The kinase Sgg modulates temporal development of macrochaetae in Drosophila by phosphorylation of Scute and Pannier

Mingyao Yang*, Emma Hatton-Ellis* and Pat Simpson‡

SUMMARY
Evolution of novel structures is often made possible by changes in the timing or spatial expression of genes regulating development. Macrochaetae, large sensory bristles arranged into species-specific stereotypical patterns, are an evolutionary novelty of cyclorraphous flies and are associated with changes in both the temporal and spatial expression of the proneural genes achaete (ac) and scute (sc). Changes in spatial expression are associated with the evolution of cis-regulatory sequences, but it is not known how temporal regulation is achieved. One factor required for ac-sc expression, the expression of which coincides temporally with that of ac-sc in the notum, is Wingless (Wg; also known as Wnt). Wingless downregulates the activity of the serine/threonine kinase Shaggy (Sgg; also known as GSK-3). We demonstrate that Scute is phosphorylated by Sgg on a serine residue and that mutation of this residue results in a form of Sc with heightened proneural activity that can rescue the loss of bristles characteristic of wg mutants. We suggest that the phosphorylated form of Sc has reduced transcriptional activity such that sc is unable to auto-regulate, an essential function for the segregation of bristle precursors. Sgg also phosphorylates Pannier, a transcriptional activator of ac-sc, the activity of which is similarly dampened when in the phosphorylated state. Furthermore, we show that Wg signalling does not act directly via a cis-regulatory element of the ac-sc genes. We suggest that temporal control of ac-sc activity in cyclorraphous flies is likely to be regulated by permissive factors and might therefore not be encoded at the level of ac-sc gene sequences.

KEY WORDS: Drosophila, Scute, Phosphorylation, Sgg, GSK-3, Bristle, Wingless

INTRODUCTION
Evolution of novel structures can result from changes in either temporal or spatial expression of genes during development. Both mechanisms appear to underlie evolution of bristle patterns in Diptera. The dorsal thorax of many dipteran flies is covered with evenly spaced mechanosensory bristles. In species of the Nematocera, a basal group, the bristles are of similar size and are not patterned, such that their number and position varies from one individual to another (McAlpine, 1981). The thorax of many species of the more recently evolved Cyclorrapha bear evenly spaced small bristles of uniform size, called microchaetae, that also vary in position between individuals (Simpson et al., 1999). However, in the lineage leading to the Cyclorrapha an evolutionary novelty, the macrochaetae, has arisen (Simpson et al., 1999). Macrochaetae are large bristles that are not evenly spaced but are arranged into stereotypical species-specific patterns (McAlpine, 1981). Their development is associated with two derived features. First, in species of Nematocera, such as Anopheles gambiae, duration of development of the imaginal thorax is very short and sensory organ precursors arise from a single phase of expression of the proneural genes that regulate bristle development (Wulbeck and Simpson, 2002; Simpson and Marcellini, 2006). In cyclorraphous flies there are two temporally separate phases of proneural gene expression during the protracted development of the thoracic imaginal epithelium, an early one for macrochaetae and a later one for microchaetae (Simpson et al., 1999; Simpson and Marcellini, 2006). Second, microchaete precursors arise from ubiquitous or very broad domains of proneural gene expression, as do the sensory organ precursors in Anopheles gambiae (Sato et al., 1999; Wülbeck and Simpson, 2000; Pistillo et al., 2002; Wulbeck and Simpson, 2002). Proneural gene expression for macrochaete development, however, is not uniform but spatially patterned such that it prefigures the sites at which macrochaete precursors arise (Cubas et al., 1991; Skeath and Carroll, 1991; Wülbeck and Simpson, 2000; Pistillo et al., 2002).

In Drosophila the proneural genes achaete (ac) and scute (sc), which encode basic helix-loop-helix transcription factors, underlie bristle development (Villares and Cabrera, 1987; Gonzalez et al., 1989; Modolell and Campuzano, 1998). Spatially restricted expression of ac-sc in discrete proneural clusters at the sites of origin of macrochaetae precursors on the thorax has been investigated. On the other hand, a number of antagonists prevent activity of ac-sc at locations outside the proneural clusters, by interfering with the accumulation of ac-sc products arising from activity of the basal promoters (Usui et al., 2008). On the other hand, a prepattern of transcription factors activates expression through an array of discrete cis-regulatory elements scattered throughout the ac-sc complex (AS-C) (Gomez-Skarmeta et al., 1995; Garcia-Garcia et al., 1999; Calleja et al., 2002). Gene duplication events at the ac-sc locus are thought to have provided material for the acquisition of the regulatory elements that have presumably evolved successively over an extended period of time (Skaer et al., 2002b; Negre and Simpson, 2009). It is not known how ac-sc expression is...
temporally regulated or whether the heterochronic shift from a singlet to two phases of expression is also linked to evolution of regulatory sequences at the ac-sc locus.

