Development 130, 3469-3478

doi:10.1242/dev.00574

PVF1, a PDGF/VEGF homolog, is sufficient to guide border cells and interacts genetically with Taiman

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Accepted 23 April 2003

SUMMARY

The border cells of the *Drosophila* ovary undergo a well-defined and developmentally regulated cell migration. Two signals have previously been shown to control where and when the cells migrate. The steroid hormone ecdysone, acting through its receptor and a coactivator known as Taiman, contributes to regulating the timing of border cell migration. PVF1, a growth factor related to platelet-derived growth factor and vascular-endothelial growth factor, contributes to guiding the border cells to the oocyte. To probe the mechanisms controlling border cell migration further, we performed a screen for genes that exhibit dominant genetic interactions with *taiman*. We identified 14 genomic regions that interact with *taiman*. Within one region, we identified *Pvf1* as the gene responsible for the interaction. Signaling by PVF1 has been proposed to guide the border cells to their proper target, but ectopic PVF1 has not been tested for its ability to redirect the border cells. We tested the ability of PVF1, as well as other factors such as Gurken, to guide the border cells to new targets. Our results demonstrate that ectopic expression of PVF1 is sufficient to redirect border cells in some egg chambers but that the other factors tested are not. These data suggest that the guidance of border cell migration is robust and that there are likely to be additional factors that contribute to long-range guidance of these cells. In addition, we find that *taiman* and *Pvf1* regulate the dynamic localization of E-cadherin in the border cells, possibly accounting for the interaction between these two pathways.

Key words: PDGF, VEGF, PVF, Ecdysone, Border cells, Cell migration, *Drosophila*

INTRODUCTION

The conversion of stationary, epithelial cells to migratory, invasive cells is an important feature of embryonic development and tumor metastasis. The border cells of the *Drosophila* ovary have emerged as a useful model system for a forward genetic approach to this problem. The border cells are a group of four to eight follicle cells that form at the anterior pole of the somatic follicular epithelium, which surrounds the germ-line-derived nurse cells and oocyte (Fig. 1A). These cells, which are recruited by two non-migratory polar cells to form a cluster (Han et al., 2000; Liu and Montell, 1999; Silver and Montell, 2001), subsequently delaminate from the epithelium and migrate through the nurse cell cluster towards the anterior border of the oocyte. Border cells complete their migration when they reach the oocyte border and align with the oocyte nucleus on the dorsal side of the egg chamber (Fig. 1A) (Montell, 1999b; Montell, 2001). It is clear that border cell migration is tightly regulated both temporally and spatially.

The border cells migrate over a long distance (~150 μm) to reach the oocyte border, raising the question of how the border cells are able to find their correct target. A putative guidance factor has been reported, platelet-derived growth factor/vascular-endothelial growth factor (PDGF/VEGF) related factor 1 (PVF1; also known as VEGF1 and Vegf17E) (Cho et al., 2002; Duchek et al., 2001; Heino et al., 2001). PVF1 protein accumulates at the highest levels in the oocyte and, to a lesser extent, in nurse cells, whereas the PVF1 receptor (PVR) is expressed in all follicle cells (Duchek et al., 2001). Loss-of-function mutations in *Pvf1* and the expression of a dominant-negative PVR cause mild border cell migration defects (Duchek et al., 2001). Misexpression of PVF1 throughout the germ line or in the border cells themselves also disrupts border cell migration (Duchek et al., 2001). Duchek et al. (Duchek et al., 2001) proposed that PVF1 secreted from the oocyte acts as a guidance factor for the border cells. However, the ability of ectopic PVF1 to guide the border cells to a new location has not been demonstrated. Furthermore, it has been proposed that another ligand, the transforming-growth-factor-α-like ligand Gurken (GRK), might function redundantly with PVF1 to guide border cells, because a null mutation in *Pvf1* results in only mild migration defects, whereas expression of dominant-negative forms of PVR and the GRK receptor [the epidermal growth factor receptor (EGFR)] together affect border cell migration more dramatically than either receptor alone (Duchek et al., 2001).

