Chapter 5

A Dose Dependent Screen for

Modifiers of Kek5

ABSTRACT

Modifier screens in *Drosophila* have proven to be a powerful tool for uncovering gene interaction and elucidating molecular pathways. Misexpression of Kek5 causes a number of adult phenotypes, of which the most overt are a rough eye and the scutellar bristle duplication. A prior modifier screen carried out by T. Evans using the rough eye phenotype proved unsuccessful (Evans and Duffy, 2006). As described in chapter three, alterations in Kek5 activity led to modifications in the scutellar bristle duplication phenotype, confirming that this phenotype is sensitive to the levels of Kek5. Therefore to identify potential interactors of Kek5, a dose dependent, genome wide deficiency screen for modifiers of the Kek5 bristle phenotype was undertaken. From this screen, four potential modifiers caused a modification of the bristle duplication phenotype, however, the effects could not be mapped to specific loci.

INTRODUCTION

The ability to perform genetic screens in *Drosophila* has helped uncover components of various biological pathways. Modifier screens, in particular, have helped elucidate signal transduction pathways (Johnston, 2002). In a modifier screen, one is looking for an enhancement or suppression of a particular phenotype associated with the gene of interest in a sensitized genetic background. To identify molecules that interact with Kek5, I undertook a dose-dependent modifier screen using deficiencies to halve the dose of a particular genomic region and assess its effect on a Kek5 dependent phenotype. Although a complete loss of *kek5* does not result in overt phenotypes, misexpression of Kek5 does result in phenotypes with high penetrance.

Previously, a rough eye phenotype due to misexpression of Kek5 in the *Drosophila* eye using *GMR>kek5* was used in a modifier screen (Evans and Duffy, 2006). This screen uncovered *wing blister* (*wb*), a member of the integrin pathway, as a potential enhancer of the rough eye phenotype of *GMR>kek5* (Martin et al., 1999). In the current study, I used the Kek5 gain of function scutellar phenotype (ectopic bristles), which is sensitive to Kek5 activity and can be easily quantified, as the basis for a modifier screen. Coupled with the knowledge that BMP signaling has been shown to affect bristle patterning and that Kek5 modulates BMP signaling, the hope was that using the scutellar phenotype might provide insight to Kek5's role in BMP signaling (Tomoyasu et al., 1998; Wharton et al., 1999). The logic was that halving the dose of a defined chromosomal region that interacted with Kek5 would result in alteration in the number of bristles based on the type of interaction (Figure 5.1). The screen uncovered two modifiers that enhanced the Kek5 bristle phenotype and two that suppressed it. However these effects were unable to be mapped to single genes.

RESULTS

In the current study, the scutellar bristle duplication phenotype displayed by *ptc>kek5*, a phenotype that is dose sensitive, was utilized in a deficiency based modifier screen. At 25^{o}C *ptc>kek5* has an average of nine scutellar bristles as opposed to four present in wild type flies (or up to six in *ptcGAL4* alone). This number increases to an average of fifteen when the temperature is raised to 28^{o}C. The screen was performed at 25^{o}C to ensure suppression as well as enhancement of the bristle duplication phenotype could be detected.

The screen was performed in a *ptc>kek5* background which results in misexpression of Kek5 in the anterior-posterior boundary of the imaginal discs and drives expression in the notum region of the wing disc that gives rise to the adult scutellum (Figure 5.1). A strain in which the *ptcGAL4* insertion was recombined with the *UAS-kek5•GFP* insertion was mated with the chromosomal deficiency stocks at 25^{o}C. FI females containing the *ptc>kek5* and a single copy of deficiency were scored for the number of scutellar bristles and screened for enhancement or suppression of the bristle duplication phenotype (Figure 5.1). A total of 311 deficiencies from the *Drosophila* Stock Center were selected to attain maximum chromosomal coverage and covered the I, II and III chromosomes (Table 5.1a and Table 5.1b).

