parts of the polypeptide (8 among the first 22 residues and 8 among the last 18 residues), while a stretch of 10 acidic residues is found in an internal region, between amino acids 135 and 163. These features may be significant for the biological activity of the *spo*IIG gene product.

The encoded protein seems to be synthesized in a very low amount as we have been unable to express it in *B. subtilis* maxicells in various experimental conditions; this suggests that the protein may have a regulatory role in sporulation. Note that the *spo*IIG gene is transcribed only in the early stages of sporulation and not during vegetative growth. This was demonstrated by hydridization experiments in which the gene was used to probe mRNAs isolated at different stages of growth and sporulation (results not shown).

To elucidate the nature of the polypeptide encoded by the *spo*IIG gene, we searched for homologies with known proteins stored in the Dayhoff protein sequence data bank (~2,300 sequences). An important homology was found with the product of the *E. coli rpo*D[13] gene, the sigma factor. Figure 3*a* shows the alignments of the two related segments of the *B. subtilis spo*IIG gene product and of the *E. coli* sigma factor. These aligned sequences exhibit a remarkable similarity: of the 65 positions compared, 29 (44.6%) are occupied by identical amino acids. When chemically similar pairs of amino acids are taken into account[14], this number rises to 44 (67.7%). It was not necessary to introduce gaps to maximize this homology. Furthermore, statistical tests[15,16] show that the similarities between the aligned sequences are highly significant; the probability that such a similarity is fortuitous is $<10^{-9}$ (Fig. 3*a*).

Analysis of the corresponding nucleotide sequences also revealed a high degree of similarity at the DNA level (100 matches over 195 positions, that is 51.3%; see Fig. 3*b*). A striking feature of the similarities is their clustering into three blocks of 34, 35 and 30 bp, where 73.5%, 80% and 70% of the respective positions are occupied by identical nucleotides. As the codon usage is not the same in *E. coli* and in *B. subtilis* (as indicated, for example, by the respective usages of the *trp*E genes of these two organisms[17,18]), such similarities strongly suggest that the two genes are evolutionarily related.

The regions shown in Fig. 3 correspond to different internal parts of the two proteins: residues 58–127 of the 239-amino acid polypeptide encoded by *spo*IIG and residues 375–439 of the *E. coli* sigma factor, a polypeptide of 613 amino acids[13]. However, their high degree of similarity strongly suggests a common function for these two protein domains. This leads to the attractive hypothesis that the *spo*IIG gene product may act as a specific sigma-like factor and that the region it has in common with the genuine *E. coli* sigma factor may similarly be involved in binding to the core RNA polymerase. This hypothesis is strengthened by the known functional and structural relationship between the *E. coli* and *B. subtilis* core RNA polymerases[19–21]. Moreover, recent nucleotide sequence analysis of the *B. subtilis* σ^{55} structural gene (R. H. Doi, personal communication) indicates that the homologous region in the *E. coli* sigma factor and the *B. subtilis spo*IIG gene product is conserved in the major sigma factor of *B. subtilis*, σ^{55}, confirming previous immunological experiments[22]. One obvious possibility is that the *spo*IIG gene encodes σ^{29}, a polypeptide associated with RNA polymerase purified from *B. subtilis* sporulating cells and conferring on it new promoter recognition specificity [23]. σ^{29} is a M_r 27,000–29,000 polypeptide[4,23,24] and appears about 1 h after the onset of sporulation[23], the exact moment at which the temperature-sensitive period starts in strain 279.1, a strain mutated in the *spo*IIG gene[8]. However, sporulation involves the expression of multiple gene sets and could rely on the presence of several alternative sigma-like proteins. The *spo*IIG gene product could equally be one of these, as yet uncharacterized, transcriptional factors.

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Note added in proof: The region of homology between the *B. subtilis spo*IIG gene product and the *E. coli* sigma factor has recently been found to be conserved also in the heat shock regulatory protein of *E. coli*[27].

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Erratum

New evidence that growth in 3T3 cell cultures is a diffusion-limited process

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BECAUSE of an editorial error, an incorrect figure was used in this letter. The correct Fig. 3 is shown below.