Factors responsible for transcriptional activation of ac-sc in proneural clusters are present in the imaginal disc for a considerable time before ac-sc expression and so do not adequately account for timing (Callega et al., 2000; Klein, 2001; Cavodeassi et al., 2002). We have started to examine temporal control by investigating the mode of action of wingless (wg), a gene for which expression coincides temporally with the initiation of expression for macrochaetes and that is essential for development of macrochaetes on the medial notum (Phillips and Whittle, 1993). The product of wg is a diffusible Wnt signalling factor that has been shown to have a permissive, rather than instructive, role with respect to the patterning of ac-sc expression (Garcia-Garcia et al., 1999). The Wg signal acts by downregulating the activity of the serine/threonine kinase Sgg (Logan and Nusse, 2004). We show that Scute and Pannier (a transcriptional activator of ac-sc) (Haenlin et al., 1997; Garcia-Garcia et al., 1999) are phosphorylated by Shaggy (Sgg) and that phosphorylation-resistant versions of these proteins are hyperactive.

We suggest that the Wg signal allows nonphosphorylated Sc to enter mitosis. Phosphorylation-resistant versions of these proteins are hyperactive. In all cases, mutations were verified by sequencing. Flies were transformed by Genetic Services, MA and Department of Genetics, University of Cambridge.

**Materials and Methods**

**Microscopy**

Confocal images were taken with a Leica SP1 or SP5. Brightfield images were taken with a Leica DMRA microscope fitted with a QImaging camera and QCapture Pro software. Images were processed in Adobe Photoshop CS and Adobe Illustrator CS. Thorax images were assembled by taking images at sequential focal planes (approximately 20 µm intervals), and the image stacks were then merged with the Stack Focuser plugin (Michael Umorin) for ImageJ (http://imagej.nih.gov/ij).

**Fixation and immunohistochemistry**

Wandering third instar larvae were fixed according to standard protocols (Sullivan et al., 2000). Primary antibodies used were: anti-GFP (Goat) 1:500 Abcam ab6673; anti-Sc (Rb) 1:1000 Y-N Jan; anti-Ac (M) 1:10 DSHB; anti-beta-Gal (Rb) 1:10,000 Cappel; anti-Hnt (M) 1:100 DSHB; anti-Wg (M) 1:200 DSHB. Fluorescence-conjugated secondary antibodies were obtained from Invitrogen and Jackson Laboratories. Wing discs were mounted in Vectashield (Vector Laboratories).

**Thorax preparations**

Adult flies were collected and stored in 70% ethanol. Thoraxes were dissected and incubated in 0.3 M NaOH at 70°C until cleared. After washing, thoraxes were mounted in Euparal (Fisher Scientific). Staples were used to raise the coverslip and prevent cuticle deformation. Bristle measurements were made with QCapture Pro software.

**Fly stocks**

The following fly stocks were used: pm^{A0257}-GAL4/TM6B (Bloomington); c765-GAL4/TM6B (Bloomington); c765-GAL4/1 (Gomez-Skarmeta et al., 1996); pm^{A090} (Ramain et al., 1993); DCl.4-lacZ (Garcia-Garcia et al., 1999); P[GFP], P[FRT]101; MKRS, P[hs-FLP]85E/DM6B (Bloomington); P[GFP], P[FRT]184; MKRS, P[hs-FLP]85E/DM6B (Bloomington); sgg-GSK-3^{A111}, P[FRT]101/FM7 (Bloomington); sgg-GSK-3^{A127}, P[FRT]184/FM7 (Ruel et al., 1993); wg^{A01}/CyO, P[act-GFP] (Bloomington); wg^{A01}/CyO, P[act-GFP] (Bloomington); DC-GAL4; UAS-ssg-GSK-3^{A01}, UAS-ssg-GSK-3^{A034} (active sgg, Bloomington); Oregon R (wild type, Bloomington).

Crosses were carried out at 25°C. Clones mutant for sgg were induced in mid first to mid second instar larvae using the FLP/FRT method (Xu and Ruben, 1993). Disks were harvested from wandering third instar larvae, or adult flies were collected for bristle analysis.

**Site-directed mutagenesis and generation of transgenic flies**

Mutagenesis was performed using the QuickChangeII kit (Stratagene), according to the manufacturer’s instructions. See supplementary material Table S1 for primer sequences. Note that Pnr exists in two isoforms (Fromental-Ramain et al., 2008), with conserved Sgg phosphorylation sites: in this work, the pnrB isoform was used.

To produce phosphorylation-resistant forms of Dm-pnrB and Dm-Sc, the appropriate sequences were cloned into the pGEM-T Easy vector (Promega) for mutagenesis. Dm-pnrB was derived from pGEX-2T Pannier (Biryukova and Heitzler, 2008), whereas Dm-Sc was PCR amplified. Mutated sequences were then subcloned into pUAST (Brand and Perrimon, 1993).