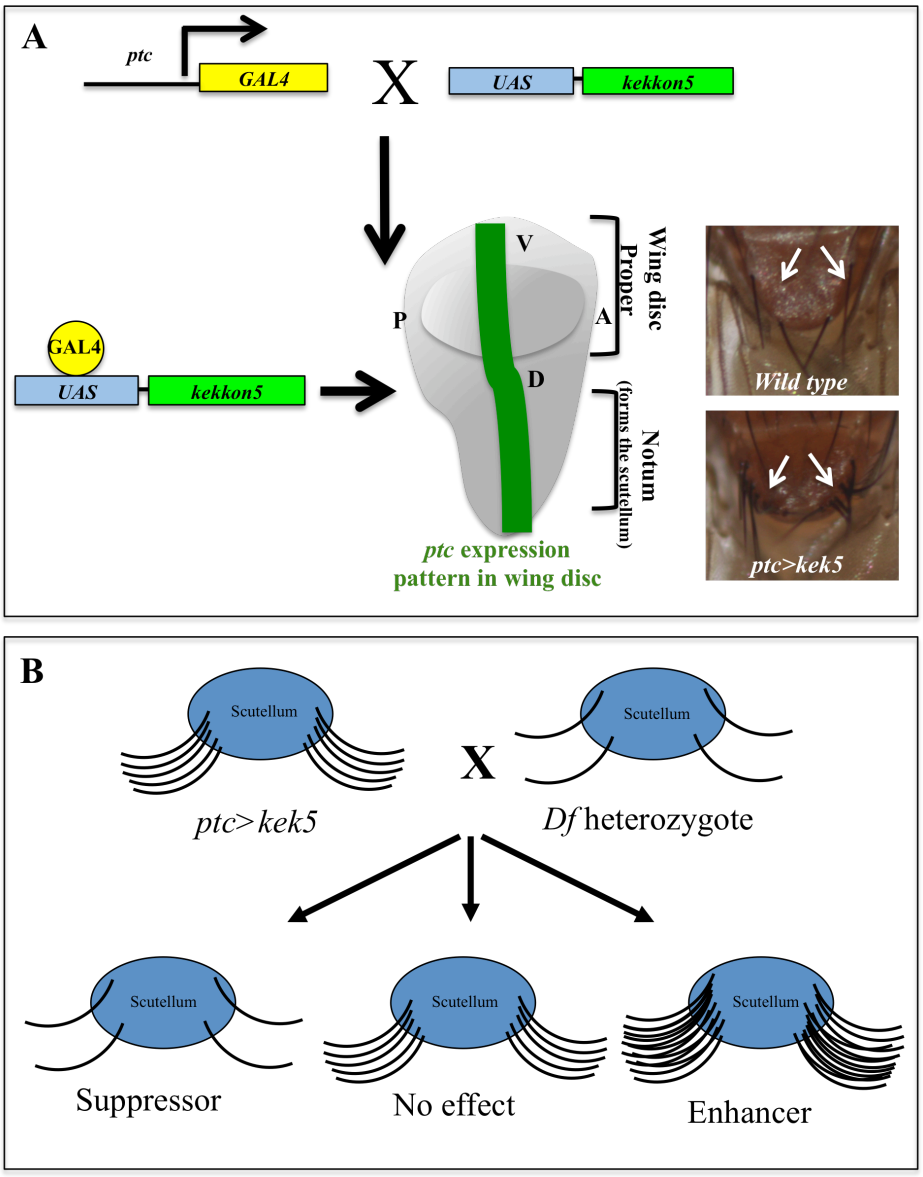

Figure 5.1: Schematic diagram of the deficiency screen. A) Kek5.GFP was expressed in the *ptc* expression domain using the UAS/GAL4 system resulting in a duplication of the scutellar bristles. Ptc expression domain lies just at the anterior side of A/P boundary. A-Anterior; P-Posterior; V-Ventral; D-Dorsal. B) For the screen *ptc>kek5* recombinant was crossed to the various deficiencies listed in Table 6.1a and 6.1b to look for suppressors or enhancers of the scutellar bristle duplication phenotype.

During the screen, I observed lethality with five deficiencies *Df(2L)Exel6011*, *Df(2R)Exel6072*, *Df(2L)Exel6027*, *Df(3R)Exel6159* and *Df(2R)Exel7171* (Table 5.1a). However, when these deficiencies were crossed with *ptcGAL4* alone they also exhibited lethality indicating

the interactions were between the deficiencies and *ptcGAL4* and were not due to Kek5 misexpression.

The results of the screen are graphed in a frequency chart (Figure 5.2) Deficiencies at the extreme ends (total of 4) of the graph showed the strongest effects and were focus of my study. These outliers included two suppressors (suppressing the number of scutellar bristles from 9 to ~3) in the chromosomal region 66A17-66B5 and 89B14-89B19 and two enhancers in regions 21B3-21B7 and 85A5-85D1 (enhancing the number of scutellar bristles from 9 to 14 and 13.57, respectively). The regions uncovered by these deficiencies did not include any obvious candidates for interactors of Kek5, such as components of BMP signaling pathway or the cell adhesion molecules of the integrin and the Cadherin–Catenin complex (Table C1).

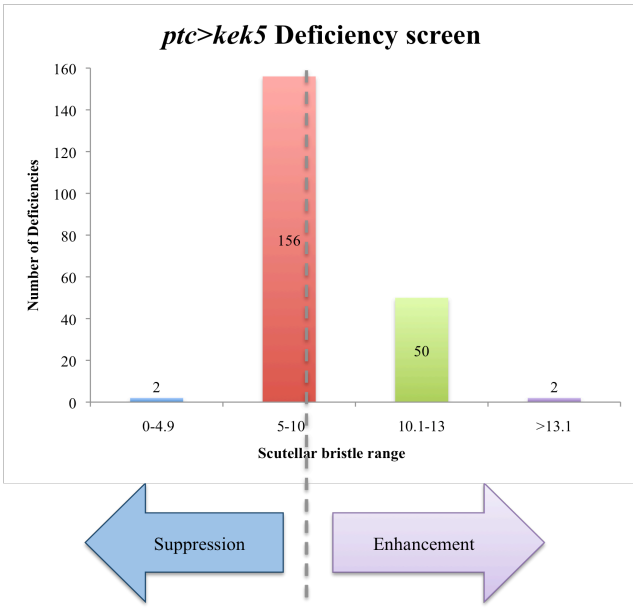

Figure 5.2: Frequency distribution chart showing the results of the *ptc>kek5* deficiency screen. The number in each bar indicates the number of deficiencies that fell in that range. Grey dotted line indicates the number of bristles in *ptc>kek5* at 25°C.

