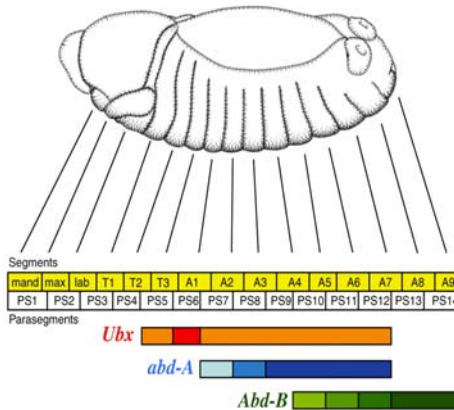


Studying functional conservation of the IAB8 enhancer in the *Drosophila* bithorax complex

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The 300 kb *Drosophila* bithorax complex (BX-C) has only three homeotic (hox) genes, *Ultrabithorax*, *Abdominal A*, and *Abdominal B*, but is able to control the developmental identity of 9 parasegments in the abdomen & posterior thorax.



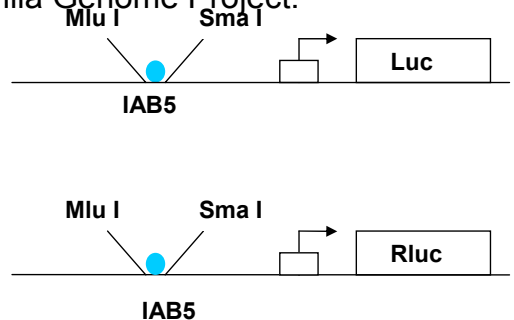
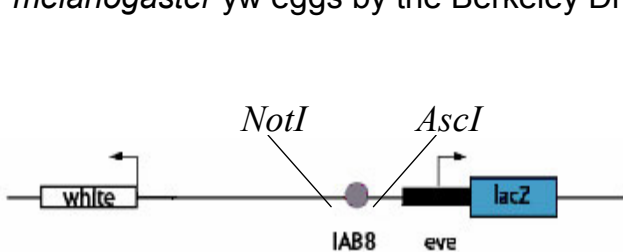
Cis-regulatory elements (CREs) are non-genic “junk” DNA sequences located near the hox genes on the same DNA strand. Because CREs regulate hox genes, they are thought to in part enable the complexity of organismal development, by varying patterns of hox gene expression across different parasegments.

Region	<i>simulans</i>	<i>Erecta</i>	<i>yakuba</i>	<i>ananassae</i>	<i>pseudo</i>	<i>Virilis</i>
BX-C	95	86	88	51	34	18
iab8 - iab5 (junk DNA)	97	86	88	47	30	12
Abd-B exons	96	99	99	67	63	53
CREs	96	85	81	45	26	13
Enhancers (Includes IAB8)	94	85	79	44	31	10
Insulators	99	79	79	27	14	11
Anti-insulator	100	97	90	56	5	0
PRE	94	67	69	37	23	19

Alignment studies done by HMC '07 graduating seniors Holly Johnsen and Christoph Rau indicate that the CREs on the *Drosophila* BX-C are drastically reduced in sequence conservation in species evolutionarily distant from *Drosophila melanogaster*.

It is a widely held belief in biology that functionally relevant sequences will tend to be more conserved on the sequence level, and this leads to **the question of whether enhancers in the bithorax complex from different species, such as the IAB8 enhancer, will function similarly even the sequence has changed.**

With that goal in mind, I built five out of seven desired transgenic constructs with the IAB8 enhancer from different *Drosophila* species driving reporter genes (lac Z and genes for red eyes), and this research will be continued in later summer and the coming academic school year. The built constructs were injected into *D. melanogaster* yw eggs by the Berkeley Drosophila Genome Project.



The aim is to quantify the relative activity of the IAB8 enhancers from different *Drosophila* species in *D. melanogaster* using *in situ* hybridization and RT-PCR.

I also collaborated with Holly Johnsen to build constructs to test a dual luciferase assay system with *Drosophila* S2 cell culture that we hope to employ in the Drewell lab.