However, it is unknown whether other ligands, such as the two other PVF homologs PVF2 (also known as Vegf27Cb) and PVF3 (also known as Vegf27Ca), participate in guiding border cell migration.

Regulation of border cell migration by a second signaling pathway might contribute to the timing of migration. The *Drosophila* steroid hormone ecdysone provides a signal for the border cells to begin migrating at stage 9 (Bai et al., 2000) and controls the movements of other follicle cells at this stage (J.A.M. and D.J.M., unpublished). The role of this pathway in border cell migration was suggested by identification of loss-of-function mutations in the ecdysone receptor co-activator *taiman* (*tai*), which cause severe border cell migration defects (Bai et al., 2000). The ecdysone pathway, via the ecdysone receptor, *tai* and as-yet-unidentified transcriptional target genes, regulates the distribution of *Drosophila* E-cadherin (DE-cadherin) in border cells (Bai et al., 2000). DE-cadherin protein is expressed at the cortex of all follicle cells and nurse cells, and is upregulated in the border cells (Bai et al., 2000; Niewiadomska et al., 1999). During migration, DE-cadherin appears to localize in a punctate pattern at the interface between border cells and nurse cells, whereas a higher level and more uniform distribution are observed between cells within the cluster (Bai et al., 2000; Niewiadomska et al., 1999). DE-cadherin is important because loss of DE-cadherin in either the border cells themselves or the nurse cells disrupts migration (Niewiadomska et al., 1999; Oda et al., 1997). Loss of *tai* in the border cells results in an abnormal accumulation of DE-cadherin at the interface between border cells and nurse cells (Bai et al., 2000). Thus, disruption of either the normal expression or distribution of DE-cadherin is associated with defective migration. An important unresolved question is how DE-cadherin is dynamically regulated at the interface of border cells and nurse cells.

To identify genes that play a role in border cell migration, we undertook a screen for mutations that exhibit dominant genetic interactions with a mutation in *tai*. 199 deficiencies were screened, 16 of which showed some degree of inhibition of border cell migration when heterozygous with *tai*. In one case, we identified a P-element insertion that showed dominant interactions with *tai* and also exhibited border cell migration defects when homozygous mutant. This P-element causes a null mutation of *Pvf1* (Duchek et al., 2001). In order to test whether PVF1 or other growth factors are capable of guiding the border cells, we ectopically expressed PVF1, PVF2 or GRK in random cells to see whether the border cells could be attracted to a new source of growth factor. PVF1 was capable of attracting the border cells to a new target but GRK and PVF2