To ensure that the drastic alteration seen in the number of scutellar bristles was due to the genes deleted in the region deleted in a particular deficiency stock and not due to additional mutations in the genetic background of that particular stock, overlapping deficiencies covering the region were tested for all 4 stocks (Figure 5.3 and Figure 5.4). None of the overlapping deficiencies tested were able to replicate the results obtained for the corresponding original deficiency. One possible explanation is that there were additional mutations in the genetic

background of the four initial deficiency stocks that were responsible for the associated suppression or enhancement. The complete table with the analysis of overlapping deficiencies and alleles of genes in the 4 respective regions that were tested can be found in Table C2.

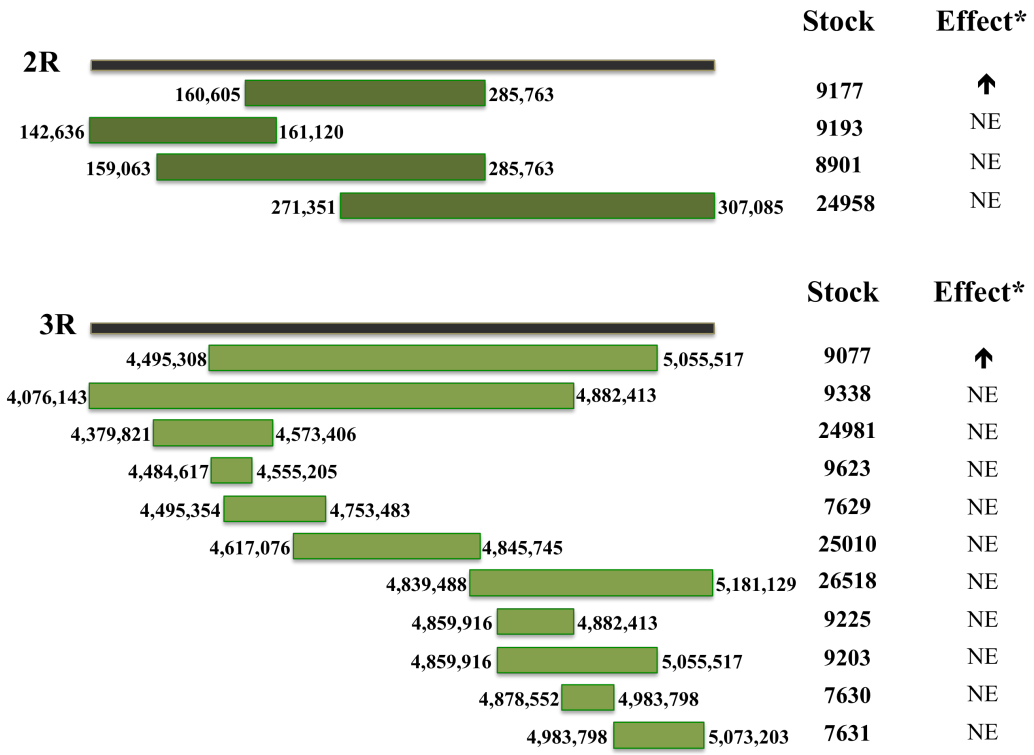

Figure 5.3: Overlapping deficiencies tested for stocks that enhanced the *ptc>kek5* bristle phenotype. Bars indicate the chromosomal region deleted in the corresponding stock. Dark green bars indicate deficiencies tested for 9177 while light green bars indicate deficiencies tested for 9077. Numbers at either end of the green bars indicate the chromosomal break points. * Effect on Kek5 bristle duplication.

