Riddle of the giant panda

SIR — The giant panda has been classified either into the Ursidae (bear family) based on comparative anatomical studies[1], immunological distances[2], DNA hybridization, isozyme electrophoresis, immunological and karyological evidence[3], and palaeontological information[4], or into the Procyonidae, based on behavioural evidence[5,6] and haemoglobin sequences[7]. This remains a controversial issue.

We have analysed mitochondrial DNA restriction-fragment length polymorphism (RFLP) in a giant panda, a lesser panda (*Ailurus fulgens*), an Asiatic black bear (*Selenarctos thibetanus*) and a sun bear (*Helarctos malayanus*), all of which had died of illness or other accidents. We purified the DNAs from liver as described in our previous report[8]. We used 15 restriction endonucleases which recognize 6 base pairs (*Xba*I, *Bgl*I, *Eco*RI, *Eco*RV, *Pst*I, *Cla*I, *Sca*I, *Xho*I, *Sac*I, *Hae*II, *Bgl*II, *Hpa*I, *Dra*I, *Sal*I and *Bam*HI to generate restriction fragments, and observed 34–45 sites in our samples. We calculated the pairwise genetic distances (number of nucleotide substitutions per site) by the method of Nei and Li[9] (see table). We have also constructed a molecular-phylogenetic tree for these four species of carnivora by using the neighbour-joining method[10] (see figure).

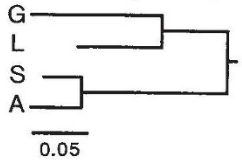
MITOCHONDRIAL DNA PAIRWISE DISTANCES OF CARNIVORES

	A	B	C	D
A—Giant panda		0.177	0.326	0.327
B—Lesser panda	0.3457		0.303	0.268
C—Asiatic black bear	0.1412	0.1628		0.072
D—Sun bear	0.1409	0.2000	0.6479	

The proportion of recognition sites shared by each pair are below the diagonal.

In our phylogenetic tree, the giant panda is more closely related to the lesser panda than to the bears. Our results indicate that the two pandas are closely related on mitochondrial DNA RFLP. So, the key point of the controversy is whether the similarities between the two pandas are all caused by convergent evolution.

There are about 1,000–10,000 copies of mitochondrial DNA in every cell; the selection pressure on this DNA is very low. So the similarities between the two pandas, at least on RFLPs from mitochondrial DNA, may not be the result of convergent evolution. If we accept that some similarities both between the two pandas and between the giant panda and the bears are due to common descent, it is certainly a fascinating evolutionary problem to determine the cause of these similarities.



Phylogenetic relationship of carnivores based on mitochondrial DNA genetic distance. Genetic distance is defined as the number of nucleotide substitutions per site. The topology was constructed using the method in ref. 10. G, giant panda; L, lesser panda; A, Asiatic black bear; S, sun bear.

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No relevance to Parkinson's

SIR — Turski *et al.*[1] report that NMDA (*N*-methyl-D-spartate) antagonists protect neurons of the substantia nigra region of the brain from toxicity produced by local administration of MPP^+ (1-methyl-4-phenylpyridinium, the active metabolite of the parkinsonism-inducing compound MPTP). We do not quarrel with the primary data, but we challenge the interpretation that these findings are relevant to Parkinson's disease.

Several investigations have shown that high concentrations of MMP^+ exert dramatic, non-selective neurotoxic actions. Selective dopaminergie neurotoxicity, the key characteristic of Parkinson's disease, occurs only when dopaminergic neurons are exposed to a limited range of MPP^+ concentrations for example, in cultures of mesencephalic neurons, 0.1–30 μM MPP^+ selectively destroys dopaminergic neurons, whereas all cells are destroyed at higher concentrations[2]. Turski *et al.* infused a 25 mM MPP^+ solution into the substantia nigra. But such concentrations of MPP^+ indiscriminately destroy all cells at the site of injection (refs 3–5; our unpublished observations). Furthermore, MPP^+ does not accumulate significantly in nigral cell bodies, but rather in the dopaminergic nerve endings in the striatum[6]. Thus, there is reason to question the rationale of direct administration of MPP^+ into the substantia nigra and, in our opinion, the method used by Turski *et al.* cannot be considered a model for Parkinson's disease.

Note also that Turski *et al.* cite evidence that the anticholinergic drugs used to treat Parkinson's disease are potent NMDA antagonists. These agents were the original treatment for this disease but were largely replaced by L-dopa, which is much more efficacious. In their long clinical use, anticholinergics have been demonstrated to have only acute efficacy and have no effect on the course of the disease, as implied by Turski *et al.* We write these comments because we are concerned that this study will become a basis for clinical trials with NMDA antagonists on Parkinson's disease in humans.

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A planet, not a plasma cloud?

SIR – Helfand and Hamilton[1] have suggested that the periodic delay and advance in arrival times of signals from the pulsar PSR1829–10, which we attributed to the existence of a planet orbiting the pulsar[2], could instead be caused by a stationary dispersing cloud of material, about 1 AU in size, quite close to the Sun on the line of sight to the pulsar. This would naturally account for the 6-month variation in pulse arrival times but, as I understand their model, when the Earth–Sun–pulsar angle is 90° the pulse arrival–time residual should be a minimum (that is, when we are seeing 'around' the dispersive cloud, the signal transmission time is shortest). This is not what is observed: as Helfand and Hamilton correctly state, at 90° (for example, at MJD 48166), we observe nearly zero residual, not a minimum. The nearest minimum is about 1.5 months away, so