ous extracts of macerated healthy tissue of brussels sprouts and tomato are compared after the manner of Tang and Bonner (*10*) with respect to auxin inactivation (Fig. 3), it is clear that brussels sprout root tissue has a greater capacity for inactivating auxin. The response of the root tissue to these three nematodes, as manifested by root gall size, appears to be a function of auxin synthesis and auxin inactivation. In the case of tomato, for example, auxin inactivation is provided only by *M. hapla* so that *M. hapla* produces small pinhead galls, whereas *M. javanica* and *M. incognita* produce large galls. In the case of brussels sprouts the auxin inactivation system provided by *M. hapla* is supplemented by that in the host tissue so that *M. hapla* produces almost invisible galls, whereas the normally massive galls of *M. javanica* and *M. incognita* are reduced to the small pinhead-sized galls normally effected by *M. hapla* on tomato.

Our experiments thus demonstrate the ability of parasitic nematodes to disturb the growth regulatory mechanisms of plants. Consideration of the systematic or superficial manifestations of host tissue response to other parasitic nematodes indicates that interference with the plant growth regulatory mechanism is a relatively common occurrence.

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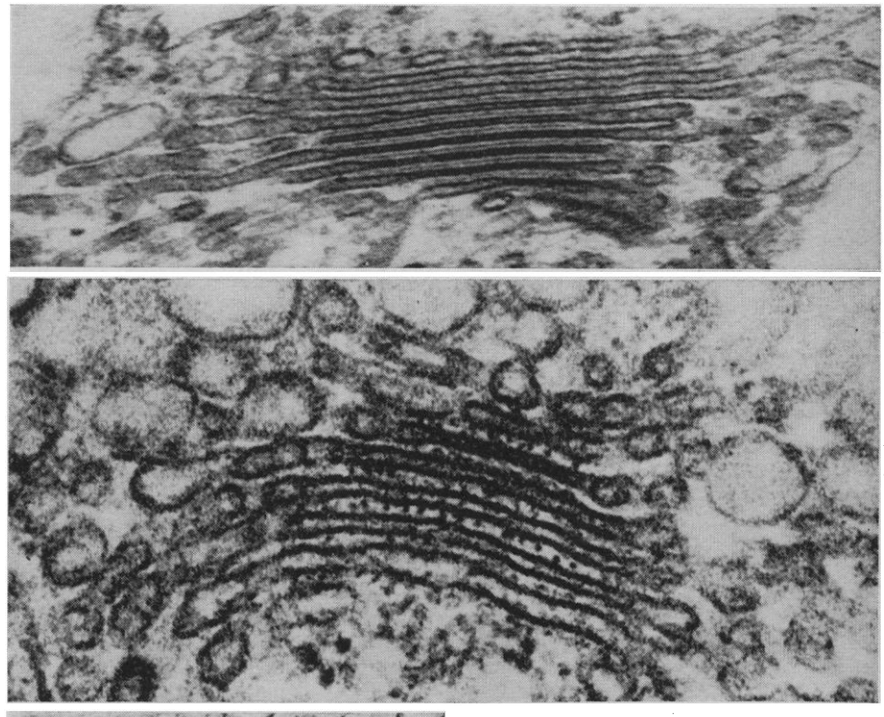
Intercisternal Elements of the Golgi Apparatus

Abstract. *In both vegetative and reproductive cells of various* Nitella *species, and in cells of other plant genera, there are fine, parallel, elongated elements lying between the cisternae of the Golgi apparatus but not in contact with the cisternal membranes.*

For some time there has been reason to believe that structural elements exist in the Golgi apparatus which have not been demonstrated in osmium tetroxide or potassium permanganate preparations. When removed from the cell the cisternae of the Golgi apparatus tend to remain associated in the typical distinct pattern of the organelle (*1*).

In both vegetative and reproductive cells of various *Nitella* spp., fixed first in cacodylate-buffered glutaraldehyde and then in osmium tetroxide, and stained first with uranyl acetate and then with lead citrate, certain views of the Golgi apparatus show an electron-dense line between some or all of the adjacent cisternae (Fig. 1). When the Golgi apparatus is viewed at what is presumed to be a 90° angle to that in which these intercisternal elements are revealed as electron-dense lines, the appearance is one of sections through individual elements (Fig. 2). This observation suggests that the elongated elements may have a definite orientation



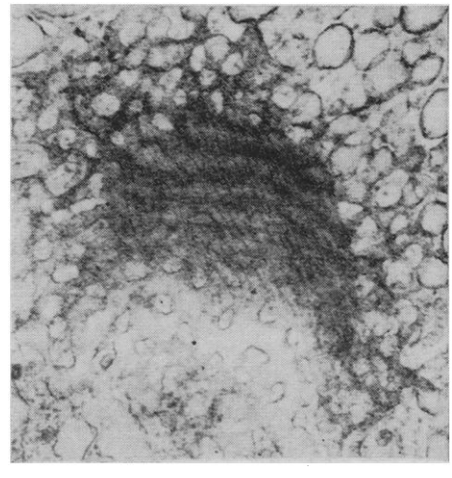


Fig. 1 (top). Electron micrograph showing electron-dense lines between cisternae of a Golgi apparatus from a vegetative cell of *Nitella* sp. (× 67,500).

Fig. 2 (center). What are presumed to be the same structures cut at an angle of approximately 90° from those in Fig. 1. From a reproductive cell of *Nitella* sp. (× 112,000).