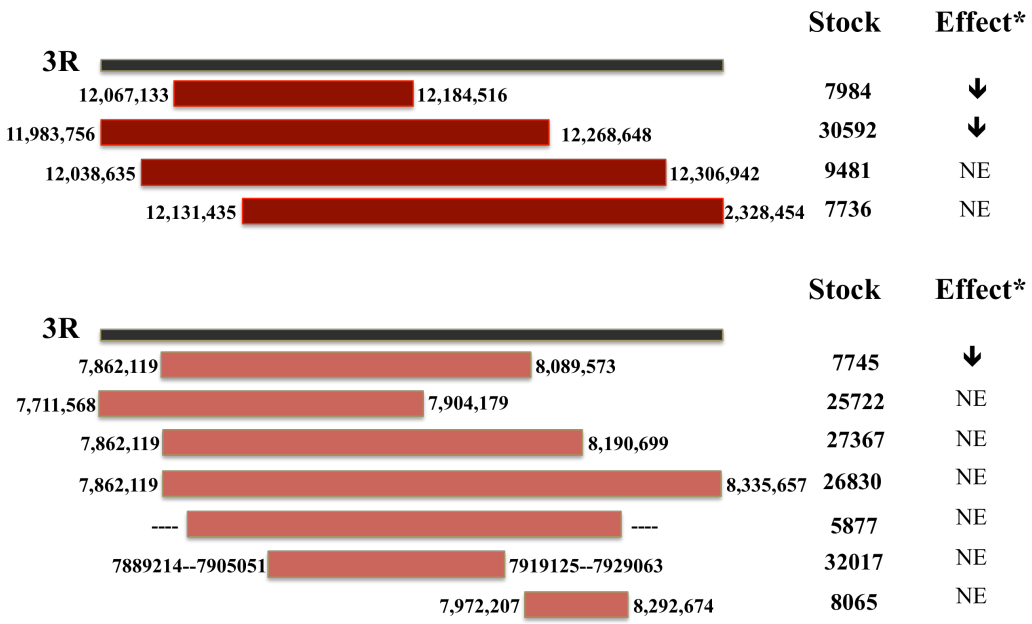

Figure 5.4: Overlapping deficiencies tested for stocks that suppressed the *ptc>kek5* bristle phenotype. Bars indicate the chromosomal region deleted in the corresponding stock. Red bars indicate deficiencies tested for 7984 and orange bars indicate deficiencies tested for 7745. Numbers at either end of the bars indicate the chromosomal break points. * Effect on Kek5 bristle duplication.

Table 5.1a: Deficiency screen looking for modifiers of scutellar bristle duplication phenotype displayed by *ptc>kek5* – Part I.

BS#	Deletion name	Deletion cytology	Effect on scutellar bristles
7495	Df(2L)Exel6009	24C3--24C8	Wk sup
7794	Df(2L)Exel7022	25B10--25C3	Wk sup
7796	Df(2L)Exel8013	25B5--25B10	Wk sup
7497	**Df(2L)Exel6011**	**25C8--25D5**	**Lethal**
7498	Df(2L)Exel6012	25D5--25E6	Wk sup
7797	Df(2L)Exel7023	25E5--25F1	NE
7724	Df(3R)Exel6256	25E6--25F2	Wk sup
7801	Df(2L)Exel7027	26F6--27B1	NE
7803	Df(2L)Exel8019	27E2--27E4	NE
7807	Df(2L)Exel7034	28E1--28F1	NE
7811	Df(2L)Exel7040	29F1--29F6	NE
7505	Df(2L)Exel6021	29F7--30A2	NE
7813	Df(2L)Exel8022	30B1--30B4	NE
7816	Df(2L)Exel7043	30D1--30F1	Wk sup
7819	Df(2L)Exel7046	31B1--31D9	NE
7820	Df(2L)Exel8026	31F5--32B3	NE
7821	Df(2L)Exel7049	32B1--32C1	NE
7510	**Df(2L)Exel6027**	**32D2--32D5**	**Lethal**
7511	Df(2L)Exel6028	32D5--32E4	NE
7512	Df(2L)Exel6029	32E4--32F2	Wk sup
7513	Df(2L)Exel6030	33A2--33B3	Mod sup
7421	Df(2L)ED784	34A4--34B6	NE
7826	Df(2L)Exel7059	34D1--34E1	NE
7521	Df(2L)Exel6038	35D6--35E2	Wk sup
7836	Df(2L)Exel9044	36C10--36D1	NE
7837	Df(2L)Exel7069	36C10--36D3	NE
7838	Df(2L)Exel7068	36C7--36C10	NE
7839	Df(2L)Exel7070	36E2--36E6	NE
7543	Df(2R)Exel6061	48F1--49A6	NE
7869	Df(2R)Exel7121	49B5--49B12	Mod sup
7544	Df(2R)Exel6062	49E6--49F1	Mod sup
7871	Df(2R)Exel8057	49F1--49F10	Mod sup

