effect of these results is to demonstrate the importance of a phased block of A_n, where n must be a significant length, and argue for the junction model. They exclude simple flexibility, although anisotropic flexibility which leads to a time-averaged net bending may still be a possibility. The dinucleotide wedge model appears to be excluded in this system by a careful analysis of the number of such steps, and whether they should add in a constructive way. Koo *et al.*[4] also ask whether one junction is more important than the other. If the vital element in creating the bend is a a non-B $5'$-A_n-$3'$ section, then there need not be equal bending at each end. By making sequences in which the $5'$ ends are phased with the helix while the $3'$ ends alternate between 7- and 13-bp periodicity, and others where the $3'$ junctions are phased correctly, the authors could show that the $3'$ junction is the more important contributer to the overall bending.

The next stage in gaining a full understanding of the bending mechanism must be to establish both the conformation of the A_n runs and that of the junction with B-DNA. In the meantime, what is the role of DNA bending? We should probably make a distinction between bent and bendable DNA. Kinetoplast DNA has a sequence which gives rise to intrinsic bending. Other sequences may be normally straight, but are relatively easily bent in response to the binding of a protein. Wu and Crothers[5] demonstrated that the DNA upstream of the *lac* operon becomes bent on binding the cyclic AMP receptor protein (CAP). It will come as no surprise if it is found that other *trans* acting factors, either prokaryotic or eukaryotic, bend their cognate DNA. The restriction enzyme *Eco*RI appears to kink and bend its substrate on binding to the GAATTC recognition sequence[17].

Sequence-directed bending of the kinetoplast DNA may be an extreme example of a more general bending that most DNA molecules are required to undergo. We have already mentioned DNA packaging in viruses. Compaction of eukaryotic DNA around the nucleosome core is another example. How may this be achieved for essentially random sequence DNA?

The answer seems to be that although the sequence itself may be random, the structure adopted is not, and forms to optimize the bending potential of the DNA. Drew and Travers[18] took a 169 bp piece of bacterial DNA and circularized it. By careful analysis of cleavage frequencies by the nuclease DNase 1, they were able to deduce which sequences lay on the 'inside' of the circle, and which lay 'outside'. Two points emerged: first, that there was indeed a defined inside and outside, rather than a population of all possible orientations; and second, that runs of A and T are positioned so that their minor grooves face in, while the less compressible G- and C-region minor grooves face outwards. Thus, the structure that is formed is the one that best optimizes these preferences.

The authors went on to show that this DNA reconstitutes a nucleosome retaining this same inside and outside, which suggests that exact nucleosome positioning of DNA is governed by the requirement for placing the most easily bent sequences at the point in the nucleosome with the smallest radius of curvature. It is clear that the significance of all these studies extends far beyond the function of an obscure suborganelle of a parasite. ☐

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Ethnic differences

Variation in human testis size

from Jared M. Diamond

THE potential harvest from studies of human testis size, a subject that has received little systematic investigation, is indicated in a paper by R. V. Short[1], who documents variations between ethnic groups which could be correlated with the incidence of dizygotic twins and breast cancer.

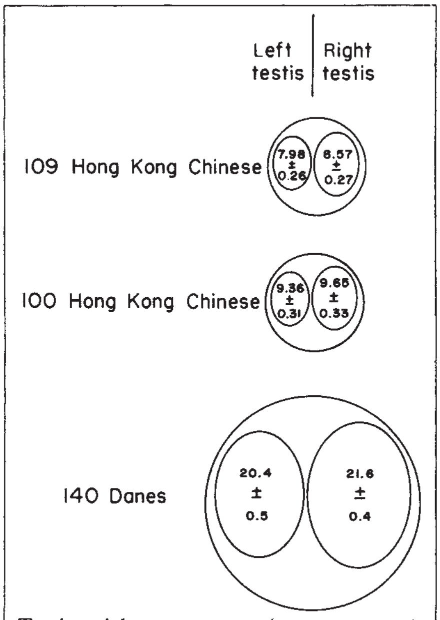
Although measurements of testis size by orchidometry in living subjects are difficult to standardize, they suggest smaller testes in Japanese and Korean men than in Caucasians. Weighing at autopsy is more accurate and showed that the size was twofold lower in two Chinese samples compared with a Danish sample (see figure). Differences in body size make only a slight contribution to these values. Could the testis size variation be a Y-chromosome trait lacking female correlates, as already documented for mice[2]? Interspecies differences in testis size among man and apes do fit this pattern, differences in the relative size of ovaries being negligible. In these species large testis size correlates with, and was probably selected by, two factors: high copulatory frequency; and high probability that a female will mate with several males during one ovulatory cycle[3]. However, evidence that these factors vary between human populations is lacking. An explicit test revealed no relation between testis size and copulatory frequency in Korean men[4].

