food and water ad libitum. Each day, beginning from the 17th to the 22nd day of gestation, females were sacrificed by ether. The fetuses, recovered on autopsy were all alive. They were weighed and their weight was recorded in mg. The mean weight of fetuses in one and the other group was calculated for each day of the observation period. The total number of observed fetuses was 145 in the experimental group, and 151 in the control group. The table shows the number of fetuses observed on individual days of fetal development in each of the 2 groups. Statistical analysis has shown that there were no significant differences between the groups with respect to the daily number of fetuses observed ($\chi^2 = 3.66$; [11, 10]).

Results and discussion. The figure displays graphically the mean values of fetal weight by day of fetal development in both, experimental and control group. The difference between the fetal weight of the experimental and control group for each day of the observation period is statistically significant at the level of $p < 0.05$ and $p < 0.01$, respectively. The difference in weight was the smallest on the 17th day of fetal development and the greatest on the 22nd day. During the period between the 17th to 22nd day the fetal weight of the experimental group increased only for 2.430 mg, and that of the control group for 4.560 mg.

These results show a negative influence of the restriction of the daily quantity of food on fetal development. The negative effect manifested itself as a statistically significant retardation in fetal b.wt between the 17th and 22nd day of the fetal development. The mechanism of the effect of restricted daily quantity of food on the weight of the fetus is very complex[6]. In parallel with the quantitative reduction of the total amount of food and its individual components, the supply of calories is reduced too. These are the factors that directly influence the fetal development.

Number of observed fetuses in the experimental and control group by day of gestation.

Days of gestation	17	18	19	20	21	22
Restrected	15	20	31	24	35	20
Unrestrected	18	16	35	19	32	31

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The relationship between basal bodies and the motility of *Polytoma papillatum* flagella

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Summary. The maternal flagellar apparatus of dividing Polytoma papillatum cells lose their basal bodies but retain their motility. It is concluded from this fact that basal bodies are neither essential for the structural maintenance of flagella nor for their motility.

During the course of vegetative cell division, the most familiar species of Polytoma and of Chlamydomonas differ in their behaviour of motion; Chlamydomonas cells lose their motility, whereas Polytoma cells retain theirs[2-7]. During division, Chlamydomonas cells lack flagella but contain basal bodies[8-11]. However, in Polytoma both flagella of the mother cell survive long enough for all the daughter cells to form their own flagellar apparatus[3,4,6]. As conjectured by Schneider[2], exactly observed by Prowazek[5] and confirmed by present electron microscopic investigation, the bases of the mother flagella of Polytoma are connected with the posterior end of one of the daughter cells until the daughters swarm out. The daughter cell, which provides locomotion for the whole maternal complex, finally leaves the mother wall by breaking away from the bases of the mother flagella with a distinctly perceptible jerk[5].

Culture conditions and all the other preparation procedures were as described previously[13].

The structural details in the flagellar apparatus of Polytoma coincide nearly exactly with those of Chlamydomonas[11,12]; for this reason we can dispense with a detailed description. Comparison of our figures using Cavalier-Smith[11] nomenclature with descriptions and illustrations of Chlamydomonas flagellar apparatus[11,12]