Table 1. Summary of positive interacting deficiences identified in the screen

Deficiency (Bloomington stock no.)	Cytology	% border cell migration defect tai^{61G1} (*n*)*	% border cell migration defect tai^{k05809} (*n*)*	Interacting region
Df(1)v-N48 (3560)	9F;10C3-5	19 (333)	13 (192)	9F-10A9
Df(1)KA7 (957)†	10A9;10F6-7	0 (≥100)	0 (≥75)	
Df(1)N19 (970)	17A1;18A2	8 (184)	10 (77)	17A1-18A2
Df(2L)Dwee-delta5 (3571)	27A;28A	15 (209)	10 (88)	27A-C1
Df(2L)BSC7 (6374)	26D10-E1;27C1	10 (98)	15 (162)	
Df(2L)J-H (1357)	27C2-9;28B3-4	0 (≥100)	1 (123)	
Df(2L)J39 (1469)	31C-D;32D1-E5	47 (131)	Lethal‡	31C-32A2
Df(2L)J2 (3366)	31B1;32A1-2	34 (85)	18 (62)	
Df(2R)M60E (2471)	60E2-3;60E11-12	9 (200)	Semi-lethal§	60E2-12
Df(3L)GN24 (3686)	63F6-7;64C13-15	22 (271)	37 (82)	63F6-64B12
Df(3L)10H	64B10-12;64C5-7	0 (≥100)	1 (≥82)	
Df(3L)AC1 (997)	67A2;67D7-13	26 (231)	14 (66)	67B1-D13
Df(3L)29A6 (2479)	66F5;67B1	0 (≥100)	0 (≥75)	
Df(3L)fz-GF3b (3124)¶	70C1-2;70D4-5	10 (281)	6 (200)	70C1-D5
Df(3R)3-4 (4787)	82F3-4;82F10-11	12 (180)	4 (265)	82F3-11
Df(3R)by10 (1931)	85D8-12;85E7-F1	14 (206)	15 (125)	85D11-F1
Df(3R)by62 (1893)	85D11-14;85F6	20 (153)	7 (97)	
Tp(3;Y)ry506-85C (1534)	87D1-2;88E5-6	8 (164)	Semi-lethal§	87D1-88E6
Df(3R)H-B79 (4962)**	92B3;92F13	20 (185)	12 (169)	92B3-F13
Df(3R)crb-F89-4 (4432)	95D7-D11;95F15	12 (272)	12 (146)	95E8-F7
Df(3R)crb87-4 (2362)	95E8-F1;95F15	13 (304)	22 (189)	
Df(3R)crb87-5 (2363)	95F7;96A17-18	0 (100)	4 (124)	
Df(3R)3450 (430)	98E3;99A6-8	11 (278)	10 (114)	98E3-99A8

*Number of egg chambers examined.

†Overlapping deficiencies are indented; deficiencies from the deficiency kit are not indented.

‡Lethal in tai^{k05809}/Df(2L)J39 females.

§Semi-lethal in tai^{k05809}/+;Df/+ females; border cell migration could not be determined.

¶Df(3L)fz-GF3b exhibits a variable phenotype and is semi-haploinsufficient; 6% of Df(3L)fz-GF3b/TM6 egg chambers have border cell migration defects (*n*=159).

**Df(3R)H-B79 removes *Stat92E*, which is haploinsufficient for border cell migration (Silver and Montell, 2001); Df(3R)H-B79/TM2 females exhibit ~10% border cell migration defect (*n*=101).

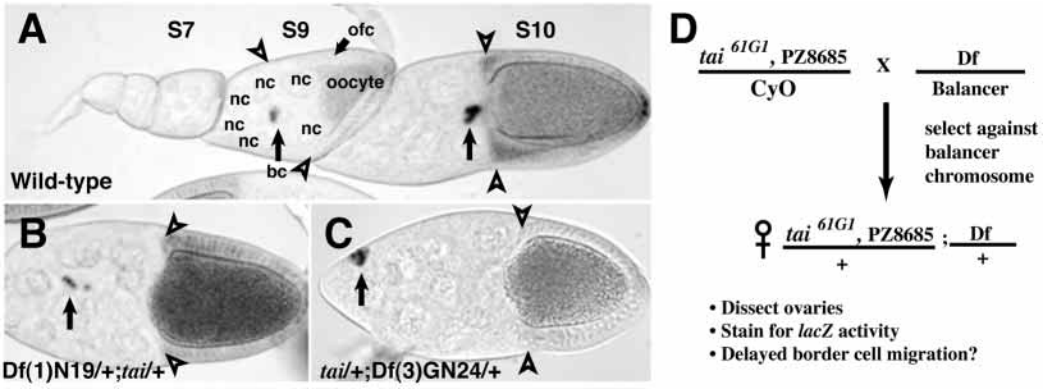

Fig. 1. Genetic screen to identify dominant interactions with *tai*. (A) Nomarski optics image of an ovariole stained for β-galactosidase activity from the enhancer trap *PZ8685*, showing the germarium stage (far left) to stage 10 (S10; far right). *PZ8685* is detected primarily in the border cells (bc, arrows), which migrate at stage 9 (S9) through the nurse cell cluster (nc). The border cells complete their migration at stage 10, when they reach the anterior border of the oocyte. (B,C) Representative examples of border cell (arrows) migration defects observed in stage 10 egg chambers heterozygous for tai^{61G1} (*tai*) and either Df(1)N19 (B) or Df(3)GN24 (C). (D) Crossing scheme used for the *tai* genetic interaction screen. The arrowheads in A-C indicate the extent of rearrangement of the outer follicle cells (ofc). Anterior is towards the left in all panels. Df, deficiency.

were not. Our results indicate that PVF1 acts as a guidance cue but additional factors likely contribute to the robust ability of these cells to find their target.

