced samples. Mean composite ratios were statistically indistinguishable (alpha=0.05) from the actual ratios of extant individuals, indicating that this method conserved each sample's central tendency. When applied to the fossil samples, joint proportions in *A. afarensis* were similar to those of humans ($p=0.851$) and significantly different from chimpanzee and orangutan proportions ($p<0.02$) while *A. africanus* was more similar to all apes ($p>0.225$) and significantly different from humans and *A. afarensis* ($p<0.04$).

These results strongly support the contention that *A. africanus* possessed more ape-like limb joint proportions than *A. afarensis*, indicating that *A. africanus* might have evolved from a more postcranially primitive ancestor than *A. afarensis*. Conversely, it is also possible that the ape-like limb joint proportions in *A. africanus* were secondarily derived, suggesting they remained under stronger selection for arboreal postures and locomotion than *A. afarensis*.

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