BS #	Deletion name	Deletion cytology	Effect on scutellar bristles
7873	Df(2R)Exel7128	50C5--50C9	NE
7875	Df(2R)Exel7130	50D4--50E4	Wk sup
7876	Df(2R)Exel7131	50E4--50F6	NE
7749	Df(3R)Exel6284	51B1--51C2	NE
7883	Df(2R)Exel7138	52D1--52D12	NE
7545	Df(2R)Exel6063	52F6--53C4	NE
7547	Df(2R)Exel6064	53D14--53F8	NE
7548	Df(2R)Exel6066	53F8--54B6	Wk sup
7551	Df(2R)Exel6069	56B5--56C11	NE
7552	Df(2R)Exel6070	57A6--57B3	NE
7554	**Df(2R)Exel6072**	**57B16--57D4**	**Lethal**
7556	Df(2R)Exel6076	57E1--57F3	NE
7566	Df(3L)Exel6087	62A2--62A6	Wk sup
7567	Df(3L)Exel6088	62B4--62B7	NE
7570	Df(3L)Exel6091	62E8--62F5	NE
7571	Df(3L)Exel6092	62F5--63A3	NE
7572	Df(3L)Exel6093	63C1--63D3	Wk sup
7573	Df(3L)Exel6094	63D2--63E1	NE
7574	Df(3L)Exel6095	63E1--63E3	NE
7575	Df(3L)Exel6096	63E3--63E4	NE
7576	Df(3L)Exel6097	63E3--63F2	Wk sup
7577	Df(3L)Exel6098	63F2--63F7	Mod sup
7583	Df(3L)Exel6104	64C8--64C13	Wk sup
7584	Df(3L)Exel6105	64C13--64D6	Wk sup
7585	Df(3L)Exel6106	64D6--64E2	NE
7586	Df(3L)Exel6107	64E5--64F5	Mod sup
7587	Df(3L)Exel6108	65A9--65A11	Wk sup
7588	Df(3L)Exel6109	65C3--65D3	Wk sup
7589	Df(3L)Exel6110	65E3--65E5	NE
7745	Df(3R)Exel6279	**66A17--66B5**	**Mod-St Sup**
7591	Df(3L)Exel6112	66B5--66C8	NE
7593	Df(3L)Exel6114	67B11--67C5	Wk sup

BS #	Deletion name	Deletion cytology	Effect on scutellar bristles
7597	Df(3L)Exel6118	70A3--70A5	NE
7608	Df(3L)Exel6129	72F1--73A2	NE
7616	Df(3L)Exel6137	78F4--79A4	NE
7623	Df(3R)Exel6144	83A6--83B6	Wk enh
7634	Df(3R)Exel6155	85F1--85F10	NE
7732	Df(3R)Exel6265	85F10--85F16	NE
7636	Df(3R)Exel6157	86B1--86B3	Wk enh
7637	Df(3R)Exel6158	86C2--86C3	NE
7638	**Df(3R)Exel6159**	**86C3--86C7**	**Lethal**
7737	Df(3R)Exel6270	89B18--89D8	Wk sup
7655	Df(3R)Exel6176	89E11--89F1	Wk sup
7663	Df(3R)Exel6184	92A5--92A11	NE
7664	Df(3R)Exel6185	92E2--92F1	NE
7739	Df(3R)Exel6272	93A4--93B13	NE
7741	Df(3R)Exel6274	94E4--94E11	NE
7746	Df(3R)Exel6280	94E5--94E11	NE
7673	Df(3R)Exel6194	94F1--95A4	NE
7674	Df(3R)Exel6195	95A4--95B1	NE
7675	Df(3R)Exel6196	95C12--95D8	NE
7676	Df(3R)Exel6197	95D8--95E1	Wk enh
7680	Df(3R)Exel6201	96C2--96C4	Wk enh
7681	Df(3R)Exel6202	96D1--96E2	NE
7682	Df(3R)Exel6203	96E2--96E6	Wk sup
7683	Df(3R)Exel6204	96F9--97A6	Wk enh
7726	Df(3R)Exel6259	98C4--98D6	Wk sup
7687	Df(3R)Exel6209	98D6--98E1	NE
7688	Df(3R)Exel6210	98E1--98F5	NE
7689	Df(3R)Exel6211	98F5--98F6	Wk sup
7691	Df(3R)Exel6213	99C5--99D1	NE
7692	Df(3R)Exel6214	99D5--99E2	NE
7693	Df(3R)Exel6215	99F6--99F8	NE
7696	Df(3R)Exel6218	100B5--100C1	NE

Interesting deficiencies are highlighted (bold). NE=No effect, ~ 10 bristles; W=weak; M=moderate; S=Strong; S=suppressor; E=Enhancer

Table 5.1b: Deficiency screen looking for modifiers of scutellar bristle duplication phenotype displayed by *ptc>kek5* – Part II.
Interesting deficiencies are highlighted (bold).