MATERIALS AND METHODS

Drosophila strains and genetics

For wild-type analysis, we used the w^{1118} strain. The following mutant alleles were used: 27C1 (Liu and Montell, 1999); tai^{61G1}, an EMS-generated null allele (Bai et al., 2000); tai^{k05809}, a P-element inserted upstream of the *tai* locus (Bai et al., 2000; Spradling et al., 1999); $Pvf1^{EP1624}$, a null allele of *Pvf1* (CG7103) (Duchek et al., 2001); $chic^{k13321}$ (Spradling et al., 1999); $slbo^{e7b}$ and $slbo^{LY6}$ (Montell et al., 1992); ecd^{1} (Garen et al., 1977); $pvf2^{c6947}$ (Cho et al., 2002); and Pvr^{c2195} (Cho et al., 2002). All deficiencies and lethal P-element alleles used in the interaction screen were obtained from the Bloomington *Drosophila* stock center except for Df(3L)10H (a gift from T. Hays). Phenotypic analyses were performed at 25°C and border cell migration was assayed at stage 10, when the outer follicle cells have completed their rearrangement (King, 1970; Spradling, 1993).

We used the FLP/FRT system (Xu and Rubin, 1993) to generate mosaic mutant follicle cell clones of tai^{61G1}, FRT^{40A} and Pvr^{c2195}, FRT^{40A}. Mosaic mutant clones marked for loss of GFP were induced as described (Bai et al., 2000; Silver and Montell, 2001) using females of the genotype hs-FLP; ubiquitin-nuclear-GFP, FRT^{40A}. Positively marked clones were induced using the MARCM system (Lee and Luo, 1999) as described (Silver and Montell, 2001).

Screen for dominant genetic interactions with *tai*

The tai^{61G1} allele was recombined with a viable enhancer trap expressed in the border cells, *PZ8685* (D.J.M., unpublished). The tai^{61G1}, *PZ8685*/CyO stock was crossed to the deficiency kit lines from the Bloomington stock center (http://fly.bio.indiana.edu/). We dissected ovaries from three to five female progeny lacking the balancer chromosomes and performed β-galactosidase activity staining. Egg chambers double heterozygous for *tai* and the deficiency were examined for delays in border cell migration compared with tai^{61G1}, *PZ8685*/CyO. A deficiency was considered phenotypic if ≥8% of the egg chambers scored showed delay of border cell migration. The average of at least two experiments is reported in Table 1. Two deficiencies were identified that exhibited partial haploinsufficiency with respect to border cell migration (Table 1).

Ectopic expression

To express genes ectopically, we used the GAL4/UAS system (Brand and Perrimon, 1993). *slbo*-GAL4 is expressed specifically in border cells (Rørth et al., 1998) and *c306*-GAL4 is expressed in a subset of anterior follicle cells, including the border cells (Manseau et al., 1997). To generate UAS-*Pvf1* flies, we subcloned a full-length *Pvf1* cDNA into pUAST (Brand and Perrimon, 1993) and injected this construct into w^{1118} flies along with the pπ25.7 (wings-clipped) source of transposase as described (Spradling, 1986). Two independent insertions were obtained, a viable insertion on chromosome 2 and a lethal insertion on chromosome 3. Additional UAS lines used were UAS-*grk*ΔTC (UAS-s-*grk*; secreted GRK) (Queenan et al., 1999) and UAS-*pvf2* ($pvf2^{d244}$) (Cho et al., 2002).

