Orthologs of the eggshell gene *Vml* contain a diverse number of coding tandem repeats.

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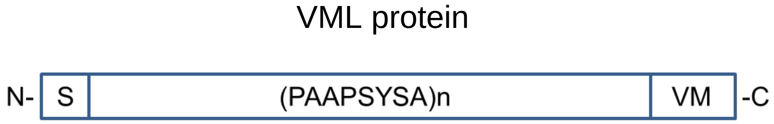
Gene *Vml* encodes a structural protein of the *Drosophila* eggshell vitelline membrane in *D. melanogaster* (Alatortsev, 2006) and participates in the establishment of the dorsal/ventral axis of the *Drosophila* embryo (Zhang *et al*., 2009). Protein VML contains an unusually large array of perfect and imperfect repeats PAAPSYSA in the central part (Alatortsev, 2006). Through genomes of 12 *Drosophila* species that were sequenced (Clark *et al*., 2007), orthologs of the *D. melanogaster* gene *Vml* were found only in closely related species *D. sechellia*, *D. simulans*, and *D. erecta* (FlyBase release FB2013_04, http://flybase.org).

For searching *Vml* orthologs in the rest of sequenced *Drosophila* species, fragments of the *Vml* gene and the FlyBase BLAST Service (http://flybase.net/blast) were used. It was found that orthologs in five *Drosophila* species (*ananassae*, *pseudoobscura*, *persimilis*, *mojavensis*, and *grimshawi*) correspond to the registered genes with unknown function (Clark *et al*., 2007). Unpredicted earlier genes were found in three species (*D. yakuba*, *D. willistoni*, and *D. virilis*). Possibly, these genes were not found earlier due to the strong searching parameters in gene finding programs used for genome annotations. All *Vml* orthologs have similar one exon gene structure and lie in synthenic regions between the corresponding orthologs of the *CG2918* and *CG2865* genes. Orthologous proteins have signal sequence for secretion at the N-end and cysteine-rich domain specific for vitelline membrane proteins (Scherer *et al*., 1988) at the C-end (Figure 1A,B). Lengths of orthologous proteins vary from 457 to 738 amino acids due to the presence of the different number of 8 aa repeats PAAPSYSA.

A



B

Species\Gene	VM domain
Dmel\Vml	-SLPSPPCPKNYVFSCSSVFTPAPCSQGYGY
Dsim\GD16605	-SLPAPPCPKNYVFSCSSVFTPAPCSQGYGY
Dsec\GM19220	-SLPSPPCPKSYVFSCSSVFTPAPCSQGYGY
Dere\GG12928	-SLPSPPCPKNYVFSCSSVFTPAPCSQGYGY
Dyak\Vml **X:6,157,204..6,158,844 [-]**	-SVPSPSCPKNYVFSCSSVFTPAPCSQGYGY
Dana\GF22208	-SVPAPPCPKSYVFSCQSVFSPAPCSQGSAY
Dpse\GA22863	-SIPAQPCPKNYVFSCLGVFQKAPCSQGLQY
Dper\GL13336	-SIPAQPCPKNYVFSCQGVFQKAPCSQGLQY
Dwil\Vml **scf2_1100000004401:330,889..332259 [+]**	-SIPAPPCPTNYVFSCNSVFKPAPCSQGSAY
Dmoj\GI21801	-SIPAPPCPANYVLSCKSVFTPAPCSQGAAY
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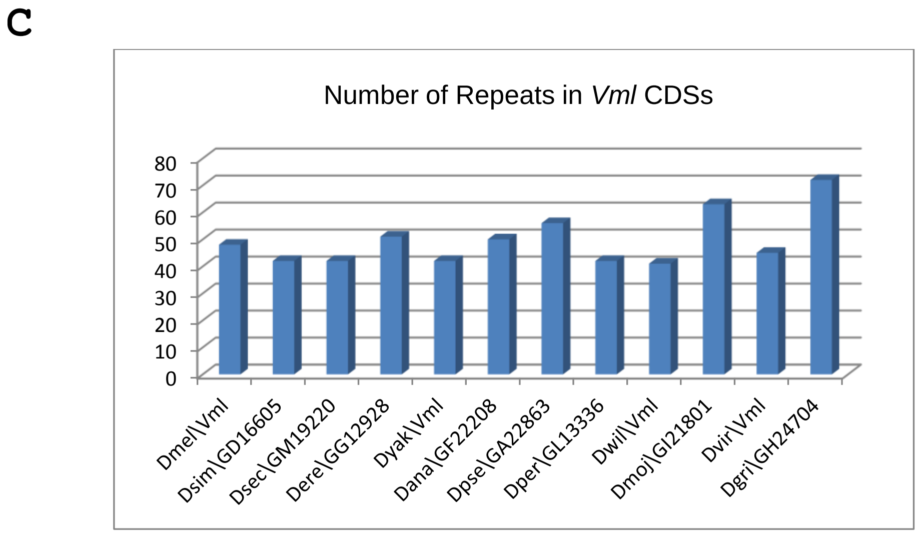

Figure 1. Structures of the VML orthologs. A, Domain structure of the VML protein: S, signal peptide; VM, domain specific for vitelline membrane proteins. B, Alignment of VM domain amino acid sequences of 12 orthologous VMLs. Orthologs found in this work are highlighted. Genome positions of orthologous genes in *D. yakuba*, *D. willistoni*, and *D. virilis* are given according to corresponding genome maps (FlyBase release FB2013_04). The VM domain sequence logo was created by WebLogo (Crooks *et al*., 2004). C, Number of 24 bp DNA tandem repeats in orthologous *Vml* coding sequences.

Quantity of 24 bp tandem repeats in orthologous genes was determined by the TRF program (Benson, 1999). It was found that orthologs contain a diverse number of coding tandem repeats (Figure 1C). Thus, *Vml* orthologs in closely related species *D. pseudoobscura* and *D. persimilis* have considerable differences in repeat number, 56 and 42 copies, accordingly. A functional consequence of this diversity between species remains unclear. Possibly, changes in repeat number participate in species-specific changes of eggshell morphology.

References: Alatortsev, V.E., 2006, Mol. Biol. 40: 330-332; Clark, A.G., M.B. Eisen, D.R. Smith *et al*., 2007, Nature 450: 203-218; Crooks, G.E., G. Hon, J.M. Chandonia, and S.E. Brenner 2004, Genome Res. 14: 1188-1190; Benson, G., 1999, Nucl. Acids Res. 27: 573-580; Scherer, L.J., D.H. Harris, and W.H. Petri 1988, Dev. Biol. 130: 786-788; Zhang, Z., L.M. Stevens, and D. Stein 2009, Curr. Biol. 19: 1200-1205.

Comparative analysis of the fragment of the Y chromosome gene *kl-2 1-beta dynein heavy chain* in *Drosophila virilis* species group (Diptera: Drosophilidae).

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Introduction

Drosophila virilis species group is one of the best studied models of speciation and microevolution (Morales-Hojas *et al*., 2011). We analysed Y chromosome DNA sequence variation