X Chromosome

BS #	Deletion Name	Deletion Cytology	Average # of bristles
1 Ptc>K5/+	CONTROL	-	8.37
2 Ptc>K5/+	CONTROL	-	10
7699	Df(1)Exel6221	1B4--1B8	5.95
9052	Df(1)ED6396	1B5--1B8	6.5
9053	Df(1)ED6443	1B14--1E1	8
7702	Df(1)Exel6225	1D4--1E3	9.21
7703	Df(1)Exel6226	1E3--1F3	8.75
7704	Df(1)Exel6227	1F3--2B1	9
7769	Df(1)Exel8196	2B1--2B5	11.33
9054	Df(1)ED6574	2E1--3A2	9.24
7705	Df(1)Exel6230	3A2--3A4	5
8031	Df(1)ED411	3A3--3A8	9.22
9348	Df(1)ED6584	3A8--3B1	9
8948	Df(1)ED6630	3B1--3C5	7.28
7707	Df(1)Exel6233	3D2--3D4	9.5
9169	**Df(1)ED6712**	**3D3--3F1**	**15**
24145	Df(1)ED6716	3F2--4B3	7.62
9055	Df(1)ED6720	4B3--4C7	6.25
8956	Df(1)ED6727	4B6--4D5	8.55
7753	Df(1)Exel6290	4F7--4F10	7.93
7708	Df(1)Exel6234	4F10--5A2	9.22
7709	Df(1)Exel6235	5A2--5A6	10.14
8949	Df(1)ED6802	5A12--5D1	8
8947	Df(1)ED6829	5C7--5F3	7.1
7713	Df(1)Exel6239	5F2--6B2	10.5
7714	Df(1)Exel6240	6B2--6C4	7.58
23670	Df(1)BSC285	6C11--6D3	10.38
9625	Df(1)ED6878	6C12--6D8	9.75
8955	Df(1)ED6906	7A3--7B2	9.06
7715	Df(1)Exel6241	8A2--8B2	7.5
8033	Df(2L)Exel8033	35B1--35B8	7.19
7770	Df(1)Exel9049	8D2--8D3	9.82

BS #	Deletion Name	Deletion Cytology	Average # of bristles
9153	Df(1)ED7005	9B1--9D3	7.91
9057	Df(1)ED7010	9D3--9D4	8.35
23672	Df(1)BSC287	10A10--10B11	10.8
9154	Df(1)ED7067	10B8--10C10	8.95
7716	Df(1)Exel6242	10D1--10D7	11.46
9171	Df(1)ED7147	10D6--11A1	7.4
9217	Df(1)ED7161	11A1--11B14	7.33
8898	Df(1)ED7170	11B15--11E8	7.2
7718	Df(1)Exel6245	11E11--11F4	7.25
8952	Df(1)ED7217	12A9--12C6	9.38
24146	Df(1)ED7225	12C4--12E8	9.75
9352	Df(1)ED7229	12E5--12F2	7.38
9218	Df(1)ED7261	12F2--12F5	10
24336	Df(1)BSC310	12F5--13A10	9.8
8035	Df(1)ED7294	13B1--13C3	10.45
9219	Df(1)ED7331	13C3--13F1	10.55
7720	Df(1)Exel6251	13F1--13F17	10
9905	Df(1)ED7364	14A8--14C6	5.17
8954	Df(1)ED7374	15A1--15E3	8.7
24429	Df(1)BSC405	16D5--16F6	9.2
24376	Df(1)BSC352	16F7--17A8	6.6
8036	Df(1)ED447	17C1--17F1	5.85
7754	Df(1)Exel6291	18A2--18A3	9.69
8951	Df(1)ED7441	18A3--18C2	7.05
23171	Df(1)BSC275	18C8--18D3	11.63
7721	Df(1)Exel6253	18D13--18F2	8.43
9351	Df(1)ED7635	19A2--19C1	9.3
7722	Df(1)Exel6254	19C4--19D1	8.3
9172	Df(1)ED7664	19F1--19F6	10.42
7723	Df(1)Exel6255	20A1--20C1	8
9156	Df(1)ED12432	20C3--20D2	9.39
9346	Df(1)ED14021	20C3--20F1	7.45

Table 5.1b Contd.

2L

BS #	Deletion Name	Deletion Cytology	Average # of bristles
9353	Df(2L)ED5878	21B1;21B3	8.11
9177	**Df(2L)ED21**	**21B3;21B7**	**13.57**
8937	Df(2L)ED62	21D1;21E2	8.77
8908	Df(2L)ED94	21E2;21E3	9.71
9176	Df(2L)ED136	22F4;23A3	9.14
8038	Df(2L)ED206	23B8;23C5	6.13
9270	Df(2L)ED250	24F4;25A7	7.5
7497	Df(2L)Exel6011	25C8--25D5	LETHAL
9343	Df(2L)ED334	25F2;26B2	11
9341	Df(2L)ED385	26B1;26D7	11.38
9060	Df(2L)ED489	27E4;28B1	11.39
8678	Df(2L)ED647	29E1;29F5	10.89
9342	Df(2L)ED680	30A4;30B12	10.45
8042	Df(2L)ED700	30E1;30E4	9.96
8043	Df(2L)ED746	31F4;32A5	9.16
7510	Df(2L)Exel6027	32D2--32D5	LETHAL
8907	Df(2L)ED775	33B8;34A3	11.57
9061	Df(2L)ED793	34E4;35B4	10.9
6963	Df(2L)ED3	35B2;35D1	9
8945	Df(2L)ED1109	36A3;36A10	9.32
8679	Df(2L)ED1303	37E5;38C6	8.48
9269	Df(2L)ED1315	38B4;38F5	11
9682	Df(2L)ED1378	38F1;39D2	8.61
9266	Df(2L)ED1473	39B4;40A5	7.5

