Proserpinaca. Gibberellic acid promotes the type of vegetative growth associated with long days. It promotes adult features typical of long-day-grown *Eucalyptus* (3) and juvenile features typical of long-day-grown *Kalanchoë* (4). It also induces erect growth of the long-day-plant *Trifolium* (5) which has an inherited light-imposed prostrate habit like that of short-day *Proserpinaca.* Low temperature has an effect opposite to that of gibberellic acid on *Proserpinaca.* It induces horizontal habit and formation of dissected leaves in long-day plants. Since photoperiod also affects habit, the response of the plant to gravity appears to be mediated by phytochrome, the pigment system which controls plant responses to photoperiod. The phytochrome system therefore interacts with temperature and externally applied gibberellic acid to control leaf shape, leaf orientation, and the geotropic response of the shoot.

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Ribosomes:
A Common Structural Feature

Abstract. A reflection between 45 and 50 Å has been observed in x-ray diffraction patterns from ribosomes extracted from Escherichia coli, Drosophila *larvae, rat liver, and rabbit reticulocytes. This spacing appears to correspond to a common substructural feature within the ribosomes. The intensity distribution is consistent with a model in which part of the RNA is in the form of four or five parallel double helices 45 to 50 Å apart.*

Knowledge of the substructure of ribosomes is of obvious importance for an understanding of the mechanism of protein synthesis. Electron-microscope studies of *Escherichia coli* ribosomes (1) have outlined the gross features; the published evidence for substructure merely indicates that it ap-

Table 1. Reflection in x-ray diffraction patterns of ribosomes. The experimental error is ± 1 Å.

Source and size of ribosomes	Spacing (Å)
E. coli, 50S	45.5
E. coli, 70S	46.5
E. coli, 100S	46.5
Drosophila larvae, 80S	48.5
Rat liver, 80S	49.5
Rabbit reticulocyte 78S	48.5

pears to be in the size range 25 to 70 Å (1, 2). Earlier studies by x-ray diffraction (3) were concentrated on the wide-angle part of the diagram and they showed that the structure of the ribonucleic acid (RNA) and protein components are somewhat independent.

The hypochromism at 260 mμ of intact *E. coli* ribosomes is the same as that of the extracted RNA (4), and since the x-ray diffraction patterns from noncrystalline fibers of ribosomal RNA are identical to those from noncrystalline transfer RNA, which has a DNA-like double helical structure (5), it is likely that sections at least of ribosomal RNA have this structure. Low-angle absolute intensity x-ray scattering measurements of RNA of high molecular weight (probably mainly ribosomal) from ascites tumor cells, *E. coli*, and yeast have been interpreted to signify short rigid rods of about 50 to 150 Å in length with a weight per unit length similar to double-stranded helical DNA, joined by small flexible regions (6). The observation of a broad reflection at 12.5 Å is consistent with the presence of RNA double helices in the intact ribosome (7).

More-detailed low-angle x-ray diffraction patterns of concentrated gels of *E. coli* ribosomes (7) indicate a linear aggregation of the particles. Only one reflection, at 45.5 Å, cannot be fitted to the predicted diffraction from such a structure. This reflection is strong and fairly sharp and occurs even in preparations for which the other reflections are diffuse or very weak. It appears to correspond to substructure within the particle (7).

Further x-ray diffraction studies have now been made of ribosomes isolated from *E. coli, Drosophila* larvae, rat liver, and rabbit reticulocytes. Specimens were prepared and x-ray diffraction photographs were taken as previously described (7). Exposure times ranged from 50 to 150 hours. A reflection between 45 and 50 Å was observed in the diffraction patterns of ribosomes

from all the sources studied, implying a common structural feature (Table 1).

The sharpness of the reflection requires at least four repeats of this characteristic distance within the ribosome, and since all ribosomes appear to have a maximum dimension of about 200 to 250 Å, the number of possible repeats is limited to four or five. A second-order reflection at 23 to 25 Å is expected, but this is very weak or absent in all the diffraction patterns; thus the transform of the repeating unit is large near 45 to 50 Å and falls nearly to zero in the 23 to 25 Å region. The equatorial intensity transform of double-helical nucleic acid (8) has this distribution, and calculation shows that an array of four or five parallel RNA double helices, 45 to 50 Å apart, gives an intensity distribution in good qualitative agreement with that observed.

Since ribosomal RNA appears to be in one or two large pieces when carefully extracted (9), and since RNA double helices are quite rigid, it is probable that the helices are arranged in short lengths connected by regions where the double-helical structure is not preserved. The structure proposed for extracted RNA (6) with lengths of 50 to 150 Å for the double-helical regions is in good agreement with this model. The protein component of the ribosome might fulfill a structural function in preserving the 45 to 50 Å spacing in the ordered RNA, perhaps interacting with the RNA in the nonhelical regions (10).

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