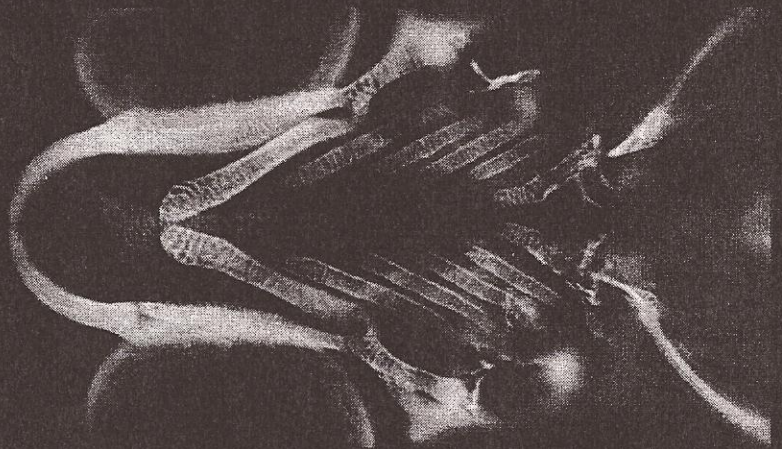
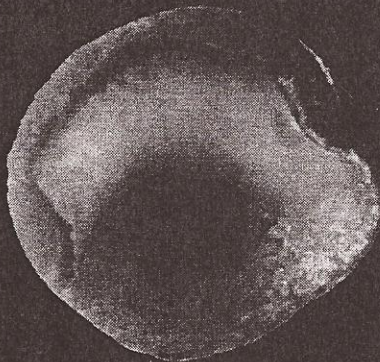


Santa Cruz
Developmental Biology Meeting
June 30th-July 3rd, 2010



“Diverse Strategies in Development”

***Diverse Strategies
in Development***

2010 Santa Cruz Developmental
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P7

In guinea pig sperm phosphorylated aldolase A probably participates in the actin polymerization during capacitation

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Upon release from the testis, mammalian sperm are unable to fertilize. To acquire the ability to fertilize they need a series of complex biochemical and physiological changes that implicate maturation and capacitation. Capacitation occurs while the cells are traveling through the female genital tract and it involves an increase in protein phosphorylation and switching to hyperactivated movement pattern. Sperm contain tyrosine kinases, PKC, PKA as well as glycogen synthase kinase. These kinases phosphorylate tyrosine and serine/threonine residues. During capacitation an increase in tyrosine phosphorylation was reported. The major phosphorylated proteins at tyrosine such as tubulin and aldolase are located in fibrous sheath. We found an increase in tyrosine phosphorylation during incubation in capacitating conditions peaking at 30 min. Also, these cells were capacitated as evidenced by hyperactivated motility and 98% acrosome reaction in response to A23187. A specific inhibitor of PKA caused a decrease in the phosphorylated aldolase levels and the F-actin concentration. The glycolytic activity of aldolase was independent of phosphorylation. We propose a possible role for phosphorylated aldolase A in the actin polymerization observed during capacitation. Probably, phosphorylation controls a non-glycolytic role for aldolase in fertilization. This work was funded by Conacyt (#59176).

P8

Elucidation of the Gene Regulatory Network in Endoderm Development by Integrating Experimental and Computational Approaches

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Emergence of the primary germ layers is among the earliest events of cell specification in animal development. While much has been learned about the gene regulatory network (GRN) describing the mesendoderm specification in frog, there remains a large gap in our understanding of these events. Traditional biochemical assays for uncovering the GRN are considered both labor and time intensive, hence we decided to take an alternative approach, which utilizes a combination of computational methods with extensive perturbation analysis, to produce a GRN. We have been generating transcriptome profiles from tightly spaced stages of early embryogenesis to permit modeling of the dynamics of changes in transcript levels. These data are incorporated along with morpholino knockdown studies to perturb relevant gene expressions. Computational modeling is then used to identify critical core networks regulating endodermal development. Although the GRN generated using this approach may lack in the details of direct physical interactions, it has the advantage of rapidly generating a global perspective.