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confirmed by both electron-polymerase chain reaction (e-PCR) and fluorescent in situ hybridization (FISH) analyses (<http://ncbi.nlm.nih.gov/genome/clone>). In addition, PTB-053J22 is fully included in another independently sequenced chimpanzee BAC clone (AC007214, RP43-135M19). Thus, it is highly likely that PTB-053J22, which we detected through this study, contains one of the breakpoints corresponding to the human (or vice versa in chimpanzee) chromosomal inversion between 12p12 and 12q15. In addition, this region in human chromosome 12 or in chimpanzee chromosome 10 is known to be inverted in gorilla and chimpanzee as opposed to human and orangutan (8, 18). We found several genes around the PTB-053J22 BESs in the following order, SCL21A14 (soluble carrier, organic anion transporter, family 21, member 14), <36 kb>, PTB-053J22-F, <5 kb>, SLC21A8 (soluble carrier, organic anion transporter, family 21, member 8, <cen>, DYRK2 (dual-specificity tyrosine-Y-phosphorylation regulated kinase 2), <330 kb>, PTB-053J22-R, <168 kb>, and IFNG (interferon- γ), based on the annotations on the corresponding NT contigs. The effect of the inversion on these genes should be the target of future studies.

To independently test our mapping procedure, we selected 15 chimpanzee BAC clones mapped to human chromosomes 1 to 8 by the BES alignment procedure (13) and subjected them to FISH analysis with both human and chimpanzee M-phase cell spreads (Fig. 3). As shown, 13 clones showed single locus signals at the corresponding positions on both human and chimpanzee chromosomes, and two clones, RP43-50L24 and RP43-60K09, showed similar signals at two loci on the human and chimpanzee chromosomes, suggesting that the mapping procedure we used in this study is reliable. We believe that the whole genome chimpanzee/human comparative map built here by the BES alignment procedure is reasonably accurate and useful for future studies. Recent development of the human-mouse comparative map (19, 20) also supports our approach.

Users of this map should still be careful in applying the information because the possibility remains that assignment of particular clones in the NT contig is incorrect or that inter- or intrachromosomally duplicated regions may be included within an insert. However, the quality of the map, and thus its usefulness, should increasingly improve as the finishing of the human genome sequence proceeds.

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- The supplemental data are available at hgp.gsc.riken.go.jp or www.sciencemag.org/cgi/content/full/295/5552/131/DC1.
- The probability equation, $N = \ln(1 - P)/\ln(1 - 1/n)$, where N is the number of clones, in this case 24,580, and n is the total size (2.7 Gb in this case) divided by the size of fractions. The estimated insert size of the BAC libraries is about 130 to 150 kb. The calculated P value is 0.694 (130-kb insert) or 0.745 (150-kb insert).
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- In total, 752 primer pairs were designed from the human chromosome 21 sequence at distances of about 50 kb (sequences of the primer pairs can be seen at *Science* Online (14)). For the reactions successful only for human DNA, we expanded the test to include two additional genomic DNA preparations from different individuals of chimpanzee (male and female) and five other primates, including gorilla (*Gorilla gorilla*), orangutan (*Pongo pygmaeus*), Old World monkey (*Macaca fascicularis*), New World monkey (*Ateles geoffroyi*), and prosimian (*Lemur catta*).
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- We thank all the members and associates (individual names can be seen at our Web site) of the Human Genome Research Group, RIKEN Genomic Sciences Center, for their enthusiastic support and stimulating discussions. Special thanks to RIKEN GSC and the National Institute of Genetics for supporting the international workshop on chimpanzee genomics, held in Tokyo, March 2001. This work was supported in part by special grants from the Ministry of Education, Culture, Sports, Science and Technology for Genome Research.

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Nucleotide Variation Along the *Drosophila melanogaster* Fourth Chromosome

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The *Drosophila melanogaster* fourth chromosome, believed to be nonrecombining and invariable, is a classic example of the effect of natural selection in eliminating genetic variation in linked loci. However, in a chromosome-wide assay of nucleotide variation in natural populations, we have observed a high level of polymorphism in a ~200-kilobase region and marked levels of polymorphism in several other fragments interspersed with regions of little variation, suggesting different evolutionary histories in different chromosomal domains. Statistical tests of neutral evolution showed that a few haplotypes predominate in the 200-kilobase polymorphic region. Finally, contrary to the expectation of no recombination, we identified six recombination events within the chromosome. Thus, positive Darwinian selection and recombination have affected the evolution of this chromosome.

