

TAF10 proteins indicate structural and functional links between histone acetyltransferase and basal transcription factor complexes

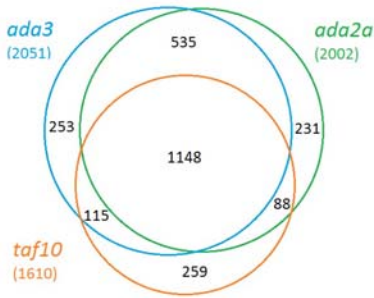


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TATA-binding protein associated factors (TAFs) have been identified as subunits of the TFIID basal transcription factor complex required for RNA polymerase II initiation. More recent studies indicate that TAFs are also present in histone acetyl transferase complexes which regulate transcription initiation and the organization of the chromatin structure. This observation raises the possibility of complex „transmutation” by which due to changes in subunit composition one type of multiprotein complex is converted to an other type as transcription initiation is progressing.

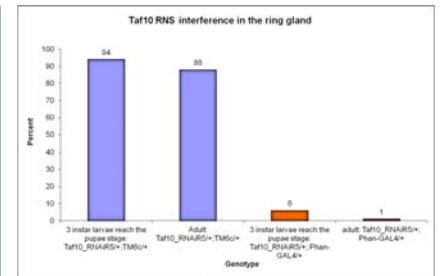
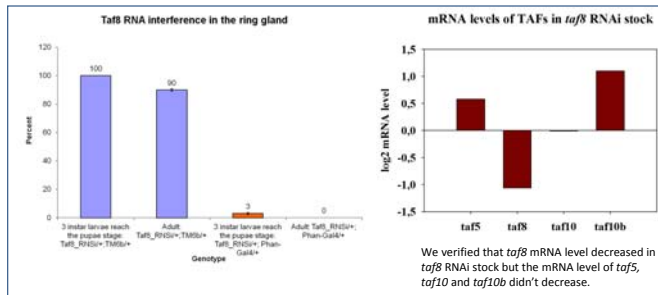
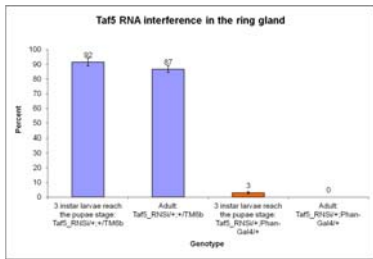
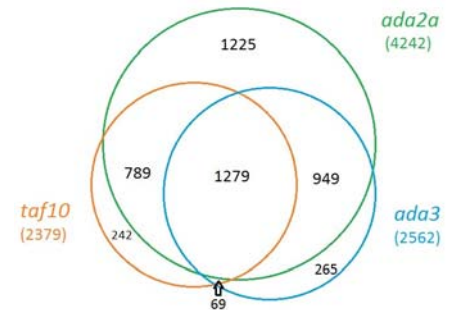
There are two major GCN5 histone acetyltransferase (HAT)-containing complexes in *Drosophila*, SAGA and ATAC. TAF10 subunits are present only in the SAGA, but not in the ATAC HAT complex. In contrast, we found that the gene expression alterations in *taf10* mutants are very similar to those observed in ATAC subunit (*Ada2a*, *Ada3*) mutants. First, we aimed to find out whether only *taf10* mutants have similar gene expression alterations to ATAC mutants or other TAFs mutants also show the ATAC-specific gene expression patterns. For this we studied the gene expression pattern of *Drosophila* stocks in which *taf5*, *taf10*, or *taf8* was downregulated by RNAi.

Upregulated genes

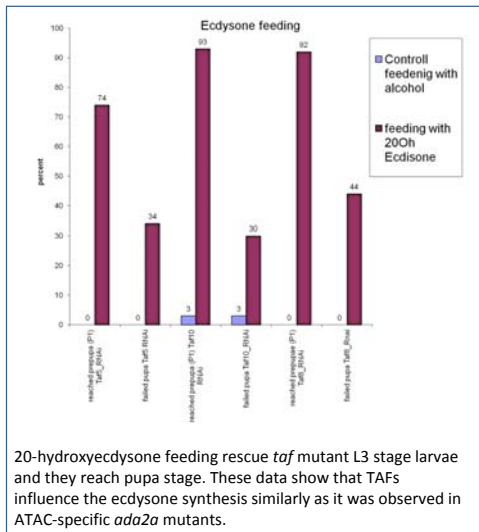


The venn diagrams show the number of upregulated and downregulated genes in *ada2a*, *ada3* and *taf10* mutant larvae. We used microarray to analyse the gene expression level in *ada2a* *ada3* and *taf10* mutant. The strong similarities between the *taf10* and ATAC mutant (*ada2a* and *ada3*) are clearly observable.

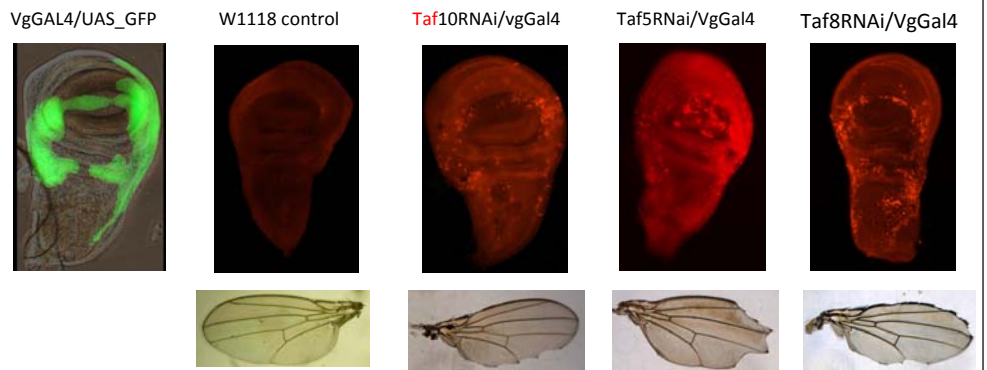
Downregulated genes



We have recently shown that *Halloween* genes, which are expressed in the prothoracic gland and have an important role in ecdysone synthesis, are regulated by the ATAC HAT complex. As a result of ecdysone synthesis failure ATAC mutants arrest development at the larval-prepupal transition though they do not present any evident defect during larval development. We silenced *taf5*, *taf8*, *taf10* genes specifically in the ring gland where ATAC-regulated ecdysone synthesis occurs at late larval stage and observed developmental arrest before the prepupal transition, while there was no detectable effect on the other larval developmental stages. This phenotype is similar to that can be seen in case of ATAC mutants.



20-hydroxyecdysone feeding rescue *taf* mutant L3 stage larvae and they reach pupa stage. These data show that TAFs influence the ecdysone synthesis similarly as it was observed in ATAC-specific *ada2a* mutants.



Decreased expression level of Taf proteins (Taf5, Taf8, Taf10) in the wing disc results in notched wing phenotype. We detected the apoptosis in wing disc with caspase-3 antibody (1:500). An UAS-GFP reporter gene was used to show the expression pattern of the *vg-GAL4* driver in the wing disc.

Our data suggest a functional interconnection between the ATAC HAT complex and the basal transcription factor TFIID. By further studies we aim to elucidate the details of the structural and functional interrelationship of the two complexes

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