tuitously, the revisions have no other appreciable effect on previously recognized important features of the amino acid sequence. Codon usage remains essentially as described before[2]. Serine remains at residue 17, a position that we have identified as the major site for phosphorylation of pp60$^{v\text{-}src}$ by cyclic AMP-dependent protein kinase (unpublished findings of J. Smart, H. Oppermann and J.M.B.). As noted previously[3], the major site of tyrosine phosphorylation in pp60$^{v\text{-}src}$ has been relocated from residue 419 to residue 416, but the adjoining amino acid sequence is unaltered for more than 40 residues on either side of the tyrosine. Sites for preferred cleavage by the V8 protease of *Staphylococcus aureus* and other proteases can still be identified in predicted regions of the sequence[2]. The chemical composition of the protein remains generally hydrophobic, and the amino acid sequence contains no recognizable domain by which the protein might insert into the plasma membrane of the host cell[4]. The revised sequence still displays provocative homologies with the amino acid sequences of other protein kinases, including the lysine at residue 295 that has been suggested by analogy to be the site of binding for nucleoside triphosphates[5].

Our previous report proposed an amino acid sequence for the protein gp37, encoded by the *env* gene of RSV. We have located an error that introduced a frameshift near the carboxy-terminus of the amino acid sequence. The revised sequence is shown in Fig. 1. The revision changes the last 6 residues of the previous version of the sequence and extends the protein by an additional 15 amino acid residues. The carboxy-terminal domain remains hydrophobic[2], however, as required by previous proposals that this portion of the molecule might be inserted into the lipoprotein envelope of the virus[6].

We have also found that our original version of the nucleotide sequence between *env* and v-*src* required revision by both the removal and addition of nucleotides. Figure 1 illustrates the two domains of the sequence where substantial changes were necessary. The revisions relocate by a few residues, but do not change the composition of either the splice acceptor site used in the genesis of *src* mRNA (marked in Fig. 1) or the large direct repeat that brackets v-*src* (as described in ref. 2). The entire untranslated sequence extending from the end of v-*src* to the 3′ end of the viral genome remains as reported by us previously[2,7], with the exception of one nucleotide which is indicated in Fig. 1.

Our revised sequence is now in general accord with all data available to us from other workers on several strains of avian leukosis and sarcoma viruses (although differences between single nucleotides still exist, as might be expected for different strains). We can offer no single explanation for the errors in our previous data; we thank several colleagues who brought to our attention the discrepancies between their results and ours and deeply regret that our errors found their way to print; we apologize to any investigator who may have been inconvenienced by the mistakes in our previous publication.

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Mean IQ differences in Japan and the United States

IN Lynn's article[1] on Japanese–US mean IQ differences, it is stated that "whereas Americans . . . have ~2% of their populations with IQs over 130, the Japanese have ~10% at this level. Among the population as a whole, 77% of Japanese have a higher IQ than the average American . . ." These calculations assume, however, that the respective variances of the American and Japanese IQ distributions are identically equal to 15 (and, of course, that the distributions are normal). My reading of the statistical source from which most of Lynn's data are obtained, namely, the Japanese and US WISC-R manuals[2,3], suggests that, in fact, the Japanese IQ variance is significantly lower. The Japanese manual (Table 3, p. 26) gives a standard deviation of the sum of scaled scores on the performance test which is 85.4% of that of the American sum of scaled scores on the same test (see Table 6, p. 23, in the American manual).

The standard deviations reported in the two manuals are comparable (that is, are in the same units) if the linear functions used to translate the raw scores into scaled scores in the two standardizations have the same slopes, as Lynn himself implicitly assumes in his calculations. Let $Y_U = a_U + bX_U$ and $Y_J = a_J + bX_J$, where Y_U and Y_J are the scaled scores on a given test for the US and Japanese samples, respectively, and X_U and X_J are the raw scores for the two samples. Only the latter are comparable, because only they are measured in the same units. Because $E(Y_U) = E(Y_J)$, by construction, $E(X_J) - E(X_U) = \frac{1}{b}(a_J - a_U)$. It is the latter which Lynn estimates, reported in the standard deviation units of X_U. In addition, the ratio of the standard deviations of X_U and X_J will be the same as the ratio of the standard deviations of Y_U and Y_J only as long as b in the two transformation equations is the same, since $\sigma_{Y_U} = b\sigma_{X_U}$ and $\sigma_{Y_J} = b\sigma_{X_J}$.

Assuming that the slopes of the transformation equations are the same, our best estimate of the standard deviation in Japanese IQ scores is 85.4% of the American standard deviation of 15, or 12.8. The proportion of Japanese scoring above 130 (on the American scale) would be, for this estimate, 6.9% rather than 10%, given a Japanese mean IQ of 111 (relative to the American mean of 100). The proportion of Japanese scoring above the American mean would be 80% rather than 77%. A calculation of the two points of intersection of the two IQ distributions shows that the relative frequency of Americans exceeds that of the Japanese for all IQs above 177 and below 104. The Japanese are relatively more numerous for all IQs between 104 and 177. These calculations, of course, are only illustrative and change quite sensitively with respect to the difference in mean IQ assumed. For example, if we use Lynn's previous estimate[4] of the Japanese–US mean IQ gap of 6.8 and still assume a 85% lower standard deviation in Japanese IQs, Americans would be relatively more frequent at all IQs above 158 and below 95, and the Japanese relatively more frequent at all IQs between 158 and 95. The proportion of Japanese scoring above 130 would be 3.5%, as opposed to the American 2.3%.

Freedman provides some interesting speculation as to why we might expect, on genetic grounds, a lower variance in various quantitative traits among the Japanese than among Americans and Europeans[5].

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