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BRIEF COMMUNICATIONS

Parthenogenesis in Komodo dragons

Should males and females be kept together to avoid triggering virgin birth in these endangered reptiles?

Parthenogenesis, the production of offspring without fertilization by a male, is rare in vertebrate species, which usually reproduce after fusion of male and female gametes. Here we use genetic fingerprinting to identify parthenogenetic offspring produced by two female Komodo dragons (*Varanus komodoensis*) that had been kept at separate institutions and isolated from males; one of these females subsequently produced additional offspring sexually. This reproductive plasticity indicates that female Komodo dragons may switch between asexual and sexual reproduction, depending on the availability of a mate — a finding that has implications for the breeding of this threatened species in captivity. Most zoos keep only females, with males being moved between zoos for mating, but perhaps they should be kept together to avoid triggering parthenogenesis and thereby decreasing genetic diversity.

Komodo dragons, the largest of the lizards, are under threat¹ as wild populations become smaller and more fragmented, as are 341 other species of reptile. At least 52 zoological institutions are cooperating in a successful international breeding programme with these lizards, but until now parthenogenesis has never been reported.

There are only two sexually mature female Komodo dragons in Europe, both of which were bred in captivity and are crucial to the success of the regional breeding programme. One of these (Flora, at Chester Zoo, UK) has never been kept with a male but has nevertheless produced a clutch of 25 eggs, of which 11 seemed to be viable. Three of these eggs collapsed early during incubation and provided embryonic material for genetic fingerprinting. The remaining eight eggs are developing normally and are expected to hatch in January 2007. Another captive-bred female (Sungai, at London Zoo, UK), now deceased, produced four viable eggs (from a clutch of 22) 2.5 years after her last contact with a male (Kimaan), which could be explained either by long-term sperm storage or by parthenogenesis; the eggs hatched 7.5 months later, and the young seem to be healthy (Fig. 1). Sungai subsequently laid a second clutch of six eggs 2 months after mating with a different male (Raja), of which just one hatched (for a full history of these animals, see supplementary information).

We analysed the parentage of the eggs and offspring by genetic fingerprinting² (see

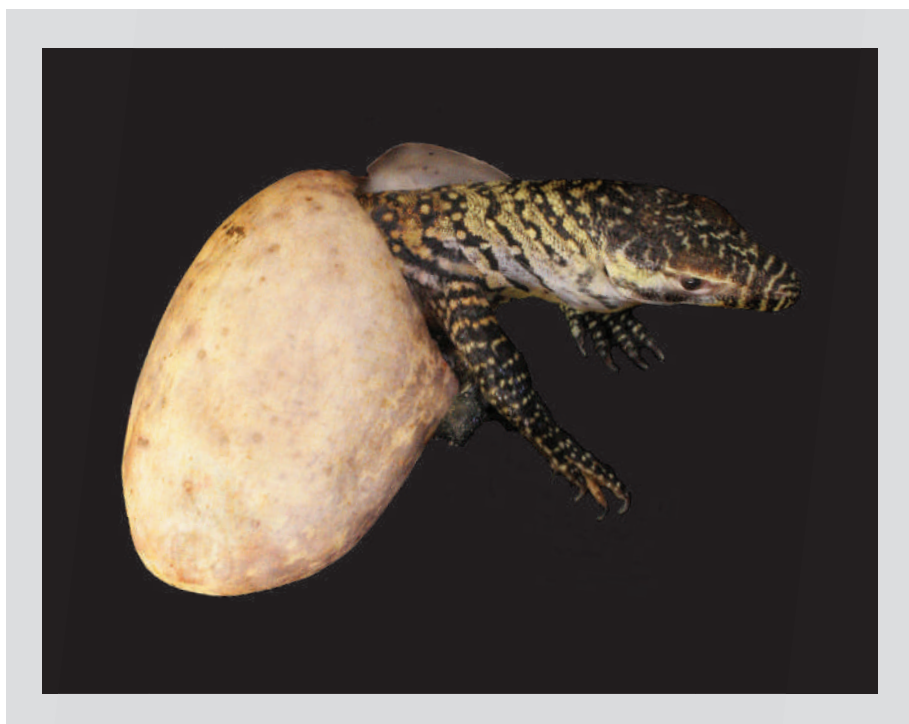


Figure 1 | Hatching of a Komodo dragon (*Varanus komodoensis*) from an egg produced asexually.