For the T123 reporter construct, putative dTcf binding sites were identified using MatInspector (Genomatix) (Cartharius et al., 2005). The DC enhancer sequence (GenBank accession no. AF132808.1) was cloned into the pGEM-T Easy vector (Promega) for mutagenesis, and then subcloned into the pStinger-GFP (DGRC) reporter construct.

Protein expression

Dm-pnrB and Dm-Sc were cloned into the pGEM-T Easy vector as described above, with the addition of EcoRI and HindIII restriction sites. They were then subcloned into the expression vector pET-40b(+) with His-Tag (Novagen) and expressed in the BL21(DE3) Escherichia coli strain (Agilent Technologies). To solubilize His-tagged fusion proteins from inclusion bodies, harvested cells were suspended in 50 mM Tris buffer with 5% sarkosyl (Tao et al., 2010). Recombinant proteins were affinity purified using Ni-NTAagarose beads (Qiagen), and checked by western blots with appropriate antibodies.

**Immunoprecipitation**

For Dm-Pnr and Dm-Sc, protein extracts were made from wild-type Drosophila larvae, and immunoprecipitation performed using the Pierce Direct IP kit (Thermo Scientific) or the protein-G-agarose kit (Roche). Immunoprecipitated Sgg and immunodepleted Sgg were prepared from extracts of Drosophila wing discs according to the method of Gogel (Gogel et al., 2006). Antibodies used were pAb-Per (Haenlin et al., 1997), pAb-Sc (Vasselin et al., 1994) and mAb-Sgg 2G2C5 (Ruel et al., 1993).

**In vitro kinase assays**

Purified recombinant His-tagged Pnr attached to Ni-NTA agarose beads (4 µg) was incubated with either immunoprecipitated Sgg kinase or immunodepleted Sgg (Sgg–) in 4 µl kinase buffer (40 mM HEPES, pH 7.4, 2 mM ATP, 5 mM MgCl2, 2 mM DTT, 10% protease inhibitor and phosphatase inhibitor cocktail (Roche) overnight at 37°C. The Sgg inhibitor LiCl (30 mM) was added to some reactions. The phospho-specific antibody pAb BUGS (Trivedi et al., 2005) was used to detect phosphorylation of the His-pnr substrate. Protein-loading levels were monitored by probing the stripped blot with a rabbit His-tag antibody (GenScript).

Se protein does not react with the BUGS antibody in vitro, so in this case kinase assays were performed using radiolabelled γ-32P-ATP. Reactions with immunoprecipitated Sgg were carried out in 20 µl kinase buffer supplemented with 200 µM cold ATP plus 2 µCi of (γ-32P)-ATP (PerkinElmer), and 1 µg of purified recombinant Sc. After incubation at 30°C for 2 hours, the reactions were terminated with SDS sample buffer followed by 12% SDS-PAGE. The gel was dried and the phosphorylated protein was visualized by autoradiography.

**Results**

**Temporal expression of wingless coincides with that of achaete-scute**

Cells for the future wing disc are set aside in the embryo of Drosophila and separation of the notum and wing pouch takes place during the first half of the second larval instar, mediated by the restriction of expression of wg to the presumptive wing blade
and of the genes of the *Iroquois* complex (*Iro-C*), which encode homeodomain-bearing transcription factors, to the presumptive notum (reviewed by Klein, 2001). At late second instar, *pannier* (*pnr*), a gene encoding a GATA factor, is expressed in the medial half of the notum where, together with U-shaped (*Ush*), it represses the *Iro-C* genes restricting their activity to the lateral notum (Sato and Saigo, 2000; Tomoyasu et al., 2000; Cavodeassi et al., 2002) (supplementary material Fig. S1A). The products of *pnr* and *Iro-C* genes directly activate *ac-sc* in proneural clusters at specific sites in the epithelium through discrete cis-regulatory elements (Cubas et al., 1991; Skeath and Carroll, 1991; Gomez-Skarmeta et al., 1995; Gomez-Skarmeta et al., 1996; Garcia-Garcia et al., 1999). However, *ac-sc* products become detectable in discs only at mid third larval instar, in spite of the fact that *Pnr* and *Iro-C* proteins are present much earlier.

Another factor that is required for *ac-sc* expression is Wg. *wingless* (*wg*) is activated by Pnr in a longitudinal stripe in the Ush-free region of the notum (Couso et al., 1993; Phillips and Whittle, 1993; Sato and Saigo, 2000; Tomoyasu et al., 2000) (supplementary material Fig. S1A,B). However, Wg does not appear to be involved in determining spatial expression of *ac-sc*; rather, it has been shown to have a permissive role (Garcia-Garcia et al., 1999). Unlike that of *pnr* and *Iro-C*, expression of *wg* does coincide temporally with that of *ac-sc*. Wg protein is first detectable at early third larval instar and accumulates substantially by mid third larval instar when Sc first becomes visible (supplementary material Fig. S1C,D).

