Mutation Notes

Genes affecting wing planarity of *Drosophila virilis* (I): *curl.*

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Organ size and shape are species-specific. Both parameters result from the coordination of cell proliferation, cell death, and arrangement of cells in specific patterns. During the last decades, our knowledge regarding the genetic basis of the cell cycle and cell survival has been greatly advanced, but the systemic relationships between gene expression patterns in cells and their proliferation only now are beginning to be established (Albagli and Pelczar, 2006). The wing of *Drosophila* is an experimental model to study the genetic mechanisms of organ patterning and growth. Due to extensive research work in this area a large number of genes, genetic interactions, several different signalling pathways that regulate strictly specific gene expression pattern in individual and general wing morphogenesis programs in *Drosophila* were described (Baena-Lopez *et al.*, 2006). Nevertheless, our knowledge about genes that affect wing planarity is still incomplete (Molnar *et al.*, 2006). There are several genes of *Drosophila melanogaster,* such as *curled* (*cu*: 3-50.0), *Curly* (*Cy*: 2-6.1), *Upturned* (*U*: 2-70.0), *Curl* (*Cu*: 2-54.6), and so on, known to produce a curled wing phenotype if mutated. But their molecular functions, as well as genetic interactions are still unclear.

A new *D. virilis* mutant was observed in a progeny of dysgenic crosses between strain 9 females (wild type Batumi population) and strain *y Bx w* males [*yellow* (*y*: 1-2.9), *Beadex* (*Bx*: 1-94.5), *white* (*w*: 1-105.0)]. This new wing mutation was genetically mapped by recombination with *Delta* (*Dl*: 2-45.0) and *ebony* (*e*: 2-83.5) to a proximal end region of the 2nd chromosome on the approximate distance of 39 genetic map units left from the *Delta* locus. Hence, more accurate chromosome localization of the new mutation is still unclear. Cytological analysis of salivary gland chromosomes, obtained from heterozygous mutant females, did not reveal obvious chromosome aberrations.

In the crosses with wild type it was shown that the newly-observed mutation is recessive, non sex-linked, controlled by single gene, and non-lethal in the homozygote.

This new mutation affected not only the wing planarity, but as well some more morphological characteristics. In general the mutant wing has a sail-like shape. Wings of the mutant flies are curled upward and diverged with an angle of about 30º relative to the longitudinal axis. High temperature in the last day of pupal life enhances curled character of the wing. The dorsal layer of wing cuticle of the mutant flies, in contrast to the wild type, is crossed with several (from 1 to 4) plications in the proximal area of wing, which are visible in an optical microscope. The normal spatial orientation of the wing hairs in the regions of plicated cuticle is altered (Figure 1).

The postscutellars of mutant flies are erected and crossed. Body color of the mutant flies is dark. Such wing phenotype has not been described earlier for *D. virilis*, but is highly similar to *D. melanogaster curled* mutant phenotype; moreover, a new curled-like mutation of *D. virilis* appeared to be located in the chromosome region that is homologous to *D. melanogaster* chromosome region,

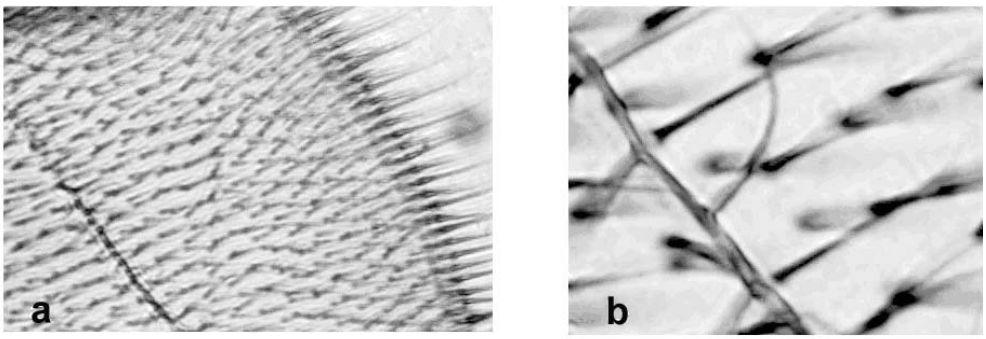

Figure 1. Cuticular plication in *D. virilis curl* wing (a) and wing hairs in the region of cuticular plication (b). Light microscopy.

where *curled* mutation is located. Thus, a new wing mutation of *D. virilis* was named *curled-like* with a symbol *curl*.

To propose a gene that causes the mentioned phenotype, a search for homologous sequences in *D. melanogaster* genome was carried out. Whiting *et al*. (1989) demonstrated sequence homology between proximal end region of the 2nd chromosome of *D. virilis* and 3R(85DE-97EF) region of *D. melanogaster* genome. According to FlyBase (http://www.flybase.org/maps), the *cu (curled)* mutation with the same phenotype is located within the bounds of 3R(85DE-97EF) region. Nucleotide sequence of *cu* genome region (FBgn0000387) contains 6 genes, named CG6629, CG33698, CG4706, Ugt86Dc, Ugt86Dd and Ugt86Di. Information about gene products and their molecular functions is presented in Table 1.

Table 1. Gene products and molecular functions of genes, located in *curled* gene genome region of *D. melanogaster*.

Gene	Product	Molecular Function	Biological Process	Flybase ID	References
CG6629	succinate dehydrogenase, complex, subunit-C, integral membrane protein	succinate dehydrogenase activity	mitochondrial electron transport, succinate to ubiquinone, succinate metabolism, tricarboxylic acid cycle	FBgn0037860	FlyBase, 1992-FlyBase curation [FBrf0105495]
CG33698	polypeptide	unknown	unknown	FBgn0053698	FlyBase Genome Annotators, 2005
CG4706	aconitate hydratase	aconitate hydratase activity	amino acid biosynthesis, tricarboxylic acid cycle	FBgn0037862	Betran et al., 2002 *Genome Res. 12(12): 1854--1859*
Ugt86Dc Ugt86Dd Ugt86Di	UDP-glucuronosyl transferase	glucuronosyltransferase activity	defense response, polysaccharide metabolism, response to toxin, steroid metabolism	FBgn0040257 FBgn0040256 FBgn0040251	Theopold et al., 1999 *Biochem. biophys. Res. Commun. 261(3): 923--927*

Thus, it is impossible to relate molecular functions of mentioned genes to the wing morphogenesis process; moreover, there is no information about expression of these genes during wing formation (Ren *et al*., 2005).

Most likely, the formation of the described phenotype is a result of complex genetic interactions, and the role of mentioned genes in this process is still unclear.

References: Albagli, O, and H. Pelczar 2006, Med. Sci. 22: 695; Baena-Lopez, L.A., and A. García-Bellido 2006, Proc. Natl. Acad. Sci. USA 103: 13734; Molnar, Cristina, Ana Lopez-Varea, Rosario Hernandez, and Jose F. de Celis 2006, Genetics 174: 1635-1659; Ren, Nan, Chunming Zhu, Haeryun Lee, Paul N 2005, Genetics 171: 625-638; Whiting J.H., J., Pliley M.D., J.L. Farmer, and D.E. Jeffery 1989, Genetics 122: 99-109.

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Waters, R.L., J.T. Smith, and R.R. Brown 1990, J. Genet. 47: 123-134.

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