Role of *cis*-regulatory module transcription in regulating gene expression

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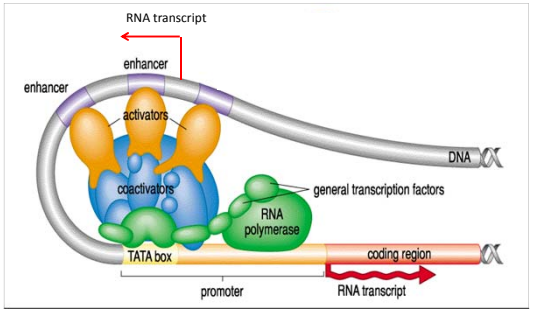
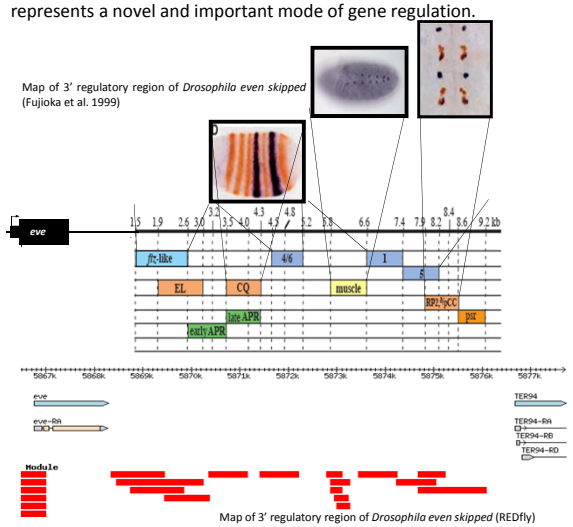
Introduction

Cis-regulatory modules (CRMs) are regions in the genome that play a key role in transcriptional regulation. CRMs are found in various regions in relation to the gene and some are capable of positively directing expression (enhancers) while others negatively direct and thus inhibit expression (silencer). Both our data and that from others has suggested that CRMs, like their corresponding genes, are transcribed into RNA (Li et al. 2007, DeSanta et al. 2010, Kim et al. 2010). A mechanism to explain this phenomenon is still unknown.

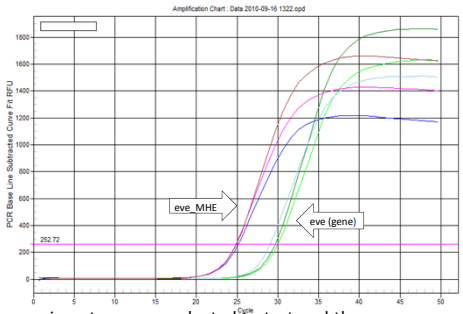


Abstract

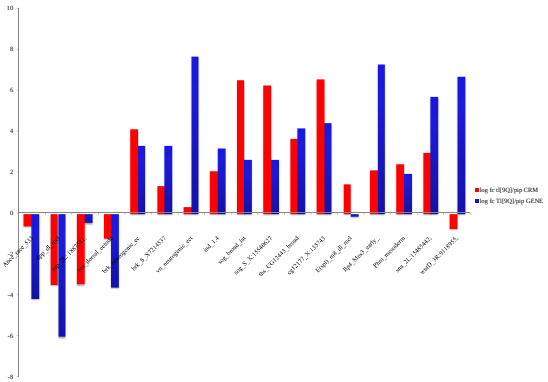
The aim of this project is to test the hypothesis that CRM transcription correlates specifically with gene expression in the tissue where the CRM is active. Our data will provide insight into the mechanisms and function of CRM transcription which potentially represents a novel and important mode of gene regulation.



Results



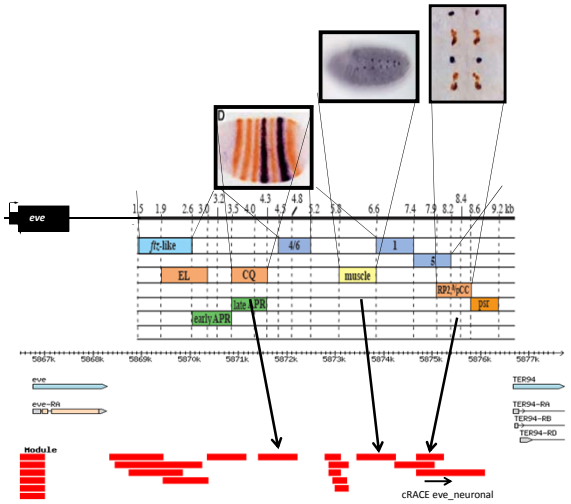
qPCR experiments were conducted to test and then compare relative levels of expression.



CRM expression is correlated with gene expression.

	Expected	Observed	Fold Enhancement
eve_MHE	middle	middle	9.7
sog_neurogenic	early	early	3.6
ato_3'F5.8	middle	late	3.5
twi_dl_mel	early	early	2.4
Hand_HCH	late	late	1.2

qPCR shows that the highest CRM/gene expression ratio correlates with the time of CRM activity. ($P(X \geq 4) < 0.05$). High CRM transcription is not correlated with degree of gene expression



5' and 3' RACE can be used to generate the regulatory regions. This is a map of one of our cloned RACE products and where it appears in relation to the eve locus.

Conclusions

Our findings show a correlation between CRM expression and the expression of the corresponding gene. When the CRM is expressed, the gene is expressed as well. Our data also point to a correlation between CRM activity and gene expression..

References

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