To make clones of cells ectopically expressing a gene under the control of GAL4/UAS, we used the 'FLP-out' GAL4 system (AyGAL4) (Ito et al., 1997). To induce clones, adult females were heat-shocked at 37°C for 1 hour and incubated for 2 days at 25°C before having their ovaries dissected. Clones were detected by expression of UAS-*lacZ* using an anti-β-galactosidase antibody. For UAS-*Pvf1* and UAS-s-*grk*, we confirmed by antibody staining that the respective proteins were expressed.

Production of antisera, β-galactosidase activity and immunofluorescence

The last 311 amino acids of PVR were cloned into the pGST-Parallel 1 expression vector (Sheffield et al., 1999). The PVR C-terminal fragment was expressed as a fusion protein in *Escherichia coli* [strain BL21(DE3)] and affinity purified. Purified protein was used to immunize rabbits and rats (Covance). Animals were boosted a total of five times, resulting in optimal signal in egg chambers at 1:1000 to 1:2000 dilution.

Ovary dissection and fixation, β-galactosidase activity staining and antibody staining were performed essentially as described (Bai et al., 2000; Montell, 1999a). The following primary antibodies were used: mouse anti-Armadillo monoclonal (N27A1; 1:75) (Developmental Studies Hybridoma Bank); rabbit anti-β-galactosidase serum (1:3000; Cappel); rat anti-DE-cadherin monoclonal (DCAD2; 1:10) (Uemura et al., 1996); rabbit anti-GFP serum (1:4000; Molecular Probes); mouse anti-PVF1 serum (1:200) (Duchek et al., 2001); rat anti-PVR serum (1:1500); mouse anti-Singed monoclonal (7C; 1:25) (Cant et al., 1994); and rabbit anti-TAI serum (1:1000) (Bai et al., 2000). Secondary antibodies conjugated to alexa fluor 488 and alexa fluor 568 (Molecular Probes) were used at a dilution of 1:400. To visualize actin, rhodamine-phalloidin (Molecular Probes), at a dilution of 1:400, was added during secondary antibody incubation. Images were