Alternatively, could the variation in human testis size be an autosomal trait with correlates in females? If male mice are selected for large or small testes, the females of these strains have correspondingly high or low ovulation rates and vice versa; similar results apply to sheep[5,6]. As a correlate of ovulatory rate in human females, Short examined the frequency of dizygotic twin births (see table). Such births are under genetic control, apparently as an autosomal recessive[7]. The dizygotic twin frequency proves indeed to be lower in Asians (average value for 14 populations, 3.9 per 1,000 births, including 4 populations transplanted to Hawaii), than in Caucasians (average for 8 populations, 7.9 per 1,000 births). All but 2 of the 14 Asian values were less than any of the Caucasian values. The differences in dizygotic twin frequency, and presumably ovulation rate, are in the same direction as the differences in testis size. The frequencies of dizygotic twins are even higher (up to 49 per 1,000 births) among African blacks (see table).

Dizygotic twinning rate per 1,000 births (from refs 1 and 7)

Population	Ethnic group	Locality	Dizygotic twinning rate
Asians	Japanese	Hawaii	2.2
	Japanese	Japan	2.3
	Chinese	Formosa	1.4
	Chinese	Hawaii	2.1
	Chinese	Malaya	2.8
	Chinese	Singapore	4.1
	Chinese	Hong Kong	6.8
	Malays	Hawaii	2.2
	Malays	Manila	2.7
	Malays	Malaya	5.2
	Hawaiians	Hawaii	3.9
	Koreans	Korea	5.1
	Koreans	Korea	5.8
	Koreans	Korea	7.9
Indians		Bombay	6.8
		Bangalore	7.3
		Calcutta	8.1
Caucasians	Europeans	Spain	5.9
	Europeans	France	7.1
	Europeans	Switzerland	8.1
	Europeans	Holland	8.1
	Europeans	West Germany	8.2
	Europeans	Norway	8.3
	Europeans	Sweden	8.6
	Europeans	Britain	8.9
African blacks	Bantu	Johannesburg	16.0
	Bantu	Leopoldville	19.0
	Yoruba	Ibadan	40.0
	Yoruba	Ilesha	49.0

The selective factor responsible for this parallel variation in men and women is open to speculation. One suggestion is that there should be strong selection against dizygotic twins in populations of small stature and slender build, because of increased maternal and infant mortality, regardless of whether those body traits are genetically or nutritionally determined. By this reasoning, small testis size in Asian men would be a by-product of selection against dizygotic twins in Asian women, assuming that testis size and ovulation rate are genetically linked in humans as they



Testis weight at autopsy, g (mean ± s.e.m.).

are for mice and sheep.

Might these dizygotic twin frequencies have any detectable correlates in the whole female population? At first, one might expect not, because even the highest recorded frequency (Yoruba women) is only 4.9 per cent. However, the probability that a single ovulation with intercourse will result in a live birth is only ¼ for humans[8]. Thus, only one-sixteenth of double ovulations should result in births of dizygotic twins, and the frequency of double ovulations should vary among human populations up to 16×4.9=78 per cent. Therefore, correlates of dizygotic twinning in the population as a whole may exist.

One possible candidate for the correlate is hormone levels, as development of two follicles doubles oestrogen production during the follicular phase of the menstrual cycle. There are indications that levels of oestradiol, follicle-stimulating hormone (FSH) and luteinizing hormone (LH) are higher in mothers of dizygotic twins than of singletons[9,10]. Yoruba women, with the world's highest frequency of dizygotic twins, have higher FSH and LH levels at the time of ovulation than do Japanese women, who have the lowest frequency of dizygotic twins[11].