supplementary information). In the clutches of both females, we found that all offspring produced in the absence of males were parthenogens: the overall combined clutch genotype reconstructed that of their mother exactly. Although all offspring were homozygous at all loci, they were not identical clones. Parthenogenesis was therefore confirmed by exclusion (clutches had different alleles from potential fathers) and by the fact that the probability of obtaining a clutch of homozygous individuals after sexual reproduction was very low ($P < 0.0001$). Sungai's resumption of sexual reproduction confirmed that parthenogenesis was not a fixed reproductive trait (that is, it is facultative) and that asexual reproduction is likely to occur only when necessary.

Parthenogenesis has been reported in about 70 vertebrate species (roughly 0.1%)^{3,4}. Our demonstration of facultative parthenogenesis in Komodo dragons is unexpected in such large reptiles. It occurs in captive snakes⁵ and has been implicated in one other species of Argus monitor lizard (*Varanus panoptes*)⁶. Our observations of two separate occurrences of parthenogenesis at two different institutions

indicate that this reproductive strategy might not be so unusual when Komodo dragons are isolated, even though reproductive plasticity in species thought to reproduce sexually is unexpected owing to the strict requirement to maintain diploidy.

Parthenogenesis presents a previously unrecognized problem for the genetic management of threatened populations. Although captive breeding can be an essential part of a species' conservation, our results indicate that studbook records of reptile species might no longer be accurate. A pressing concern with parthenogenesis is instantaneous homozygosity of the entire genome, as this inbreeding carries an associated risk of reduced fitness and an increased probability of extinction^{7,8}. It is noteworthy, however, that the four Komodo dragon parthenogens at London Zoo are healthy and growing and behaving normally. It is common practice to keep extra females without males in captivity to maintain a sex-ratio bias towards the reproductively limiting sex and, because these are solitary animals, to reduce the risk of aggressive interactions. However, they are then subjected to strong selective pressures — as experienced by island

colonists of a sexually reproducing damselfly (*Ischnura hastata*), for example, that became exclusively parthenogenetic⁹. Parthenogenesis can also bias the sex ratio: in *Varanus* species, females have dissimilar chromosomes (Z and W), whereas the combination ZZ produces males¹⁰, so the parthenogenetic mechanism can produce only homozygous (ZZ or WW) individuals and therefore no females.

Parthenogenesis in wild Komodo dragons could be adaptive, given that viable offspring are always male and that sexual reproduction can resume, albeit between related individuals, in a colony founded by a single unfertilized female. Fewer than 4,000 Komodo dragons remain in the wild, of which perhaps fewer than 1,000 are mature females (T. Jessop, personal communication). Our discovery of the potential for asexual reproduction in this species, and possibly in other reptiles presumed

until now to be exclusively sexual, calls for further investigation into the genetic load experienced by the parthenogens, the frequency with which asexual offspring occur in captive and in wild populations, and the fitness consequences associated with facultative parthenogenesis.

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MICROBIAL ECOLOGY

Human gut microbes associated with obesity

Two groups of beneficial bacteria are dominant in the human gut, the Bacteroidetes and the Firmicutes. Here we show that the relative proportion of Bacteroidetes is decreased in obese people by comparison with lean people, and that this proportion increases with weight loss on two types of low-calorie diet. Our findings indicate that obesity has a microbial component, which might have potential therapeutic implications.

Trillions of microbes live in the human gut, helping to break down otherwise indigestible foods¹. Transplanting the gut microbiota from normal mice into germ-free recipients increases their body fat without any increase in food consumption², raising the possibility that the composition of the microbial community in the gut affects the amount of energy extracted from the diet².

