TOPIC: CONTROL OF CLEAVAGE PATTERNS,CHEMICAL CHANGES AND SIGNIFICANCE

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AUTHOR:NIRMAL KUMARI

CONTROL OF CLEAVAGE PATTERNS

A simple way to regulate cell divisions differentially during development would be to express all but one of the required factors constitutively, and to then modulate expression of the single remaining, rate-limiting factor. Our findings are consistent with this type of regulation, and suggest that stg mRNA is the rate-limiting factor whose expression governs mitotic patterns after interphase 14. The most suggestive of these findings are first, that stg mRNA is expressed in a spatio–temporal pattern that anticipates the mitotic pattern, and second, that the stg gene is required zygotically for initiation of the first patterned mitosis. Since cell-cycle arrest occurs earlier in stg mutants than in any other characterized zygotic mutant, it seems likely that maternal supplies of other cell-cycle factors persist past the time when stg

becomes required. The work of Lehner and O'Farrell on Drosophila cyclin A provides a clear example of a product that is required for mitosis yet seems not to be rate-limiting during the first zygotically controlled divisions. In contrast to stg, cyclin A derived from maternal mRNA is sufficient to support divisions through mitosis 15, and the level of cyclin A protein has little influence on the timing of mitoses.

We have demonstrated directly only that stg is required for mitosis 14, but our observations of mitotic patterns in hypomorphic and temperature-sensitive stg mutants suggest that stg is required for subsequent embryonic mitoses (Edgar, unpublished data). In addition, clonal analysis has indicated that stg is required for cell divisions in the imaginal discs during metamorphosis (Terle and Saint, personal communication). Although such observations do not address whether stg continues to be rate-limiting during later mitoses, the continued correlation of stg expression with mitotic patterns suggests that stg expression could determine the timing of all the postblastoderm divisions.

Perhaps our most significant finding is that the pattern of embryonic cell divisions may be predicted from the expression pattern of stg messenger RNA. This implies

that the mitotic pattern may be controlled through differential rates of stg transcription and/or RNA degradation. While we know little about RNA degradation in Drosophila, recent studies have defined a plethora of factors involved in generating complex spatio–temporal patterns of transcription during embryogenesis these factors are encoded by the “selector” genes that set up patterns and determine cell identities in the embryo. To date, most of the selector genes studied at the molecular level encodes DNA binding proteins of the zinc finger or homeodomain types that reside in the nucleus, and are widely believed to be transcription factors. This is fitting, since it has long been thought that selector genes determined cell fates by modulating the expression of “cytodifferentiation” genes encoding products directly responsible for cell structure, movement, and division. Our understanding of stg’s function clearly classifies it as a cytodifferentiation gene, and thus as a likely target of selector-gene regulation.

There are more compelling reasons than theory, however, to believe that stg is a selector-gene target. One is that the selector-gene expression patterns exhibit uncanny similarities to the stg expression patterns. Preceding mitosis 14, stg expression along the dorsoventral axis of the embryo is broken up into at least six distinct patterns

that fall into the six dorsoventral domains defined by selector genes such as zerknüllt, twist, and those of the spitz group. Along the anteroposterior axis, stg expression is divided into different patterns in the head, thorax, abdomen, and tail, regions that are determined by differential expression of selector genes of the gap and homeotic classes (Gaul and Jäckle, 1987. Within these regions, stg expression occurs in reiterated patterns with double- and single-segment periodicity that resembles pair-rule and segment-polarity gene expression patterns.

In theory, the various selector-gene expression patterns subdivide the embryo into enough uniquely specified domains to account for virtually all aspects of stg expression during cycle 14. Moreover, the patterns of mitosis 14 are altered in predictable ways in many selector-gene mutants (Foe, personal communication). We expect that the altered patterns of mitosis in these mutants will be correlated with altered patterns of stg expression. Accordingly, we would like to propose that stg activity, and thus the mitotic pattern, isregulated at the transcriptional level by a variety of selector-gene products. Much of this regulation may be indirect, but the relative timing of selector-gene and stg expression suggests that direct interactions, perhaps using

combinations of selector-gene encoded transcription factors, are involved.

CHEMICAL CHANGES DURING CLEAVAGE

Significant chemical changes go on in the fertilized egg during cleavage. They are:

Increase of nuclear material: During cleavage a steady increase in nuclear material (predominantly DNA) is observed. Cytoplasm of the egg is the source of such nuclear material. Cytoplasmic DNA contained in mitochondria and yolk platelets are available.

RNA synthesis: During cleavage messenger RNA (mRNA) and transfer RNA (RNA) are synthesized during cleavage, especially in late stages.

Synthesis of proteins: Throughout the period of cleavage there is steady and spectacular increase in protein synthesis.

SIGNIFICANCE OF CLEAVAGE

It converts a unicellular zygote into a multicellular embryo.

It maintains the cell size and nucleo-cytoplasmic ratio of the species.

Cleavage produces large member of cells or blastomeres required for the building of offspring's body.

During cleavage quick mitotic division of blastomeres occurs following which there is no growth of blastomeres.

Cleavage brings about the distribution of cytoplasm among the blastomeres.

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