Fig. 3 (left). An oblique cut showing the elongate, parallel character of the elements. From the same material as Fig. 1 (× 39,200).

between the cisternae. This hypothesis is supported by the observation of oriented elements in sections cut parallel or obliquely to the long plane of the cisternae (Fig. 3). Preliminary measurements indicate that these elongated elements are of the order of 70 to 80 Å in diameter. The elements are apparently essentially parallel, and appear, at least in some instances, to be arranged in lines from one intercisternal space to the next. In our preparations these elements were not in direct contact with the membranes of the cisternae.

What appear to be the same structures have now been demonstrated in several types of cells of different organisms. Whether they can be equated with the fine electron-dense lines seen earlier by Mollenhauer and then by others in this laboratory in cells of the root apex of maize has not yet been established. It is clear, however, that with the procedures used it is possible to demonstrate in some cells definite intercisternal structures in the Golgi apparatus. In some instances these intercisternal elements are more apparent toward one face of the apparatus than the other, possibly in relation to a progression of changes across the apparatus as seen in the production of secretory product (*2*). In other instances they are seen between all the cisternae. The difference could represent stages in the ontogeny of the apparatus. The demonstration of these intercisternal elements strengthens the concept of the apparatus as an organelle of which the cisternae are units, as opposed to the concept of the cisternae as simply being grouped in a Golgi zone. The elongated character of these elements and their parallel arrangement indicates a polarity that may prove to be important. Further study should clarify the functional aspects of these newly observed structures.

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Immunoglobulin Structure: Amino- and Carboxyl-Terminal Peptides of Type I Bence Jones Proteins

Abstract. *Analysis of the amino acid sequence in Bence Jones proteins permits study of the structure of L-chains of normal immunoglobulins. An amino-terminal octadecapeptide containing the sole methionine residue occurs in many but not all immunoglobulins of antigenic type I. The carboxyl-terminal octapeptide appears invariant in type I proteins and ends in cysteine, which may have a cross-linking function.*

The structure of the polypeptide L-chains of the immunoglobulins is deemed related to antibody function; however, on the basis of antigenic characteristics and peptide maps two wholly different types of L-chains exist, type I and type II (*1*). These are structurally similar to the two types of Bence Jones proteins and differentiate each of the three classes of serum immunoglobulins (γ_G, γ_A, and γ_M) into the corresponding two antigenic types (*2*). By comparison of the tryptic peptide maps of type I Bence Jones proteins, type I globulins from the serums of patients with lymphomatous diseases, and normal human γ-globulin we have established that all proteins of this antigenic type contain many tryptic peptides in common (*3*). Whether these peptides represent an identical L-chain or the common portion of a similar L-chain has yet to be established. However, since individual Bence Jones proteins of type I contain a common structural moiety, yet differ in some peptides, we have assumed that, in general, type I L-chains contain a fixed portion and also a mutable portion in which antibody specificity may reside (*4*). The fixed portion contains a series of tryptic peptides previously designated B_1, B_2, B_6, B_7, B_9, B_{11}, B_{13}, and B_{15} (*3–5*); the sequence of most of these has since been determined in our laboratory. A paramount question is whether type I L-chains share many identical sequences but differ at fixed points, for example, in the amino- or carboxyl-terminal peptides, or whether the differences in sequence are randomly located. Our results suggest that an octapeptide COOH-terminal sequence is identical but that differences occur in the NH_2-terminal portion.

A type I Bence Jones protein (Ag) was purified on a diethylaminoethyl (DEAE)-Sephadex column, reduced with mercaptoethanol, and alkylated by reaction with monoiodoacetic acid. A tryptic digest was prepared (with the *p*H-stat), and the soluble peptides were removed and fractionated. Seven basic peptides were separated from the fraction containing the neutral and acidic peptides by chromatography in a gradient elution system (0.5*M* pyridine–0.02*M* acetic acid to 2*M* pyridine–1*M* acetic acid on IRC-50, the column being 1.8 × 150 cm). The column was operated at 50°C, with a flow rate of 80 ml per hour. The fraction containing the neutral and acidic peptides was separated into a series of peptides by chromatography on Dowex 50-X2 (column, 1.8 × 150 cm) with a gradient elution system from 0.1*M* pyridine–formic acid (*p*H 3.1) to 1*M* pyridine–acetic acid (*p*H 5.0) at 40°C with a flow rate of 80 ml per hour. In all, 19 peptides have been obtained in yields ranging from 22 to 70 percent of theoretical. This excludes minor peptides and those present in the insoluble "core." The amino acid composition of many of these peptides is in accord with that previously reported (*5*).

By use of the dinitrophenyl (DNP) method and the phenylthiohydantoin method the probable sequence has been determined thus far for 11 peptides and partial sequences of others; this accounts all told for about one-half of the molecule. We confirm the sequence Gly-Glu-CySH (*6*) found in another type I Bence Jones protein by Milstein (*7*) for the tryptic peptide of this composition (B_1), which we previously reported to be COOH-terminal (*5*, *8*). For the COOH-terminal peptic peptide Milstein found the sequence Lys-Ser-Phe-AspNH_2-Arg-Gly-Glu-CySH; we have established the sequence of our tryptic peptide B_9 as: Ser-Phe-AspNH_2-Arg. Since B_1 and B_9 are present in the tryptic peptide maps of all type I Bence Jones proteins and immunoglobulins investigated in our laboratory, as well as in normal 7*S* γ-globulin, we suggest that this octapeptide sequence may be an invariant part of the structure of type I L-chains. Its apparent function is to provide the COOH-terminal cysteine residue which