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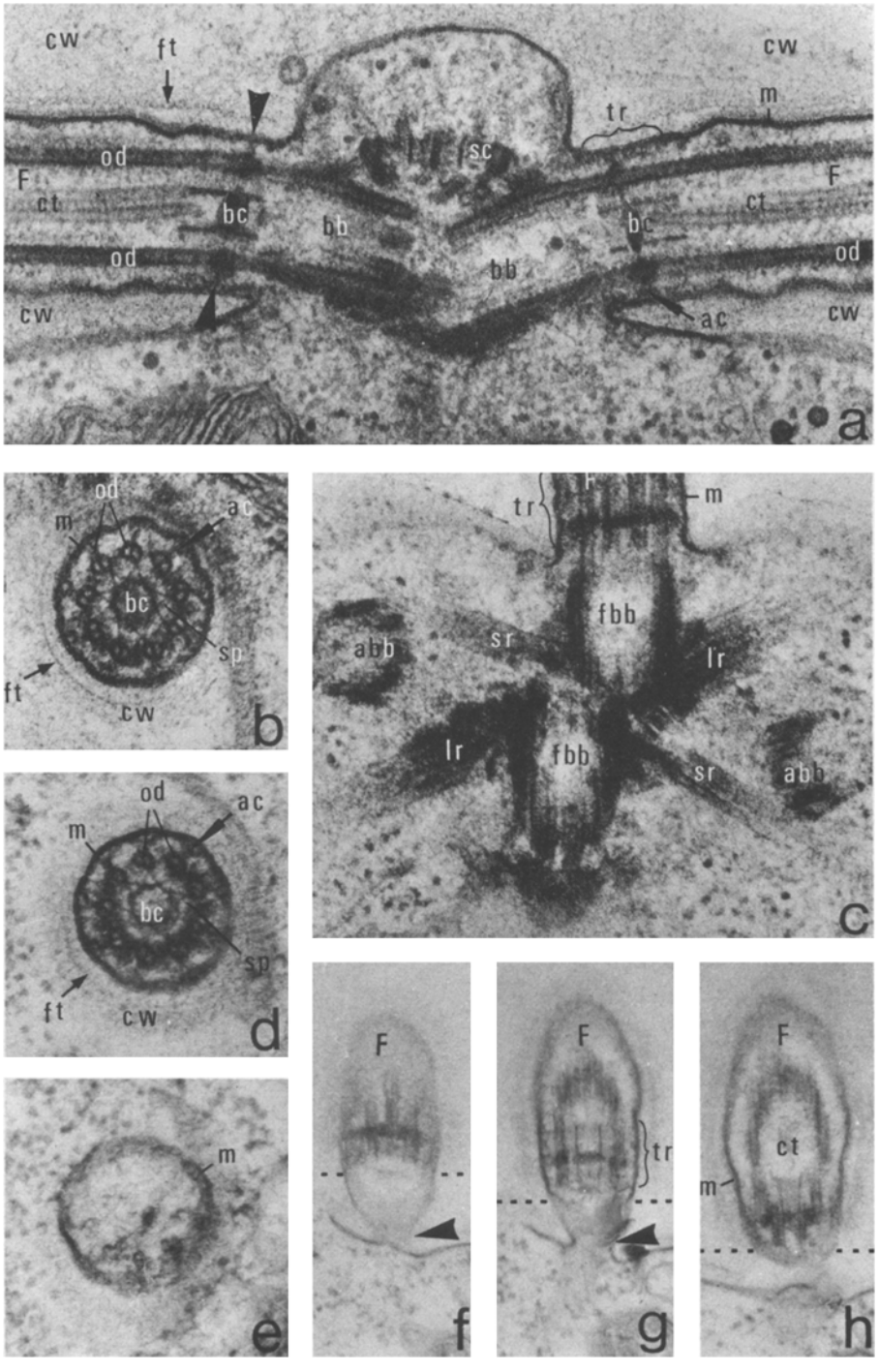
also provides information about the construction of flagella in the interphase cells of Polytoma (figure, a–c). Despite the overall similarities in ultrastructure, 2 distinct differences are visible: 1. The flagella of Polytoma are oriented to one another at a more obtuse angle than in Chlamydomonas (Pol. ca. 140°; Chl. 70–100°); 2. 2 additional basal bodies, besides the basal bodies bound to the flagella, are generally found not only in interphase



a A view of both flagella (F) in a longitudinal section showing the orientation of the basal bodies (bb) in a Polytoma interphase cell: distal striated connection (sc), transitional region (tr), central pair of tubules (ct), flagellar tunnel (ft) in the cell wall (cw), basal cylinder (bc) and annular connexion (ac) joining the outer doublets (od) to the flagellar membrane (m). ×85,000. *b* Transverse section of flagellum in an interphase cell at the plate-like transitional region (indicated by arrow-heads in *a*) shows the star pattern (sp) surrounding the basal cylinder (bc). Other abbreviations as in *a*. ×85,000. *c* A section perpendicular to that of figure *a* demonstrating the presence of 4 basal bodies (2 flagella-bound ones [fbb] and 2 additional ones [abb]). 4 roots (bands of tubules), 2 of them smaller (sr) than the other 2 (lr) form an X-configuration. Other abbreviations as in *a*. ×72,000. *d*, *e* 2 adjacent transverse sections through one of the maternal flagella of a Polytoma division stage which contains 4 separate daughter cells. *d* At the level of the proximal part of the basal cylinder of the transitional region. Notice the star pattern (sp). *e* At the point of basal body detachment. Diameter of flagellum is already slightly reduced. ×82,000. *f–h* 3 adjacent, slightly oblique longitudinal sections through one of the maternal flagella of a Polytoma division stage, which contains 8 separate daughter cells, demonstrating the flagellar constriction (arrow) and the point of basal body detachment (dotted lines). ×56,000.

cells[13], but also in cells just going through cytokinesis. These additional basal bodies are physically attached to 2 small roots which form an X-configuration with 2 larger roots (figure, c). In Chlamydomonas, extra basal bodies are present as a rule only in predivision (preprophase) cells[9–11].