**Loss or gain of function of wingless and shaggy/GSK-3 affect the time of birth of bristle precursors**

Binding of Wg to its receptor leads to inactivation of Sgg, and it has previously been shown that, although loss of function of *wg* leads to a loss of macrochaetes in the medial notum, loss of function of *sgg* causes the opposite phenotype of additional macrochaetes (Simpson and Carteret, 1989; Couso et al., 1993; Phillips and Whittle, 1993; Neumann and Cohen, 1996). Correspondingly, expression of a constitutively active form of Sgg (*SGG10S9A*) mimics *wg* mutants and results in a loss of macrochaetes on both the medial and lateral notum (Fig. 1) (Bourouis, 2002).

In addition to bristle loss it was noted that the bristles that do form after expression of constitutively active Sgg appeared smaller (Papadopoulou et al., 2004). Similarly, we find that hypomorphic mutants of *wg* display some macrochaetes with shorted shafts (Fig. 1D). For these studies we focussed on *wg*<sup>Sp-1/wg*<sup>CX4</sup>, a viable allelic combination. In flies of this genotype, expression of *wg* on the notum is strongly reduced, being restricted to the posterior notum (supplementary material Fig. S1F). We have quantified the number and size of dorso-central (DC) bristles after loss of function of *wg* or gain of function of *sgg*. The anterior DC bristle (aDC) is missing in 61% of *wg*<sup>*Sp-1/wg*<sup>CX4</sup> male flies. When present, the aDC in flies of this genotype is 14% shorter (212 µm ± 4.3, n = 15) than in control siblings (246 µm ± 4.8, n = 37; P<0.01) (Fig. 1D,E).

We used the driver *c765-Gal4*, which gives a generalized expression over most of the thorax (Gomez-Skarmeta et al., 1996), to overexpress wild-type Sgg (*UAS-sgg/GSK-3<sup>WT</sup>*) and constitutively active Sgg (*UAS-sgg/GSK-3<sup>act</sup>*) (Bourouis, 2002). Overexpression of Sgg/GSK-3<sup>WT</sup> does not cause loss of bristles but the length of the posterior DC (pDC) bristle shaft is decreased by about 15% (281.9 µm ± 4.8, n = 58) when compared with wild type (333 µm ± 2.37, n = 39) (Fig. 1B,E). Nearly 20% of flies overexpressing Sgg/GSK-3<sup>act</sup> are missing all DC bristles and the remainder display a single tiny pDC that is 46% shorter in length (178.7 ± 5.9, n = 38) than seen in wild type (Fig. 1C,E).

The results show that loss of function of *wg* or gain of function of *sgg* results in a loss of bristles, as well as the development of smaller bristles. Bristle length correlates with the time of precursor formation (Skaker et al., 2002a; Usui-Ishihara and Simpson, 2005) because the size of the bristle is proportional to the number of endocycles undergone by the socket and shaft cells (Szuplewski et al., 2009). Smaller bristles are therefore likely to be due to delayed segregation of bristle precursors. A delay in precursor formation could also lead to bristle loss because precursors need to form within a defined period of competence (Rodriguez et al., 1990). This is consistent with the preferential loss of the aDC, as the precursor of the aDC is known to form later than that of the pDC (Huang et al., 1991). To determine whether precursor development is delayed in *wg* mutants, we examined the time of precursor formation in *wg*<sup>*Sp-1/wg*<sup>CX4</sup> flies using an anti-Hindsight (Hnt) antibody (Lai, 2003). In white prepupae, 10.5% of discs displayed two Hnt-expressing DC precursors, 60.5% displayed a single DC precursor and 29% had no DC precursors at all (n = 38). Nearly 40% of adults of this genotype bear two DCs and the remainder have a single one, so the segregation of about 40% of the expected precursors must occur after pupariation. In control discs from white prepupae of *wg/Cyo* siblings, 80% of discs displayed two DC precursors and the remainder had a single one (n = 15), so only 10% of precursors segregate after pupariation (Fig. 1F,G).

We conclude that *Wg* acts through *Sgg* to regulate the time of birth of bristle precursors. Loss of function of *wg* leads to a delay in the formation of DC bristle precursors that can lead to the
development of smaller bristles and might also cause an absence of bristles. A gain of function of sgg is likely to have a similar effect. The additional bristles that develop after loss of function of sgg could therefore result from an extended period of precursor segregation provided by an earlier start.

