

Acknowledgments: We thank P. Taghert for freely sharing information regarding their studies of the 39BC interval, and T. Laverty and G. Rubin for providing the P element stocks used in this study.

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Alatortsev, V.E. Institute of Molecular Genetics, Russian Academy of Sciences, Kurchatov Sq. 46, Moscow, 123182, Russia. An indication on overlapping functions of the *Vinculin* and α -catenin loci in *Drosophila melanogaster*.

Vinculin, a conservative protein of the cellular cytoskeletal and anchorage system, was localized in adherent contacts of cells (Geiger *et al.*, 1980; Burridge *et al.*, 1988; Geiger *et al.*, 1990). Vinculin is homologous to the other peripheral cytoplasmic protein, α -catenin, in vertebrates (Kemler, 1993). Recently the *Vinculin* and α -catenin genes were described in

Drosophila melanogaster (Alatortsev *et al.*, 1997; Oda, *et al.*, 1993). Structures of the corresponding *Drosophila* proteins are compared in this note.

Alignment of the vinculin (962 amino acids) and α -catenin (935 amino acids) sequences revealed that internal repeats and proline-rich domain are unique to the *Drosophila* vinculin. However, vinculin and α -catenin contain three extended regions of homology which occupy greater parts of their sequences (Figure 1). These regions lie within the highly conservative N- and C-domains of vinculin, as well as in the central part of the vinculin sequence. Given this multiple homology, it is possible to suggest that vinculin and α -catenin have some functions in common.

Interestingly, sequence of the central part of vinculin is variable in different vinculins (Weller *et al.*, 1990). High level of similarity between vinculin and α -catenin found for central region (71.5%) reflects co-evolution of two proteins in *Drosophila* and represents a special indication on overlapping functions of the *Vinculin* and α -catenin genes.

Acknowledgment: This work was partly supported by an RBRF grant.

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Figure 1 (next page). Alignment of amino acid sequences of the *Drosophila* vinculin (Dmvincp) and α -catenin (Dmcatp) produced with the help of the GENESEE program (Brodsky *et al.*, 1995). Standard parameters were used. Only regions with reliable homology are shown. The meaning of signs at the top of the alignment is following: '-' - the average weight of column pair exchanges is less than weight matrix mean value; '.' - is less than mean value plus one SD; '+' - is less than mean value plus two SD; '*' - is more than mean value plus two SD.