This variation in female hormone levels may contribute to the distribution of the incidence of breast cancer, which is known to be related to oestrogen levels. Even after all other risk factors for breast cancer have been taken into account, the incidence among Japanese women remains inexplicably low. Perhaps this puzzle, the so-called 'Japanese factor' of breast cancer[12], is related to low double-ovulation frequencies and low hormone levels.

Short's intriguing study[1] raises more questions than it solves. The nature of the causal links, if any, between testis size, dizygotic twins and breast cancer remains to be clarified. Another study shows no relation betwen dizygotic twinning and breast cancer[13]. The primary observations of variation need extension — for example, do Yorubas have large testes as well as frequent dizygotic twins? It remains unknown whether differences in testis size arise from differences in tubule number, diameter or length, or in interstitial cells. What is clear from Short's work is that variation in human sex organs and function warrants serious study. ☐

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Astrophysics

Galaxy distances and deviations from universal expansion

from J. Richard Bond and Sidney van den Bergh

Two major findings involving large-scale structure in the Universe dominated discussion at a recent meeting*. The first of these was the result of the deep (out to $\sim 150\ h^{-1}$ Mpc) extension of the Harvard/Smithsonian Center for Astrophysics redshift survey[1] that most galaxies and clusters in the Universe appear to lie on the surfaces and along the intersections of huge bubble-like structures (Hubble bubbles) enclosing voids with typical diameters $\sim 25\ h^{-1}$ Mpc, where h is the Hubble constant in units of 100 km s^{-1} Mpc^{-1}. This work, which was discussed last month in these columns[2], confirms the picture reviewed by Oort in 1983 that superclusters, filaments and voids dominate structure on the largest scales[3]. A graphic example of the sort of structure which now seems pervasive is provided by the Perseus–Pisces supercluster, discussed at the workshop by M. Haynes (Arecibo Observatory). It is characterized by large-scale filamentariness stretching from the Perseus to the Pisces clusters, accompanied by holes in the apparently evacuated surroundings. N. Bahcall (Space Telescope Science Institute) presented a strong case that Abell clusters have the remarkably large correlation length $\sim 25\ h^{-1}$ Mpc; Bahcall also suggested that superclustes defined by associations of rich clusters have an even larger correlation length. B. Tully (Hawaii) showed tentative evidence from the distribution of rich clusters that an extremely large ($\sim 300\ h^{-1}$ Mpc) flattened structure exists of which the Local Supercluster is a small part.

The second major discovery reported at the meeting was that regions of the Universe with dimensions $\gtrsim 50\ h^{-1}$ Mpc are streaming with velocities of many hundreds of kilometres per second relative to the absoulte standard of rest provided by the cosmic microwave background (CMB). Previously it had been thought that the 610 ± 50 km s^{-1} motion of the Local Group relative to the microwave background resulted from a superposition of Local Group infall into the Virgo cluster and infall of the Virgo cluster into the Hydra–Centaurus supercluster. It now turns out that the Hydra–Centaurus supercluster was something of a red herring — Infrared Astronomical Satellite (IRAS) observations show that this complex does not have a massive extension hiding behind the dusty clouds of the Southern Milky Way. To cause the observed motion of the Local Supercluster would require the Hydra–Centaurus supercluster to have $\gtrsim$ five times as large a mass-to-light ratio as the Virgo cluster. Furthermore the attraction by Hydra–Centaurus is partially offset by the Perseus–Pisces supercluster that is pulling us in the opposite direction.

New techniques, developed independently by G. Djorgovski (Harvard) and by D. Burstein (representing a large international group), make it possible to determine the absolute magnitudes of elliptical galaxies with an accuracy of ~ 0.5 mag (apart from an arbitrary zero point) and hence the distances to clusters to an accuracy of 5–10 per cent. Using this distance indicator, Burstein reported that Hydra–Centaurus is also moving with a velocity ~ 700 km s^{-1} relative to the microwave background as part of a relatively coherent streaming motion extending over at least $\sim 40\ h^{-1}$ Mpc. Work on the original Rubin–Ford[4] sample of spiral galaxies, extending from $\sim 35\ h^{-1}$ Mpc to $\sim 65\ h^{-1}$ Mpc, reported by C. Collins, R. Joseph and N. Robertson (Imperial Col-

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*NATO Workshop held at Kona, Hawaii, 13–17 January 1986.