Detecting evolutionary forces that shape the structure of genetic variation at the genomic level often relies on understanding the effects of natural selection on nearby linked loci (1–4), for which the fourth chromosome of *Drosophila melanogaster* is a classical model system (5–7). It has been thought to undergo no meiotic recombination except under certain experimental conditions (e.g., the interchromosomal effect introduced for the purpose of mapping)

(8, 9). Two genetic models—“selective sweep” by the hitchhiking effect (1, 10), in which an advantageous allele is selected for and fixed in species rapidly, and the background selection model, in which deleterious mutations are selected against (2, 10)—predicted a lack of variation throughout the chromosome, which has been supported by limited data (6, 11). We have reexamined the level of variation and recombination in the fourth chromosome using a chromosome-wide assay of nucleotide variation.

We first investigated within-species nucleotide variation in two adjacent regions from the 102F cytological position of the fourth chromosome of *D. melanogaster*: (i) 4257 base pairs (bp) of the *CG11091* locus, and (ii) 847 bp of an intron of the *toy* gene. *CG11091* and *toy* are separated by ~10 kb. We directly

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polytene chromosomes (21) to ascertain the gene order within the haplotype region; this did not reveal any inversion. An alternative scenario of positive selection would involve the major haplotype undergoing a selective sweep, being driven by selection toward fixation. However, that the two haplotypes are polymorphic in all locations argues against this possibility.

Because our results contrast with those from previous studies of *ci* in *Drosophila*, we sequenced 10 *ci* genes from our worldwide sample and again found no polymorphism (Fig. 2). The lack of variation at *ci* implies different evolutionary histories in different chromosomal regions and the existence of recombination between *ci* and *CG11091-toy*. We investigated these conjectures by examining patterns of linkage disequilibrium throughout the euchromatic region of the chromosome by sequencing an additional 15 gene regions (22) (Fig. 2). We also sequenced seven related genes in *D. simulans*, the sibling of *D. melanogaster*, to further investigate the role of selection and to determine the ancestral haplotype.

First, we found that the chromosome could be divided into three discrete domains: (i) the 200-kb dimorphic domain containing the *CG11091-toy* region with its characteristic two-haplotype organization of variation; (ii) a polymorphic proximal domain in which no such haplotype organization is seen; and (iii) a domain, distal to the centromere, where levels of variation are low. The first domain has the highest level of variation in comparison with the two other domains, although its average silent nucleotide diversity, 0.0021, is lower than the average nucleotide diversity in the genome (13). The latter two domains, both proximal and

distal to the dimorphic domain, show no such dimorphism, and varying levels of polymorphism. Although many genes in these two domains show levels of polymorphism characteristic of regions of reduced recombination (13), 3 out of 11 gene regions in these areas show relatively high levels of nucleotide diversity (0.0012 to 0.0019). The boundaries between these domains can be narrowed to two short regions of 15 kb (boundary 1 between the regions *CG11153* and B) and 7 kb (boundary 2 between *toy* and *plexA*).

A statistical test for heterogeneity of variation among gene regions, based on the χ^2 - Kreitman-Hudson test statistic (23), shows, for all 18 gene regions, significant heterogeneity ($P \ll 0.0001$). This further indicates that the fourth chromosome is not evolving as a single unit; different regions appear to have different evolutionary histories.

All but one of the five gene regions in the dimorphic domain in the additional survey show the same haplotype structure as the *CG11091-toy* region; locus A, however, shows no variation. This domain thus displays linkage disequilibrium over some 200 kb. The major haplotype is less diverse than the minor haplotype: The major haplotype cluster contains 9 segregating sites (one indel site included), whereas the minor haplotype cluster contains 30 such sites (2 indel sites included) (Fig. 2). In the *CG11091-toy* region, the worldwide sample reveals that for the within-minor haplotype group $\pi = 0.0015$, and for the within-major haplotype group $\pi = 0.0004$. Consistent with these observations, the *D. simulans* outgroup sequences in gene regions *CG11152* and *CG11091* reveal that the minor haplotype is ancestral.