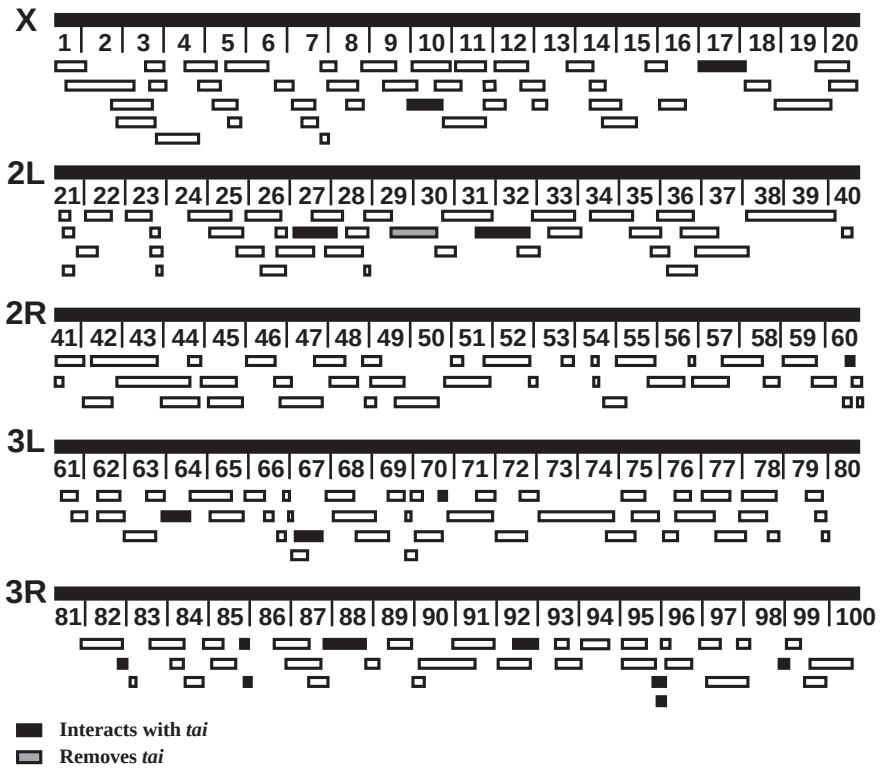

Fig. 2. All deficiencies screened for dominant interaction with *tai*. The Bloomington Stock Center deficiency kit was screened for dominant genetic interaction with *tai*, indicated by the boxes below each chromosome arm (thick black lines). The identity of the chromosome arms are indicated on the left. The size of the box corresponds to the cytological breakpoints for the deficiency, indicated by the numbers below the chromosome arms. White boxes represent deficiencies that were tested but had no interaction with *tai*. Black boxes represent deficiencies that interacted with *tai* (Table 1). The gray box represents the deficiency that removes the *tai* locus at the 30A6 region.

captured with the Ultraview confocal microscope or with a digital camera on a Zeiss Axioplan fluorescent microscope.

RESULTS

Screen to identify loci that exhibit dominant genetic interactions with *tai*

The ecdysone signaling pathway, via *tai*, plays an important role in border cell migration, but little is known about the mechanisms by which this pathway facilitates migration or how it interacts with other pathways that affect border cell migration. In order to gain further insight into these questions, we performed a screen for dominant genetic interactions with *tai* (Fig. 1D). This type of screen has previously been successful at identifying members of genetic pathways that are missed in other types of screens (e.g. Cox et al., 2000; Firth et al., 2000; Halsell and Kiehart, 1998; Jackson and Berg, 1999; Simon et al., 1991). We found that *tai* exhibited dominant genetic interactions with 27C1, a mutation that causes border cell migration defects in mosaic clones (data not shown) (Liu and Montell, 1999). Approximately 18% of egg chambers (n=88) that were heterozygous for both *tai* and 27C1 displayed defects in border cell migration, whereas egg chambers that were heterozygous for just *tai* or 27C1 were indistinguishable from the wild type (data not shown). This finding suggested that other genes required for border cell migration might also show dominant interactions with *tai*.

In order to maximize the number of genes that could be tested for interaction with *tai*, we screened a collection of deficiencies, which in total removes ≥75% of the genome, for loci that showed border cell migration defects when doubly heterozygous with a null allele of *tai* (tai^{61G1}) (see Materials and Methods; Fig. 1D). Of 199 deficiencies tested, 16 deficiencies, defining 14 separate interacting regions, exhibited a border cell migration defect in heterozygous combination with *tai* (Figs 1, 2, Table 1). The proportion of egg chambers with border cell migration defects varied between 8% and 47%, depending on the deficiency (Fig. 1B,C, Table 1). In order to confirm that the deficiencies specifically interacted with *tai*, we re-screened the interacting deficiencies with another *tai* allele, tai^{k05809}, which is a P-element insertion allele (Table 1). Most of the deficiencies interacted with both *tai* alleles with a few exhibiting different strengths of interactions (Table 1). In several instances, we were able to define smaller interacting regions by testing overlapping deficiencies (Table 1).

In order to identify individual genes that were responsible for the dominant interactions, several lethal P-element alleles that map to ten of the regions were tested but none exhibited an interaction with *tai* (data not shown). In a separate screen, we identified a homozygous viable P-element insertion that caused mild border cell migration defects (E.M.P. and D.J.M., unpublished; Fig. 3C). This P-element allele, EP1624, maps to 17E4-6, a region deleted by the interacting deficiency Df(1)N19 (Table 1). EP1624 has been shown to be a null allele of the *Pvf1* locus (Duchek et al., 2001). We tested whether EP1624 interacted with *tai* and found that about 6% of the double heterozygous egg chambers had border cell migration defects, compared with 1% of tai^{61G1}/CyO egg chambers (Fig. 3A-C; P<0.006, Student's t-test). This effect was similar in strength to the interaction of Df(1)N19 with *tai* (Table 1).

