As a result of progress in microscopic instrumentations, microscopists feel that they are only in the beginning of a new era of subatomic microscopic imaging [1]. The biologist could study the components of cells. Moreover, the great value has definition of elementary structure of the sample, and also computation and characterization the received images[2-3].

The aim morphometric and stereometric computations analysis TEM, SEM have been carried software programs structures of bioorganic(virus,bacteria, yeast, protozoa).

The investigation objects were the rotaviruses, virus-symbionts, bacteria, candida, entamoeba. The identifications of organic and inorganic particles conducted by means of transmission (TEM) and scanning electronic microscope (SEM) and SEM microanalysis. For preparing electronic-microscopic preparations of biological samples were standart methods. Computer morphometric and stereometric analysis of electronic microscopic pictures was performed according to the softwar computer programs.

TEM the virus-symbionts of entamoeba are shown to have stick-type form: surface square - 11036 nm2. The application of direct TEM method allows visualization of the surface of E. coli: there is a large number of fimbria. Computer stereometric TEM analysis of these fimbria points out that their diameter is 8-15 nm. Morphometric SEM analysis of the C. guilliermondii(Cg) after x-ray radiation allow to consider the relation of squareof destructive structures to the total square cell of Cg is equal to 26,2773 :73,723. The length of ribonucleoprotein helical-like nanoparticles and crystal body in the vegetative and cyst forms of protozoa was found to 300 nm (diameter - 40 nm)and intracitoplasmatic cylindrical structure of hematophage Ent.histolytica (Fig.1,2). The computer three-dimensional visualization has allowed to transform the image of the plane of cellular structures in the measurement using for building of cordinate of brightness, and also with the help softwar service of programs to show certain colour spectra of the one-colour image.

References

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Fig. 1: TEM. Computation of ribonucleoproteid spiral aggregates of chromatoid body of Entamoeba according to the softwar computer programs.

Fig. 2: TEM Intracitoplasmatic cylindrical structure of hematophage Ent. histolytica computer analysis according to the softwar computer programs.