By pooling all 16 loci that contain polymorphisms, we have estimated a minimum number of six recombination events (R_m) by the four-gamete method (Fig. 2) (24). However, because we have not obtained a continuous sequence along the entire chromosome, the true R_m for the fourth chromosome is in all probability larger. Thus, to calculate an upper bound on R_m , we identified one event in *CG11093* from 20,010 nt that we sequenced, yielding a R_m density of $1/20,010 = 0.05/\text{kb}$ in 10 chromosomes. To calculate a lower bound, we assume a R_m density of six events/1156-kb nucleotides (the chromosomal euchromatin length) = $0.0052/\text{kb}$ in these chromosomes. Although these results cannot be directly compared with the experimental recombination estimates, it is informative to compare them with the estimates from other population genetic data. The *Adh* gene in a moderate-recombination region has a R_m density of 1.84 events per kilobase in 11 alleles (24). Thus, qualitatively, rates of recombination on the fourth chromosome are 37- to 354-fold lower than those on normal autosomes. The amount of recombination observed here is low, consistent with genetic analysis of the chromosome (8). In contrast to previous predictions (1-3, 6), however, such a low rate has a considerable effect on the structure of genetic variation on the chromosome.

Recombination caused by crossovers at each end of the dimorphic domain may account for the different evolutionary histories of the three chromosome domains as described above. The genome sequence (25) reveals that both putative boundary regions contain many repetitive sequences that may facilitate genetic recombination.

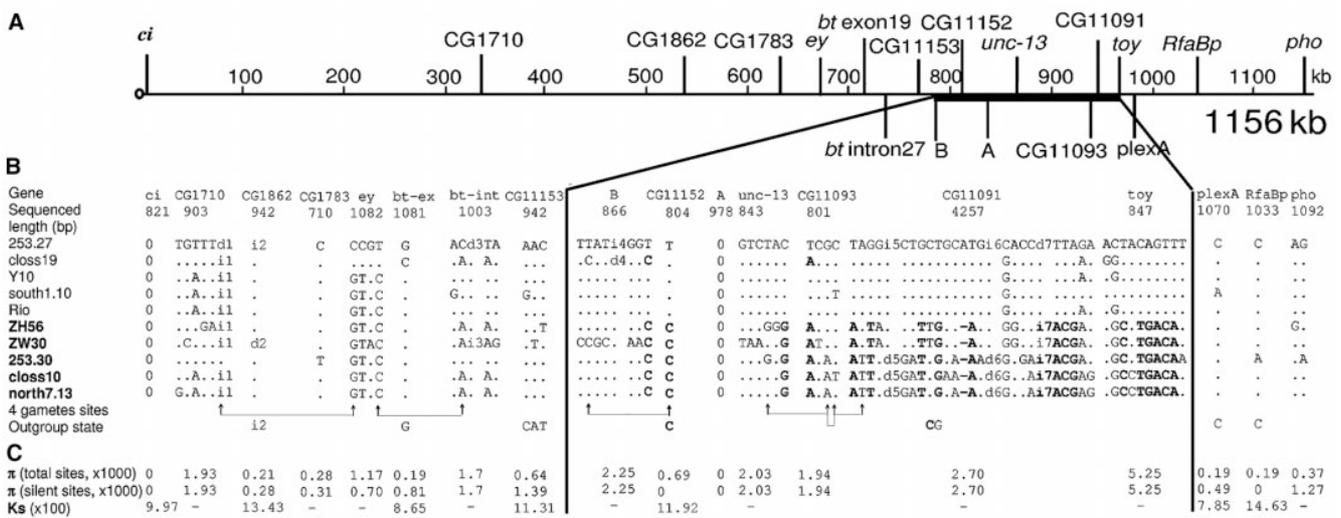


Fig. 2. Distribution of variation on the *D. melanogaster* fourth chromosome. (A) The surveyed 18 gene regions along the *D. melanogaster* chromosome in the map (25) with the gene order between *CG11153* and *pho* corrected on the basis of our FISH experiments. (B) Segregating sites in the nonrandomly sampled 10 chromosomes with dimorphism shown in bold type. Arrows indicate the minimum number of recombination (R_m) sites identified by the

four-gamete method (24). *Drosophila simulans* is the outgroup. i/d denotes indel polymorphism of various lengths indicating presence (i) or absence of nucleotide sequences (d). Seven indel polymorphic sites are shown: i1/d1 = 16 bp, i2/d2 = 2 bp, i3/d3 = ~1 kb, i4/d4 = 13 bp, i5/d5 = 2 bp, i6/d6 = 11 bp, i7/d7 = 18 bp. (C) K_s : synonymous divergence per nucleotide site between *D. melanogaster* and *D. simulans*.