PVF1 is normally expressed only in the germ line but misexpression of PVF1 in the border cells disrupts border cell migration in a similar way to that seen with *Pvf1* loss of function (Fig. 3D) (Duchek et al., 2001). Because the loss-of-function and misexpression phenotypes of *Pvf1* are similar, we

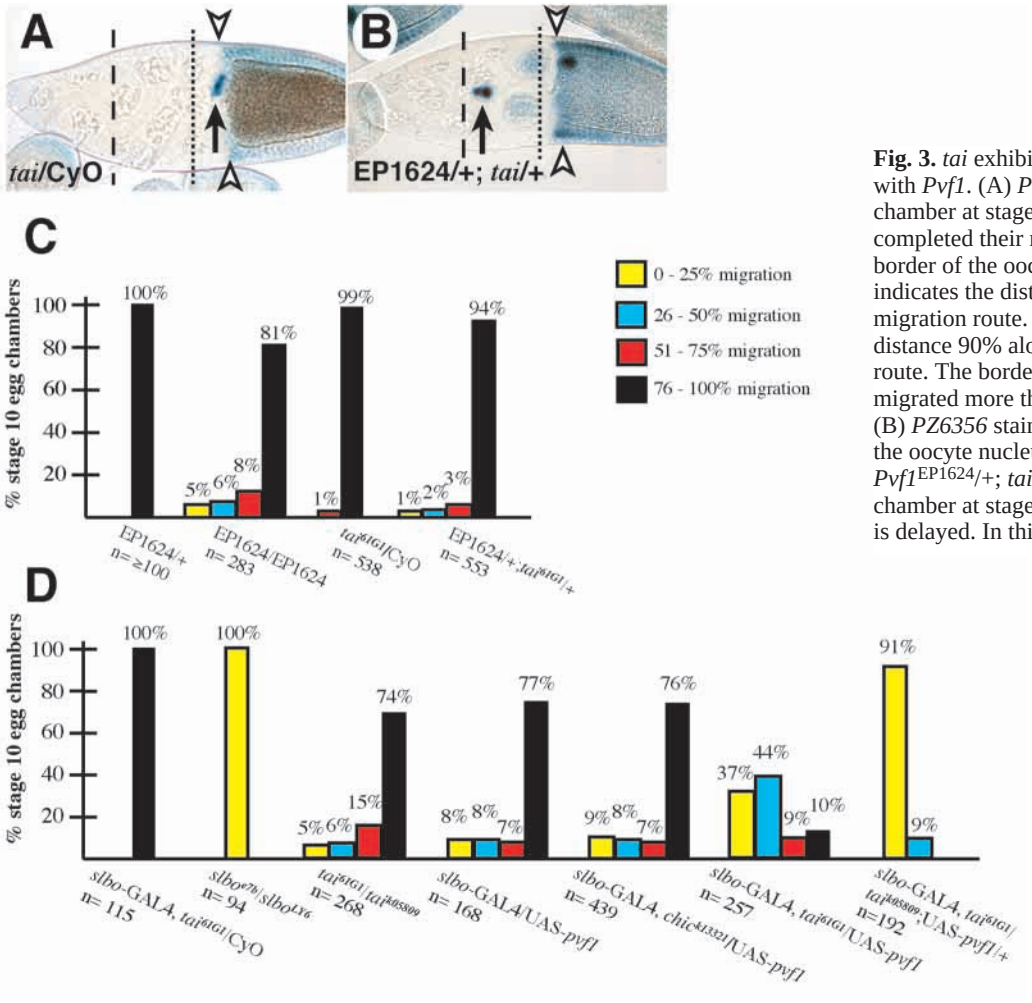

Fig. 3. *tai* exhibits dominant genetic interactions with *Pvf1*. (A) *PZ8685* staining in a tai^{61G1}/CyO egg chamber at stage 10. The border cells (arrow) have completed their migration and reside at the anterior border of the oocyte (arrowheads). The dashed line indicates the distance 50% along the length of the migration route. The dotted line indicates the distance 90% along the length of the migration route. The border cells in this egg chamber have migrated more than 90% of the normal distance. (B) *PZ6356* staining, which labels the border cells, the oocyte nucleus and some nurse cell nuclei, in a $Pvf1^{EP1624}$/+; tai^{61G1}/+ double heterozygous egg chamber at stage 10. Border cell migration (arrow) is delayed. In this egg chamber, the border cells have migrated ~60% of the normal distance. (C,D) Quantitation of border cell migration shown as the proportion of egg chambers in which the border cells migrated 0-25% (yellow), 26-50% (blue), 51-75% (red) and 76-100% (black) of the normal distance. Border cell migration was assayed in the indicated genotypes at stage 10. The number of egg chambers examined is indicated (n). (C) Interaction of *tai* with $Pvf1^{EP1624}$ (EP1624). (D) Interaction of *tai* with *slbo*-GAL4/ UAS-*Pvf1*.

examined whether loss of *tai* could enhance the PVF1 misexpression phenotype. As previously reported (Duchek et al., 2001), PVF1 misexpression in the border cells caused a minor delay in border cell migration (23% of egg chambers; Fig. 3D), with most clusters migrating varying distances along the length of the egg chamber (Fig. 3D), whereas *tai* heterozygotes did not exhibit migration delays (Fig. 3C,D). By contrast, misexpression of PVF1 in a *tai* heterozygous mutant background resulted in 90% of the egg chambers exhibiting border cell migration defects (Fig. 3D). Most of the delayed border cell clusters (81%) migrated ≤50% the