Investigation of P. papillatum division stages with 2, 4 and 8 separate daughter cells, either completely enclosed within the mother wall or just leaving the opened mother wall, revealed that the flagella-bound basal bodies of the mother cell, without exception, detach from their axonemes at the proximal end of the plate-like transitional region (triplet-to-doublet transition) (figure, d, e). This event of detachment corresponds to that of Chlamydomonas[9–11]. The mother flagella are constricted at the point where they join the posterior end of the daughter cell (figure, f–h). Corresponding indentations in Chlamydomonas[9,10] were interpreted as the places at which flagellar abscission or breakage occurs. Withdrawal[8] or regression[11] of the flagella are also suggested; these are the results of a gradual shortening or disassembly which probably starts at the flagellar tip and proceeds sequentially to the base until it reaches the point just below the transitional region. Resorption of flagellar protein prior to cytokinesis and re-utilization of protein during the formation of daughter cell flagella have been taken into consideration[14].

Light microscopic observation confirmed the motility of Polytoma papillatum division stages containing 2 and 4 separate daughter cells. From the present experiments, it was determined that: a) In contrast to theories of Lenhossék[15] and Henneguy[16], basal bodies are not kinetic centers. b) In contrast to the supposition of Johnson and Porter[9], basal bodies are not essential for the maintenance of flagella. Thus, flagellar motility in Polytoma clearly does not depend on the presence of basal bodies. Reactivation experiments with ATP also showed that in cilia and flagella lacking basal bodies the mechanism of flagellar motility takes place in the axonemes[17].

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Steroid metabolism by mouse preimplantation embryos in vitro

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Summary. Mouse preimplantation embryos were incubated with radioactive pregnenolone, progesterone or dehydroepiandrosterone for various periods of time. These substrates were not converted to metabolites even after incubation of 120 h. We suggest that preimplantation mouse embryo does not possess enzyme activities for steroid metabolism.

The idea that the blastocyst could contribute to the implantation by its own steroid hormone production has been proposed by Dickman et al.[2]. The pioneer work of early steroid metabolism was done by Huff and Eik-Nes[3] in 1966. They demonstrated that 6-day-old rabbit blastocysts possessed enzyme systems for synthesizing cholesterol and pregnenolone in vitro from acetate. Progesterone was metabolized further to 5β-pregnandione, 3α-hydroxy-5β-pregnan-20-one and 20α-hydroxy-4-pregnen-3-one.

Competitive protein-binding techniques have revealed endogenous levels of progestins (progesterone [0.003 to 0.165 nmoles/ml], 20α-hydroxy-4-pregnen-3-one and 17α-hydroxy-4-pregnene-3, 20-dione) in rabbit blastocysts[4].

Perry et al.[5] using radioimmunoassay found progesterone, estrone and 17β-estradiol in pig blastocysts. Incubation studies still indicated weak $\Delta^5$3β-hydroxysteroid dehydrogenase, 17–20-desmolase, aromatase, 17β-hydroxysteroid dehydrogenase and 3-sulphatase activities.

The presence of $\Delta^5$3β-hydroxysteroid dehydrogenase has been shown histochemically in rat[2,6,7], mouse[8] and hamster[9,10] preimplantation blastocysts, and it was concluded that these embryos could synthesize progesterone. The biochemical studies of Chew and Sherman[11] with preimplantation mouse blastocysts did not support these results. The authors suggested that the apparent discrepancy may be explained by the histochemical method. Dickman and coworkers[8] used dehydroepiandrosterone instead of pregnenolone as substrate.

However, the mammalian embryos bath in a steroidal environment which offers them the possibility to bind and metabolize steroids. Our aim was to show biochemically what kind of steroid metabolism may occur in preimplantation mouse blastocysts.

Table 1. Pregnenolone incubations

Amount of incubations	n	Stage	Incubation time (h)	Recovery in percent of dose Substrate	Metabolites
3	10	2–3	14	93.2 ± 3.0	0
3	50	2–3	24	84.6 ± 3.6	0
1	5	4–5	48	87.5	0
6	10	3–5	48	89.1 ± 1.8	0
3	10	3–4	120	83.0 ± 3.4	0

n, Amount of embryos in incubation.

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