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Given that recombination does occur on the fourth chromosome, the maintenance of the huge dimorphic domain is anomalous—we would expect it to be eroded by recombination. However, it seems plausible to suppose that the dimorphism is the joint product of balancing selection on a locus within the region, and a low rate of recombination such that variation linked to one balanced allele is seldom, if ever, recombined into association with the other allele.

The significantly reduced variation outside the dimorphic domain could be due to either a reduced mutation rate, hitchhiking with positive Darwinian selection, or background selection. The first hypothesis, which predicts that low divergence between species will correspond to low variation within species, was not supported by the observed typical level of silent site substitutions, K_s ($K_s = 0.0785 \sim 0.1463$) (Fig. 2) (3, 6). For the second and third hypotheses, a Tajima's D test on pooled data from all seven gene regions in the centromere-proximal nondimorphic domain shows no significant bias in the polymorphism spectrum ($D = -0.9745$, $P = 0.1739$) and thus does not support a recent selective sweep over this long region (26). This leaves the possibility that other forms of selection—e.g., background selection or directional selection in local regions delineated by recombination—may play a role. Even if selective sweep does occur in some local regions, the low recombination rate would render it a slow process and make it unlikely to be global.

Previous studies, both theoretical and empirical, had concluded that the fourth chromosome lacks variation. However, we have found that it not only harbors high levels of nucleotide variation throughout the chromosome, but also has a unique dimorphism that extends across a long chromosome domain, suggesting the importance of positive Darwinian selection (balancing selection) in the evolution of this chromosome. These results may be viewed as empirical support for Dobzhansky's "coadapted gene complex" idea (27), with each haplotype representing a distinct complex. The evolution of such a complex—if it is to occur at all—is most likely to occur in regions of low recombination like the one in question. These results provide a starting point for reassessing the genetic and evolutionary forces that affect both

this chromosome in particular, and low recombination regions in general.

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Role of Cell-Specific SpoIIIE Assembly in Polarity of DNA Transfer

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SpoIIIE mediates postseptal chromosome partitioning in *Bacillus subtilis*, but the mechanism controlling the direction of DNA transfer remains obscure. Here, we demonstrated that SpoIIIE acts as a DNA exporter: When SpoIIIE was synthesized in the larger of the two cells necessary for sporulation, the mother cell, DNA was translocated into the smaller forespore; however, when it was synthesized in the forespore, DNA was translocated into the mother cell. Furthermore, the DNA-tracking domain of SpoIIIE inhibited SpoIIIE complex assembly in the forespore. Thus, during sporulation, chromosome partitioning is controlled by the preferential assembly of SpoIIIE in one daughter cell.

Table 1. Neutrality tests of haplotype structures in the *D. melanogaster* fourth chromosome genes.

Tests	Tested statistics	Observed values	Probability
K test	Haplotype number K	5	0.0435
H test	Haplotype diversity H	0.618	0.0055
HP test	Number of alleles with ≤ -1 segregating site	8	0.0050

The spore formation pathway of *Bacillus subtilis* provides a valuable system for studying how bacterial cells establish the cellular polarity necessary for development (1, 2). Early in sporulation, a polar septum is synthesized in the space between two domains of an asymmetrically partitioned chromosome (3). After divi-

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sion, the forespore contains the origin proximal 30% of its chromosome, whereas the remaining 70% must subsequently be transported through the septum. This striking chromosome movement is accomplished by the SpoIIIE DNA translocase (4, 5), a bifunctional protein that also participates in membrane fusion after the phagocytosis-like process of engulfment (Fig. 1A) (6). The NH₂-terminal membrane domain of SpoIIIE is necessary and sufficient for localization to the septum, whereas the COOH-terminal domain moves along DNA in an adeno-