2R

BS #	Deletion Name	Deletion Cytology	Average # of bristles
8939	Df(2R)ED1618	42C3;43A1	8.9
9062	Df(2R)ED1673	42E4;43D3	7.53
8931	Df(2R)ED1715	43A4;43F1	7.55
8941	Df(2R)ED1725	43E4;44B5	8.75
9275	Df(2R)ED1735	43F8;44D4	9.4
9063	Df(2R)ED1791	44F7;45F1	10.75
9277	Df(2R)ED2098	47A7;47C6	8
9344	Df(2R)ED2155	47C6;47F8	9.25
8910	Df(2R)ED2219	47D6;48B6	10.2
7916	Df(2R)Exel8056	49C2;49E1	8.6
9268	Df(2R)ED2308	49D3;49E7	7.35
8913	Df(2R)ED2354	50E6;51B1	7.77
9064	Df(2R)ED2426	51E2;52B1	10.81
8914	Df(2R)ED2436	51F11;52D11	9.67
8915	Df(2R)ED2457	52D11;52E7	9.88
7885	Df(2R)Exel9060	52E11;52F1	8
7886	Df(2R)Exel7142	53B1;53C4	9.29
7888	Df(2R)Exel7144	53C8;53D2	6.61
9213	Df(2R)ED3181	53C9;53F10	9.44
7887	Df(2R)Exel7145	53D4;53D12	9
7890	Df(2R)Exel7149	54C10;54D5	8.29
7891	Df(2R)Exel7150	54E1;54E9	8.5
9066	Df(2R)ED3610	54F1;55C8	7.4
8918	Df(2R)ED3683	55C2;56C4	9.08
9067	Df(2R)ED3728	56D10;56E2	10.1
7896	Df(2R)Exel7162	56F11;56F16	10.2
7897	Df(2R)Exel7163	57A2;57A6	8.45
7898	Df(2R)Exel7164	57A6;57A9	8.19
7554	Df(2R)Exel6072	57B16--57D4	LETHAL
8942	Df(2R)ED3923	57F6;57F10	9.25
9158	Df(2R)ED3943	57F10;58D7	9.45
9223	Df(2R)ED3952	58B10;58E5	9.56
7901	Df(2R)Exel7170	58B1;58C1	9
7902	Df(2R)Exel7171	58C1;58D2	LETHAL
9068	Df(2R)ED4061	60C8;60D13	9.67

Table 5.1b Contd.

3L

BS #	Deletion Name	Deletion Cytology	Average # of bristles
8046	Df(3L)ED4079	61A5;61B1	9.3
8047	Df(3L)ED201	61B1;61C1	6.9
8048	Df(3L)ED4177	61C1;61E2	9.26
8054	Df(3L)ED4256	62A3;62A6	10.6
8096	Df(3L)ED4287	62B4;62E5	9.82
8057	Df(3L)ED4288	63A6;63B7	9.95
8058	Df(3L)ED4293	63C1;63C1	9.7
8060	Df(3L)ED4341	63F6;64B9	8.64
8061	Df(3L)ED210	64B9;64C13	8.95
7927	Df(3L)Exel7210	65A1;65A5	8.3
7928	Df(3L)Exel8101	65A3;65A9	7.47
8063	Df(3L)ED211	65A9;65B4	11.7
7929	Df(3L)Exel8104	65F7;66A4	8.43
8065	Df(3L)ED4408	66A22;66C5	9.04
8066	Df(3L)ED4421	66D12;67B3	8.95
7933	Df(3L)Exel9048	67D1;67D2	8.24
9355	Df(3L)ED4457	67E2;68A7	9.89
8068	Df(3L)ED4470	68A6;68E1	9.7
8069	Df(3L)ED4475	68C13;69B4	8.16
8070	Df(3L)ED4483	69A5;69D3	12.1
8072	Df(3L)ED4486	69C4;69F6	12.35
8097	Df(3L)ED4502	70A3;70C10	10.18
8073	Df(3L)ED4543	70C6;70F4	8.2
8074	Df(3L)ED217	70F4;71E1	8.8
8077	Df(3L)ED220	72D4;72F1	9.28
8079	Df(3L)ED223	73A1;73D5	7.94
8098	Df(3L)ED4674	73B5;73E5	9.1
8099	Df(3L)ED4685	73D5;74E2	10
8080	Df(3L)ED224	75B1;75C6	9.65
8081	Df(3L)ED225	75C1;75D4	10.42
8082	Df(3L)ED4782	75F2;76A1	10.1
8083	Df(3L)ED4786	75F7;76A5	9.95
8087	Df(3L)ED229	76A1;76E1	6.92
8088	Df(3L)ED4858	76D3;77C1	9.67
7949	Df(3L)Exel9065	78D4;78D5	9.09
8101	Df(3L)ED4978	78D5;79A2	11.8
8089	Df(3L)ED230	79C2;80A4	11.39
8102	Df(3L)ED5017	80A4;80C2	9.18