The dorsocentral enhancer of achaete-scute does not contain functional dTCF binding sites

Expression of ac-sc for DC bristle development depends on the activity of a cis-regulatory element called the DC enhancer (DCE) (Gomez-Skarmeta et al., 1995; Garcia-Garcia et al., 1999). In wg+/wg− mutants, a transheterozygous combination in which Wg protein levels are significantly reduced in the notum region of third instar wing discs (Klein et al., 1998), expression of the DCE-lacZ enhancer gene is notably reduced (Garcia-Garcia et al., 1999). Here we have examined the activity of DCE-lacZ in clones of cells mutant for null alleles of sgg, sgg0127 or sggMG. The DCE-reporter transgene is ectopically expressed in large sgg clones (Fig. 2A). Thus, Wg signalling is required for activation of the DCE in its normal spatial domain.

If Wg acts via the canonical Wnt signalling pathway, then the DCE should contain a functional dTCF binding site(s). A search for the dTCF consensus sequence (van de Wetering et al., 1997), using MatInspector (Cartharius et al., 2005) (see Materials and methods), identified three potential binding sites (supplementary material Fig. S2). Two of the sites are conserved in the D. virilis DCE (not shown). To determine whether the DCE sites are functionally relevant, all three sites in a DCE-GFP enhancer construct were mutated. At least two bases of the core TTGA motif were altered for each site and the modified construct was named DCE\textsuperscript{T123}-GFP (supplementary material Fig. S2). The expression pattern of DCE\textsuperscript{T123}-GFP was compared with the unmodified DCE-lacZ reporter in transheterozygous flies. The expression patterns correspond almost perfectly, demonstrating that the predicted dTCF sites are not required for normal DCE activity (Fig. 2B). This suggests that the sites are not functional and that Wg acts on the DCE via a noncanonical Wnt signalling pathway.

Pannier is a target for phosphorylation by Sgg

Activation of ac-sc transcription via the DCE is through the GATA factor Pnr (Garcia-Garcia et al., 1999). The phosphorylation predication network NetPhosK 1.0 Server (Blom et al., 2004), reveals two potential sites that fit the consensus for phosphorylation by Sgg (at amino acids at 101 and 391) in Pnr\textsubscript{β} of D. melanogaster. They display homology with the GSK-3β-phosphorylation site of the mouse MAP1B (microtubule associated protein) (Fig. 3A), a peptide of which was used to raise the BUGS phospho-antibody (Trivedi et al., 2005). This antibody has been successfully used to detect phosphorylation by Sgg of D. melanogaster Futsch (Gogel et al., 2006). Therefore, we used this antibody to determine whether Sgg can phosphorylate Pnr.

Immunoprecipitation (IP) was used to obtain an enriched Pnr extract from wild-type larvae. Western blot analysis showed that the phospho-antibody BUGS robustly recognized a protein at about 60 kDa, which is the size expected for Pnr, as indicated by the Pnr antibody (Fig. 3B). This result suggests that D. melanogaster Pnr is phosphorylated at a site with the consensus sequence for phosphorylation by Sgg that is recognized by the phospho-antibody BUGS.

To determine whether Sgg can indeed phosphorylate Pnr, we employed an in vitro kinase assay. Recombinant His-tag Pnr was incubated with Sgg, obtained through IP from a Drosophila wing disc extract. As a control, recombinant Pnr was incubated with the immunodepleted extract (see Materials and methods). A western blot showed that the recombinant pnr protein alone displayed no immunoreactivity with BUGS (not shown). By contrast, after incubation with Sgg, the phospho-antibody BUGS can recognize Pnr, thus indicating that Pnr has been phosphorylated by Sgg in vitro (Fig. 3C). Immunodepleted Sgg showed reduced kinase activity towards Pnr. Furthermore, in this assay, phosphorylation of Pnr by Sgg was inhibited by lithium chloride, a specific GSK-3 inhibitor (Cohen and Frame, 2001).

In summary, these findings show that the pAb BUGS specifically recognizes a Pnr phospho-serine epitope, indicating that Pnr is phosphorylated by Sgg in vitro.

A phosphorylation-resistant form of Pannier induces ectopic bristles

To test the significance of the Sgg phosphorylation sites in Pnr we mutated the central serine residues at the two sites to alanines (Fig. 3A). Transgenic flies carrying the mutated Pnr, designated Pnr\textsubscript{MUT}, in a UAS vector were crossed to various Gal4 drivers. The results were compared with expression of a wild-type version of Pnr, UAS-Pnr\textsubscript{WT}. Both Pnr\textsubscript{WT} and Pnr\textsubscript{MUT} induced additional macrochaetes on the lateral notum of flies of the genotype c765-Gal4>UAS-Pnr. Overexpression of Pnr\textsubscript{WT} caused the production of an average of 9.5 extra macrochaetes per thorax (n=108) and that of Pnr\textsubscript{MUT}, 19 extra macrochaetes per thorax (n=100) (Fig. 3D) (note that these numbers do not include the 11 macrochaetes normally found on the wild-type thorax). The phosphorylation-resistant form of Pnr therefore displays stronger bristle-inducing activity.

