is strengthened by two other experiments. When a solution of 50 mgm. of the toxin is incubated for 30 min. at 37° C. with a suspension of 100 mgm. of human erythrocyte stroma in saline[7] the toxin is completely absorbed and after centrifugation the supernatant contains neither agglutinating nor toxic activity. Moreover, when a saline solution of phaseolotoxin *A* in a concentration of 25 mgm./ml. is heated to 80° C. for 60 min. the activities are not completely destroyed, although the solution becomes milkily turbid due to partial denaturation and precipitation. Hæmagglutinating and toxic activity, however, are reduced to the same extent, namely, to about 50 per cent. Boiling for 30 min. uniformly abolishes both activities completely.

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CELL PHYSIOLOGY

Nuclear Origin of Ribonucleic Acid

Living hyphæ of *Neurospora crassa* were centrifuged and their contents stratified in distinct layers. Starting at the centrifugal end, the layers were as follows (Fig. 1): glycogen, ergastoplasm (microsomes), mitochondria, nuclei, 'supernatant' cytoplasm, vacuoles and fat. Each fraction could be identified by cytochemical reactions. It was found that most of the cytoplasmic ribonucleic acid resided in ergastoplasm, some in mitochondria, and none was detectable in the 'supernatant'. Nuclei were relatively poor in ribonucleic acid.

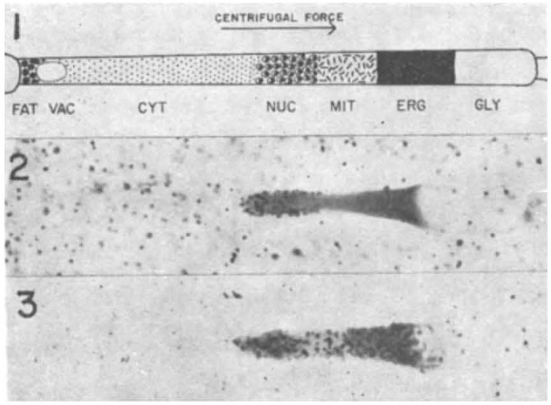

Fig. 1. Schematic presentation of a centrifuged hypha of *Neurospora*. *FAT*, fat; *VAC*, vacuole; *CYT*, 'supernatant' cytoplasm; *NUC*, nuclei; *MIT*, mitochondria; *ERG*, ergastoplasm (microsomes); *GLY*, glycogen. Centrifugal direction is to the right in all figures

Fig. 2. Autoradiograph of a centrifuged hypha fed tritiated uridine for 1 min. prior to centrifugation, stained with hæmalum. β-tracks in the nuclear layer; deeply stained layer, free of tracks, is ergastoplasm; glycogen and 'supernatant' not stained

Fig. 3. Autoradiograph of a centrifuged hypha fed tritiated uridine for 1 min. and unlabelled uridine for 1 hr., prior to centrifugation. β-tracks densest in ergastoplasm, less dense in nuclei and mitochondria; no significant increase of tracks over background in glycogen and 'supernatant'

The fact that nuclei became clearly separated from the cytoplasmic ribonucleic acid enabled us to localize the site of formation of ribonucleic acid. Mycelium, in its active growth phase, was fed tritiated uridine (uridine-5,6-^{3}H, 640 mc. per m.mole, 100 μgm./ml.) for given times, centrifuged and fixed. The mycelium was then washed in cold 5 per cent trichloracetic acid so that only nucleosides which were incorporated into ribonucleic acid remained. The preparation was mounted on a slide and covered with photographic emulsion[1]. After exposure and development, the autoradiographs showed tracks of β-decay at the sites of uptake of the precursor.

At short feeding times, from 1 to 4 min., the label appeared only in the nuclear fraction (Fig. 2). After 4 min., more and more label was found in cytoplasmic ribonucleic acid. In 1 hr., ergastoplasm was labelled much more heavily than the nuclei (Fig. 3), and some activity was found also in mitochondria, while the 'supernatant' remained virtually inactive. In brief, the distribution of the label became roughly proportional to the relative content of ribonucleic acid in the different fractions. When tritiated uridine was fed for 1 min. only and then washed out and replaced with an excess of non-labelled uridine, the label again appeared first in nuclei, to appear in the ergastoplasm only after several minutes. The labelling of ergastoplasm increased with time at the expense of nuclear label.

These results demonstrate that all the cellular ribonucleic acid is formed in nuclei and that it migrates into the cytoplasm later. Previous work of several investigators indicated that ribonucleic acid originated in nuclei[2] and the present experiments substantiate this hypothesis. These findings suggest that ribonucleic acid is a direct product of gene action. Ribonucleic acid is formed in nuclei, the seat of chromosomes and genes; it migrates into the cytoplasm; and it is required for the synthesis of proteins. A detailed report of this investigation will be published elsewhere.

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Hæmoglobin and 'Apparent Protein' in the Human Red Cell

The concentration C_{Hb} of hæmoglobin is conventionally measured by dividing the hæmoglobin in gm. per cent by the fractional concentration ρ, allowance being made for incomplete packing in the hæmatocrit tube. If a high-speed hæmatocrit is used, ρ can be found with an error of about ± 1 per cent, and the hæmoglobin concentration can be measured by the cyanmethæmoglobin method with an error of about the same magnitude.