3R

BS #	Deletion Name	Deletion Cytology	Average # of bristles
9224	Df(3R)ED5071	81F6;82E4	7
8680	Df(3R)ED5138	82D5;82F8	12.06
8967	Df(3R)ED5147	82E8;83A1	9.41
8965	Df(3R)ED5156	82F8;83A4	9.67
9159	Df(3R)ED10257	83A7;83B4	12.74
8103	Df(3R)ED5177	83B4;83B6	8.79
7952	Df(3R)Exel7283	83B7;83C2	7.13
9199	Df(3R)ED5187	83B7;83B8	9.89
9339	Df(3R)ED5197	83B7;83D2	8.88
8681	Df(3R)ED5196	83B9;83D2	9.73
8685	Df(3R)ED7665	84B4;84E11	9.84
8682	Df(3R)ED5230	84E6;85A5	10.56
9077	**Df(3R)ED5330**	**85A5;85D1**	**14**
9202	Df(3R)ED5327	85D1;85D1	8.94
9204	Df(3R)ED5339	85D1;85D11	9.43
9082	Df(3R)ED5474	85F11;86B1	10.37
7638	Df(3R)Exel6159	86C3--86C7	LETHAL
9084	Df(3R)ED5518	86C7;86E13	9
8920	Df(3R)ED5559	86E11;87B11	11.92
9087	Df(3R)ED5610	87B11;87D7	9.8
9088	Df(3R)ED5612	87C7;87F6	7.16
8921	Df(3R)ED5623	87E3;88A4	10.71
9279	Df(3R)ED5642	87F10;88C2	7.45
9090	Df(3R)ED5644	88A4;88C9	6.94
7981	Df(3R)Exel8162	89A5;89A8	10.36
7982	Df(3R)Exel7327	89A8;89B1	7.68
7983	Df(3R)Exel7328	89A12;89B6	6.05
7985	Df(3R)Exel7330	89B13;89B17	7.5
7984	**Df(3R)Exel7329**	**89B9;89B13**	**3.33**
7988	Df(3R)Exel8165	89E8;89E11	7.74

8104	Df(3R)ED5780	89E11;90C1	10.85
9208	Df(3R)ED5815	90F4;91B8	8.58
6962	Df(3R)ED2	91A5;91F1	9.87
8964	Df(3R)ED6025	92A11;92E2	10.94
9487	Df(3R)ED10845	93B9;93D4	12.17
8962	Df(3R)ED6076	93E10;94A1	12.35
8923	Df(3R)ED6085	93F14;94B5	10.4
8684	Df(3R)ED6096	94B5;94E7	6.74
8963	Df(3R)ED6103	94D3;94E9	6.6
7990	Df(3R)Exel9012	94E9;94E13	7.84
7991	Df(3R)Exel9013	95B1;95B5	9.33
7992	Df(3R)Exel9014	95B1;95D1	9.71
9211	Df(3R)ED6220	96A7;96C3	9.9
7994	Df(3R)Exel9056	96C4;96C5	7.95
8105	Df(3R)ED6232	96F10;97D2	9.87
9478	Df(3R)ED6235	97B9;97D12	8.17
9210	Df(3R)ED6255	97D2;97F1	8.79
8960	Df(3R)ED6265	97E2;98A7	8.33
8961	Df(3R)ED6310	98F12;99B2	10.35
8925	Df(3R)ED6316	99A5;99C1	11
7997	Df(3R)Exel7378	99F8;100A5	8.33
7919	Df(3R)Exel7379	100B2;100B3	6.52

DISCUSSION

Altering the levels of Kek5 has been shown to have a multitude of effects such as defects in crossvein patterning (BMP signaling), scutellar bristle duplication and cellular defects (Arm upregulation, epithelial cell extrusion and large cell) (Evans et al., 2009; this work). In an attempt to identify molecules that interacted with Kek5, a genome-wide deficiency screen was performed to look for modifiers of the *ptc>kek5* bristle duplication phenotype. The reasons for selecting this phenotype were its overt and quantifiable nature and sensitivity to variation in levels of Kek5. By varying the amount of GAL4 produced (by changing the temperature), the strength of the phenotype could be varied; 9 bristles at 25^{o}C increases to 15 bristles at 28^{o}C in *ptc>kek5* flies. Thus, we were hopeful to uncover modifiers of Kek5 activity through this screen. However, while the screen uncovered two suppressing and two enhancing strains, these effects could not be mapped to single loci. One possible explanation is that the observed modifications were due to something in the genetic background of the respective stocks, specifically on the deficiency chromosome, but distinct from the region uncovered by the deficiency itself.

MATERIALS AND METHODS

Drosophila genetics

All the screen crosses were performed at 25^{o}C. The screen was performed by mating *ptc>kek5* recombinant virgins with males from the deficiency stocks and *ptc>kek5/Df* F1 progeny were examined for the number of scutellar bristles. Deficiency stocks used in the screen are listed in Table 5.1a and Table 5.1b.

ACKNOWLEDGEMENTS

I want to thank the Bloomington Drosophila Stock Center for maintaining and providing all the deficiency stocks.

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