We also tested whether the phosphorylation-resistant form of Pnr rescues the DC bristles missing from pnr\textsubscript{TV6}/pnr\textsubscript{MD237} transheterozygotes. panner\textsubscript{TV6} is a null allele and pnr\textsubscript{MD237}
contains a Gal4 insert at the pnrl locus that drives expression over the medial half of the notum (Heitzer et al., 1996). We found that rescue of DC bristles after expression of Pnr WT was poor (0.4 bristles per thorax, \(n=113\)), but that rescue after expression of Pnr MUT was significant (4.6 bristles per thorax, \(n=181\); Fig. 3E). Finally we tested for rescue of DC bristles in the wgSp-1/wgCX4 mutant using the MD237-Gal4 line. Overexpression did indeed lead to bristle rescue and again, PnrMUT rescued with a greater efficiency (Fig. 3F). Therefore PnrMUT is able to bypass the hyperactivity of Sgg caused by the loss of Wg signalling.

Taken together, these results indicate that the phosphorylation-resistant form of Pnr is hyperactive. We conclude that Pnr is phosphorylated by Sgg and that the phosphorylated form is less active. This suggests that inactivation of Sgg by the Wg signal leads to the accumulation of nonphosphorylated Pnr and consequent enhanced transcriptional activity.

**Scute is a target for phosphorylation by Sgg**

Clones of cells mutant for sgg also display ectopic macrochaetes outside the positions of proneural clusters within which the extant bristles form (Simpson and Carteret, 1989; Phillips et al., 1999).
Furthermore they bear additional microchaetes. It has been shown that formation of ectopic bristles correlates with accumulation of the ac protein (Phillips et al., 1999). Here we show that sc is also expressed at ectopic locations in sgg null clones (Fig. 2C). Expression of ac-sc at these ectopic locations is unlikely to be driven by the activity of specific cis-regulatory sequences that bind Pnr or the products of the Iro-C, neither of which affects microchaetes. Instead it probably results from increased transcription mediated by the basal promoters of ac and sc (Martinez and Modolell, 1991). A possible explanation for the effects of sgg mutants on ectopic ac-sc expression would be that either Ac or Sc themselves were targets for phosphorylation by Sgg.

The phosphorylation prediction network NetPhosK 1.0 Server predicts two potential Sgg phosphorylation sites in Drosophila Sc at the positions of amino acids 85 and 268 (Fig. 4A) (Blom et al., 2004). These sites are not conserved in Ac and indeed we were unable to detect any sites in Ac that meet the criteria for a consensus sequence for Sgg phosphorylation. Multiple protein sequence alignment analysis with ClustalW2, reveals that the consensus motif at amino acid 268, but not that at amino acid 85, is highly conserved among sc proteins in cyclorrhaphous Diptera (supplementary material Fig. S3). We employed an in vitro kinase assay to examine possible phosphorylation of Sc by Sgg. The BUGS antibody did not identify any signal in IP sc protein, which displays a different sequence for Sgg phosphorylation from that of Pnr (Fig. 3A and Fig. 4A). Therefore, we used traditional radiolabelled [γ-32P]ATP to test for protein kinase activity (see Materials and methods). Activity of Sgg should result in the incorporation of radiolabelled phosphate from [γ-32P]ATP into the sc protein if Sc is phosphorylated by Sgg. Incubation of His-tag recombinant Sc with Sgg revealed kinase activity: a positive band of about 75 kDa indicated phosphorylated Sc (Fig. 4B). No kinase activity was detected when the recombinant sc protein was incubated in the absence of Sgg. Treatment with the Sgg inhibitor LiCl prevents phosphorylation of Sc (Fig. 4B). The result shows the presence of kinase activity and suggests that Sgg can phosphorylate Sc in vitro.

**A phosphorylation-resistant form of Scute displays hyperactivity**

To test the significance of Sgg phosphorylation of Scute we performed site-directed mutagenesis at the conserved consensus site (amino acid 268). Serines in the Sgg site at amino acid 268 as well as a possible priming phosphate site located at n+4 (Cohen and Frame, 2001) at amino acid 272, were mutated into alanines (Fig. 4A) and the resulting protein designated ScMUT. Transgenic flies carrying the mutated ScMUT in a UAS vector were crossed to various Gal4 drivers. The results were compared with expression of a wild-type form of Sc, ScWT. We found that the phosphorylation-resistant ScMUT displays increased proneural activity and therefore induces development of a greater number of additional bristles than ScWT. With many Gal4 lines, expression of either ScWT or ScMUT induces so many ectopic bristles that counting bristles to obtain numbers for comparison was not possible (data not shown). We therefore used the DC-Gal4 line that drives expression exclusively at the site of the DC proneural cluster. About 28% of DC-Gal4>UAS-ScWT flies display more than two DC bristles per hemithorax (Fig. 4C). This number increases to 76% in DC-Gal4>UAS-ScMUT flies (Fig. 4C). Expression of a phosphorylation-resistant form of Scute therefore mimics sgg loss of function in the notum, suggesting that phosphorylation of Sc by Sgg reduces activity.

