Small genomes for better flyers

SIR — Genome size (nuclear DNA content) is both lower and more uniform in birds than in other tetrapods. The mean DNA content for 165 avian species was reported to be 2.82±0.33 pg per cell[1], as opposed to a mean of about 8 pg per cell in mammals[2,3]. Because avian genomes are smaller on average than those of their closest relatives the reptiles, as well as those of amphibians and mammals, it seems likely that this is a derived character rather than a primitive one[1]. One way in which a reduction of genome size has been achieved is by the loss in birds of the pattern of short period sequence interspersion, which is known to be correlated with reduced genome size[4]. To test whether genome size reduction in birds has extended to protein-coding genes themselves, we compared 111 introns and 141 exons, homologous between humans and chickens, for 31 genes whose sequences were available in the database.

Human introns were significantly longer than their chicken homologues (244.9±82.5 base pairs; a in the figure). By contrast, although exons averaged slightly larger in human than in chicken (2.3±1.3 base pairs), the difference was not statistically significant. The slope of the plot of logarithms of corresponding intron lengths in chicken against human (0.37) was significantly less than 1.0, indicating a negative allometric relationship (b in the figure). The equivalent plot of exon lengths also showed significant negative allometry, but

the slope (0.98) for exons was significantly greater than that for introns (c in the figure). The strong negative allometry in the case of introns indicates that DNA loss from chicken genes has occurred disproportionately in long introns.

Alignment of human and chicken introns suggested that DNA loss has occurred by multiple separate deletion events scattered throughout the intron, rather than by deletion of a single large stretch of DNA (data not shown). DNA loss in avian introns was not correlated with a significant change in nucleotide content. The mean per cent G+C in human introns was 56.5±1.2, whereas that in chicken was 54.6±1.3. On the other hand, at third-codon positions in exons, human genes were significantly more G+C-rich (G+C = 70.4±1.3%) than their chicken homologues (G+C = 67.5±1.5%; $P<0.05$; paired-sample t-test).

It has been proposed that modern birds are all descended from one lineage that survived a catastrophic event 65 million years ago[5]. A mutation occurring during such a severe bottleneck, even a disadvantageous one, could become fixed by genetic drift[6], but the present results suggest that genome compaction in birds did not occur through such a mutational event. The fact that numerous independent deletions in large introns have contributed to genome compaction suggests that reduction of avian genome size occurred gradually over a long period. A

pattern of persistent reduction of genome size is consistent with long-term directional selection favouring small genome size in birds.

The metabolic demands of flight may place a constraint on genome size[1,7,8]. Genome and cell size are correlated in vertebrates, and avian cells are generally smaller than those of mammals[8]. As the surface-to-volume ratio of a cell is negatively related to cell volume, small cell volume permits a greater rate of gas exchange per unit volume. Further, bats (order Chiroptera) have much smaller genomes than other mammals[9], whereas among avian families genome sizes tend to be larger in flightless birds and weak flyers than in strong flyers (data not shown). Thus, it would seem that reduced genome size is an adaptation for flight in vertebrates.

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Making a better superconductor

SIR — In a recent News and Views[1], Grant eloquently captured the excitement surrounding the recent progress at Los Alamos on ion-beam-assisted deposition (IBAD) technology. IBAD offers a fresh path for making long-length, flexible, high-temperature superconducting (HTS) wires. Here I give an industrial perspective on this development from a manufacturer of HTS wires and wire products.

At American Superconductor (ASC) we consider IBAD to be a very positive development and share Grant's enthusiasm. If manufacturing issues can be resolved, this technology using the $YBa_2Cu_3O_{7-y}$ (YBCO) superconductor promises to extend the range of application of HTS wires, particularly at high fields and temperatures, beyond that expected from the deformation-processed wires based on $Bi_2Sr_2Ca_2Cu_3O_{10}$ (BSCCO).

For commercial applications, it is important to consider the engineering current density J_e, which divides the current by the full cross-section of the wire, rather than the HTS current density J_c, which divides the current only by the cross-section of the

a, Mean length of 111 homologous introns and 141 homologous exons from 31 genes of human (open columns) and chicken (hatched columns). (GenBank accession numbers are available from the authors on request.) Paired-sample t-tests of the significance of the difference between human and chicken give: introns, $t = 2.97$, $P<0.004$; exons, $t = 1.75$, not significant. b, Natural logarithm of chicken intron length against the natural logarithm of the length of the corresponding human intron. The slope of the regression line is significantly different from zero ($t = 5.47$, $P<0.00001$) and from 1.0 ($t = 9.16$, $P<0.00001$). c, Corresponding log plot for exons. The slope of the regression line is significantly different from zero ($t = 156.97$, $P<0.00001$) and from 1.0 ($t=2.66$, $P<0.01$). The slopes of the regression lines for introns and exons are significantly different from each other ($z = 8.88$, $P<0.00001$).