line. The histamine is partly in mast cells, but partly also in nerve terminals. It is distributed unequally in the various regions of the brain, the region richest in histamine being the hypothalamus, within which different nuclei have widely different contents. The l-histidine decarboxylase that produces the neuronal histamine is also present and achieves a rapid rate of histamine synthesis, naturally followed by rapid breakdown. In experiments in which mechanical lesions were made in the medial forebrain bundle (an area associated with reward), a decrease of the histamine content and of its synthesising enzyme suggested that a tract of histaminergic fibres had been severed. All this evidence, much of which can also be found in a well-documented paper by M. Garbard and colleagues (*Science*, **186**, 833; 1974), encourages the belief that histamine should be added to the list of putative mediator or modulator substances involved in brain function.

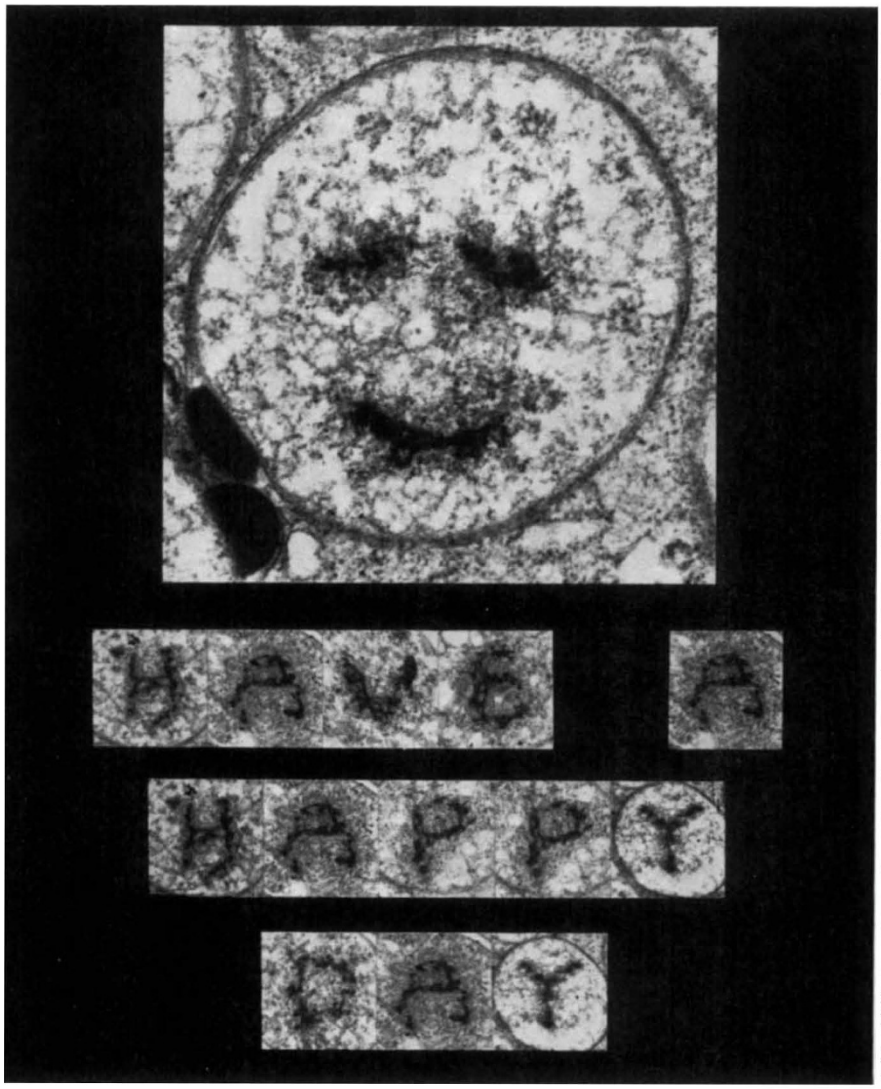
One of the best ways of deciding whether a putative mediator is a really serious candidate is to study the effects of its specific antagonists. Such tests, with the classical anti-histamines, whose development was started by Daniel Bovet and colleagues before the second World War, have clearly indicated that histamine plays a part in anaphylactic bronchoconstriction in the guinea pig and in nasal and dermal allergy in man. This criterion also suggested that histamine might be involved in such central nervous activities as wakefulness and motion sickness, because conventional anti-histamine drugs have sedative, hypnotic and anti-emetic properties.

These anti-histamines, however, failed in several directions in which they were at first expected to act; for example they did not inhibit gastric secretion induced by histamine. This difficulty led to the recognition of H_1 and other (later called H_2) receptors (Ash and Schild, *Br. J. Pharmac. Chemother.*, **27**, 427; 1966) and to the development of antagonists for the H_2 receptor and agonists for both types of receptor that were selective to the point of specificity (Black, Duncan, Durant, Ganellin and Parsons, *Nature*, **236**, 385; 1972).

As so often happens, the availability of a specific receptor antagonist enables the action of the agonist to be clarified. In this issue of *Nature*, Baudry, Martres and Schwartz (page 362), report some insights gained from using specific H_1 and H_2 receptor antagonists (mepyramine and metiamide respectively) and an H_2 agonist (4-methylhistamine) to analyse the mechanism whereby histamine stimulates cyclic AMP formation in slices of guinea-pig cerebral cortex, an effect first observed some years ago in rabbit cortex by Kakiuchi and Rall (*Molec. Pharmac.*, **4**, 379; 1968). The study of Baudry and colleagues shows that histamine acts on both H_1 and H_2 receptors to stimulate cyclic AMP formation, because it is not until both types of receptor are blocked that the effect of histamine is obliterated. This finding fits with clinical experience, in that the central nervous effects of antihistamines of classical type are usually evident, but seldom intense. It would be interesting to know whether both H_1 and H_2 receptor blockers, given together, would produce profound sleep.

Cracking the genetic code is peanuts

from A. S. Craig and K. L. Giles



Genetic material of bacteroids in peanut root nodules, showing the only message de-coded to this date. Magnifications various.

DURING a study of the fine structure of root nodules from peanut (*Arachis hypogaea*) some features of considerable interest have been found. Routine electron microscope preparations of nodule tissue revealed plant cells full of large spherical bacteroids whose nuclear (genetic) material stained unusually heavily.

It did not pass our notice that the form of the genetic material in section often took on the appearance of letters of the Roman alphabet. Armed with a knowledge of the genetic code one might have expected to find only the letters A, C, G and T. But so many were the letters found that it was possible to place several interpretations on them, one of which is shown. On these preliminary findings we are preparing a model of the genetic code based not so much on the idea of a macromolecular databank, as on a form of sophisticated semaphore.