We also tested the ability of ScMUT to rescue missing DC bristles in the wg/CX4 mutant using the DC-Gal4 line. We find that rescue by ScMUT is more effective than rescue by ScWT (Fig. 4D). This suggests that, as for Pnr, the Wg signal, through inactivation of Sgg, leads to the accumulation of nonphosphorylated Sc that displays increased transcriptional activity.

**DISCUSSION**

**Inactivation of Sgg by Wingless at mid third larval instar allows accumulation of Scute for macrochaete development in Drosophila achaete-scute products become detectable in wing discs only at mid third larval instar (Romani et al., 1989; Cubas et al., 1991; Skeath and Carroll, 1991).** The known upstream regulators, Pnr and the Iro-C genes, are selector genes that pattern the medial and lateral halves of the notum, respectively (Calleja et al., 2000; Mann and Morata, 2000). Therefore their activity is not restricted to ac-
sc activation and bristle patterning and they are expressed for a considerable period before ac-sc gene products are detected (Calleja et al., 2000; Klein, 2001; Calleja et al., 2002; Cavodeassi et al., 2002; Ghazi, 2003; Ikmi et al., 2008). Furthermore, although activation of ac-sc in proneural clusters by Pnr and Iro-C dramatically increases transcription at these sites, the ac-sc genes are also expressed at low levels over the entire disc epithelium, presumably through activity of the basal promoters (Martinez and Modolell, 1991; Ayyar et al., 2007). Indeed maintenance of proneural genes in an active state of basal transcription is a general feature of neuroepithelia (Bertrand et al., 2002). So what prevents accumulation of Ac-Sc at earlier stages in disc development?

We have shown that Sc is phosphorylated by Sgg, an enzyme that is expressed constitutively. Furthermore a mutated form of Sc that is resistant to phosphorylation has significantly greater bristle-forming activity than the wild-type protein. This suggests reduced transcriptional activity of phospho-Sc. One possibility is that the turnover of phospho-Sc is rapid, owing to phosphorylation-dependent ubiquitination and degradation (Ciechanover, 1998). It has been reported that mutations in the GSK-3β consensus motif in β-catenin abolishes ubiquitination and leads to protein stability (Yost et al., 1996; Aberle et al., 1997). GSK-3β also induces ubiquitination and degradation of Drosophila myc (dm – FlyBase) protein through the proteasome pathway and mutation of residues in the phosphorylation domain affects stability of this protein (Galletti et al., 2009). Indeed it has been shown that mutation of the phosphorylation site SPTS to APAA stabilizes the Sc protein (M. Kiparaki and C. Delidakis, personal communication). This suggests that before expression of wg at the mid third larval instar, the stability and transcriptional activity of any Sc present, whether derived from transcription mediated by the basal promoter or enhanced by Pnr and the Iro-C proteins, would be reduced through phosphorylation by Sgg.

Development of neural precursors requires high levels of Sc, which are needed for the process of lateral inhibition and singling out of precursors as well as for autoregulation (Culi and Modolell, 1998; Bertrand et al., 2002). During this process in Drosophila, Sc binds its own promoter, through a specific regulatory sequence, the sensory organ precursor enhancer (SOPE), to further activate transcription in presumptive precursors (Culi and Modolell, 1998). Therefore, any factors that diminish the activity of Sc itself have the potential to prevent sufficient accumulation to allow selection of precursors and maintenance of precursor cell fate. Expression of wg at mid third larval instar would lead to inactivation of Sgg. The consequent accumulation of a more active nonphosphorylated form of Sc might allow levels of Sc to accumulate sufficiently for precursor cell development. Achaete does not appear to be a target for Sgg. However, this protein has been shown to be dispensable for bristle development (Marcellini et al., 2005).