The relative abundance of the two predominant bacterial divisions (deep evolutionary lineages or superkingdoms) in mice differs between lean and obese animals: mice that are genetically obese (*ob/ob*) have 50% fewer Bacteroidetes, and correspondingly more Firmicutes, than their lean (+/+) siblings³. In an accompanying Article⁴, we show that the gut microbiota in these *ob/ob* mice are more effective at releasing calories from food during digestion than are the +/+ microbiota: this trait is transmissible to germ-free recipients, resulting in greater adiposity.

To investigate the relation between gut microbial ecology and body fat in humans, we studied 12 obese people, who were randomly assigned to either a fat-restricted (FAT-R) or to a carbohydrate-restricted (CARB-R) low-

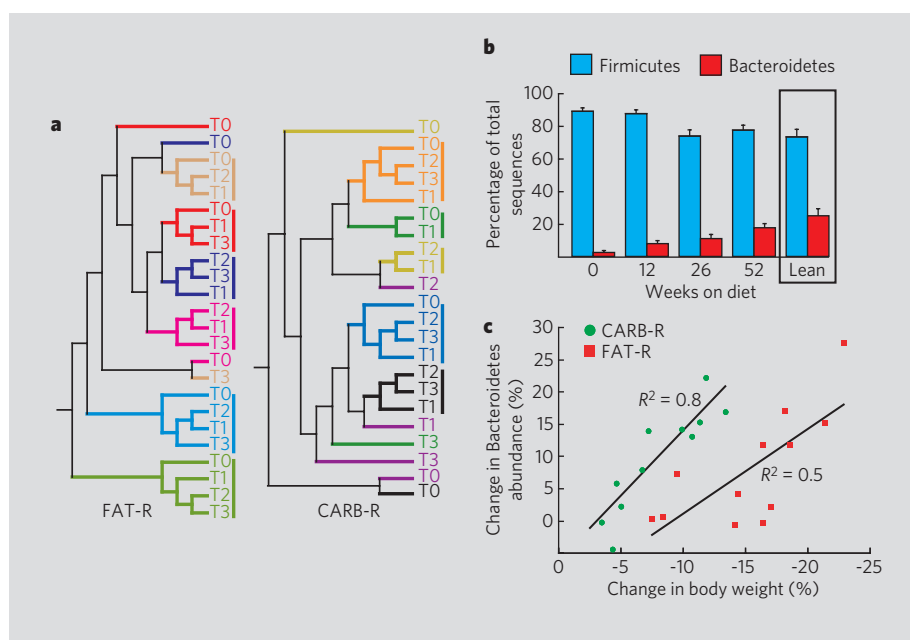


Figure 1 | Correlation between body-weight loss and gut microbial ecology. **a**, Clustering of 16S ribosomal RNA gene sequence libraries of faecal microbiota for each person (in different colours) and time point in diet therapy (T0, baseline; T1, 12 weeks; T2, 26 weeks; T3, 52 weeks) in the two diet-treatment groups (fat restricted, FAT-R; carbohydrate restricted, CARB-R), based on UniFrac analysis of the 18,348-sequence phylogenetic tree. **b**, Relative abundance of Bacteroidetes and Firmicutes. For each time point, values from all available samples were averaged (n was 11 or 12 per time point). Lean-subject controls include four stool samples from two people taken 1 year apart, plus three other stool samples⁶. Mean values $\pm$ s.e. are plotted. **c**, Change in relative abundance of Bacteroidetes in subjects with weight loss above a threshold of 2% weight loss for the CARB-R diet and 6% for the FAT-R diet.

calorie diet. The composition of their gut microbiota was monitored over the course of 1 year by sequencing 16S ribosomal RNA genes from stool samples (for details, see supplementary information).

The resulting data set of 18,348 bacterial 16S rRNA sequences revealed that most (70%) of the 4,074 identified species-level phylogenetic types (phylotypes) were unique to each person (see supplementary information). Despite the