Two patterns were found in the C14 distribution of the E. coli amino acids from tracer expts. with C14O2, C14H3COOH, CH3C14OOH, aspartic acid (I) and glutamic acid (II), both C14-uniformly labeled, and 1-C14-glutamic acid. The one family with the specific activity pattern like (I) included diaminopimelic acid (III), lysine (IV), threonine (V), isoleucine (VI), and methionine (VII). The other family which followed the pattern of II was proline (VIII) and arginine (IX). The distinction was also shown in the location of the isotope within the mols. of each member. C14-VIII was incorporated into the bacterial protein but was not converted to II or IX. A similar result was obtained for C14-IX. When cold glutamic-γ-semialdehyde was added to the C14-glucose medium, no C14 was found in the bacterial VIII, whereas all other bacterial amino acids were radioactive. From various expts., it was proposed that the syntheses of VIII and IX was, resp., as: II → glutamic-γ-semialdehyde → VIII, and II → N-acetyl-II → Nα-acetylornithine → ornithine → citrulline → IX; and the relations of the members of the I family were as follows:IV←I ↑III →homoserine↑VII→V→α-ketobutyric acid ↑α-aminobutyric acid ↓ →α-keto-β-methylvaleric acid → VI. Yeast (Torulopsis utilis), mold (Neurospora crassa), and algae (Chlorella pyrenoidosa) behaved in certain aspects similar to E. coli B.