We find that Pnr is also a target for phosphorylation by Sgg and, that, like Sc, a mutated phosphorylation-resistant form of Pnr is hyperactive. So phosphorylation of Pnr might also result in ubiquitination and increased degradation, a situation that would be modified by Wg signalling at mid third larval instar. The effects of phosphorylation on Pnr and Sc appear to be quantitative, rather than all or nothing. Pannier has other targets before Wg signalling and activation of ac-sc (the iro genes and wg itself) and if the sole function of Wg were to be the inactivation of Sgg then one would expect loss of scgg function to have no bristle phenotype. So de-phosphorylation might just give an extra little boost to the system. Interestingly it has been shown that the Drosophila transcription factor Mad is also a target of Sgg and that phosphorylation-resistant Mad proteins are hyperactive (Eivers et al., 2009). Mad is activated by Dpp/TGFβ signalling, which in turn regulates expression of both pnr and the Iro-C genes in the thorax (Sato and Saigo, 2000; Tomoyasu et al., 2000; Shi and Massague, 2003; Letizia et al., 2007; Formental-Ramain et al., 2008) (Fig. 5). Thus, it appears that inactivation of Sgg by the Wg signal can stimulate the levels of Sc via multiple routes: by increasing the levels of expression of pnr and the Iro-C genes as well as the activity of Pnr and Sc themselves. Thus, expression of wg at mid third larval instar might result in levels of Sc sufficient for macrochaete development. It is not known how the second phase of ac-sc expression for microchaetes is regulated.

Wingless is unlikely to be the only factor regulating temporal ac-sc expression. Indeed, although loss of sgg function can affect bristles over the entire notum, the effects of wg appear to be restricted to the medial notum (Phillips and Whittle, 1993). Other factors must be involved on the lateral notum. One possibility is Nfk-B/Rel, a factor that is required for functioning of the SOPE and singling out of precursors, and that also indirectly affects the
stability of sc transcripts (Culi and Modolell, 1998; Ayyar et al., 2007). Another event that coincides with the accumulation of ac-sc products at mid third larval instar is a small peak of 20H-ecdysteroid (not associated with a moult) (Berreur et al., 1979; Riddiford, 1993). Indeed ecdysone has been implicated in temporal regulation of expression of the proneural gene atonal and the development of atonal-dependent sense organs (Niwa et al., 2004).

An ancient function of Wingless might have been co-opted for temporal regulation of ac-sc expression

Wingless signalling has important functions in the thorax, likely to be ancient, that are linked to the development and patterning of flight muscles. So wg was probably already expressed on the notum of the ancestor of the Cyclorrapha, before the evolution of macrochaetes. The rapid development of the notum and short pupal period in many Nematocera leaves little requirement for any temporal control of expression (McAlpine, 1981). By contrast, the prolonged period of growth and patterning during the larval and pupal life of Drosophila allows time for two discrete phases of proneural gene expression (reviewed by Simpson and Marcellini, 2006). Wingless might then have been co-opted for the regulation of ac-sc and the evolution of macrochaetes in the lineage leading to the Cyclorrapha. Our results suggest that the Wg signal does not involve transcriptional regulation of target genes but instead is mediated simply through inactivation of Sgg. The phosphorylation sites are strongly conserved in the sc genes of C. vicina and C. capitata (supplementary material Fig. S3), two other species of Schizophora, suggesting a conserved mechanism of regulation by Wg and Sgg. By contrast, the same sites are not conserved in the other genes of the Drosophila AS-C, or in the ac-sc homologues of A. gambiae, although other potential Sgg phosphorylation sites can be detected in these proteins. Phosphorylation of Sg by Sgg could have been recently acquired in the Cyclorrapha. The ac and sc genes themselves have arisen from duplication events thought to have taken place during evolution of the Cyclorrapha (Skauer et al., 2002b; Negre and Simpson, 2009). Phosphorylation of Pnr by Sgg might also have been acquired in the lineage leading to the Schizophora, as one of the sites is conserved in the pnr protein of C. vicina, but not that of Megaselia abidita or A. gambiae (supplementary material Fig. S4).

Uniform proneural gene expression, together with Notch-mediated lateral inhibition (Heitzler and Simpson, 1991), is sufficient to generate a pattern of evenly spaced, but randomly positioned, bristles such as that seen in Nematocera and for the microchaetes of the Cyclorrapha (Wülbeck and Simpson, 2000; Pistillo et al., 2002; Wülbeck and Simpson, 2002). For this process, the SOPE, a very ancient regulatory element that predate the Diptera (Ayyar et al., 2010), is the only cis-regulatory element of ac-sc that would be required. Factors that act through the SOPE could be co-opted to modulate the temporal activity of ac-sc. This includes factors regulating activity of Sc, which itself binds the SOPE (Culi and Modolell, 1998). Control at this level could be superimposed on the ancestral state without the need to acquire new regulatory sequences for the binding of novel transcriptional repressors and activators. By contrast, the spatially restricted expression underlying the macrochaete pattern is linked to changes at the AS-C complex and the acquisition of novel cis-regulatory elements that possibly arose in association with gene duplication events (Skauer et al., 2002b; Negre and Simpson, 2009). This illustrates the power of evolution to make use of factors acting both in cis and in trans to effect morphological change.

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Competing interests statement

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Supplementary material

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References