normal distance (Fig. 3D). We further lowered the dosage of *tai* using a viable combination of *tai* alleles (tai^{61G1}/ tai^{k05809}), which on its own exhibited a minor delay in border cell migration (26% of the egg chambers; Fig. 3D). Lowering *tai* gene dosage in this genetic background dramatically enhanced the PVF1 misexpression migration defect, such that all egg chambers were defective (Fig. 3D). Most border cell clusters (91%) migrated less than 25% of the normal distance, resembling the *slow border cells* (*slbo*) mutant phenotype (Fig. 3D). If this were simply an additive phenotype, we would expect approximately 50% of the border cells to fail to migrate and just a few clusters (13%) to migrate less than 25% of the normal distance. Identical results were obtained using a different GAL4 driver, *c306*-GAL4 (data not shown). The interaction between misexpressed PVF1 and loss of *tai* appeared to be specific because lowering the gene dosage of *chickadee* (*chic*), another gene required for border cell migration (Verheyen and Cooley, 1994), did not enhance the PVF1 misexpression phenotype (Fig. 3D). These data together demonstrate that *tai* and *Pvf1* genetically interact to control border cell migration.

tai and *Pvf1* affect DE-cadherin distribution in the border cells

To investigate the basis for the genetic interaction between *Pvf1* and *tai*, we first tested whether ecdysone signaling affected expression of either PVF1 or its receptor PVR. TAI is expressed in all follicle cells (Fig. 4A) (Bai et al., 2000), as is PVR (Fig. 5A,B) (Duchek et al., 2001). Because TAI encodes a transcriptional regulator, we examined the expression of PVR protein in follicle cells that were mutant for *tai*. No change in the levels of PVR expression was observed either in the columnar follicle cells surrounding the oocyte (Fig. 4C,D) or in the border cells (Fig. 4F). PVF1 was also expressed normally in *ecdysoneless* mutant egg chambers (data not shown), which are defective in the synthesis of ecdysone. We then examined the expression of TAI protein in *Pvf1* mutant egg chambers (Fig. 4A,B). *Pvf1* mutant egg chambers displayed normal levels of TAI protein in border cells and other follicle cells (Fig.

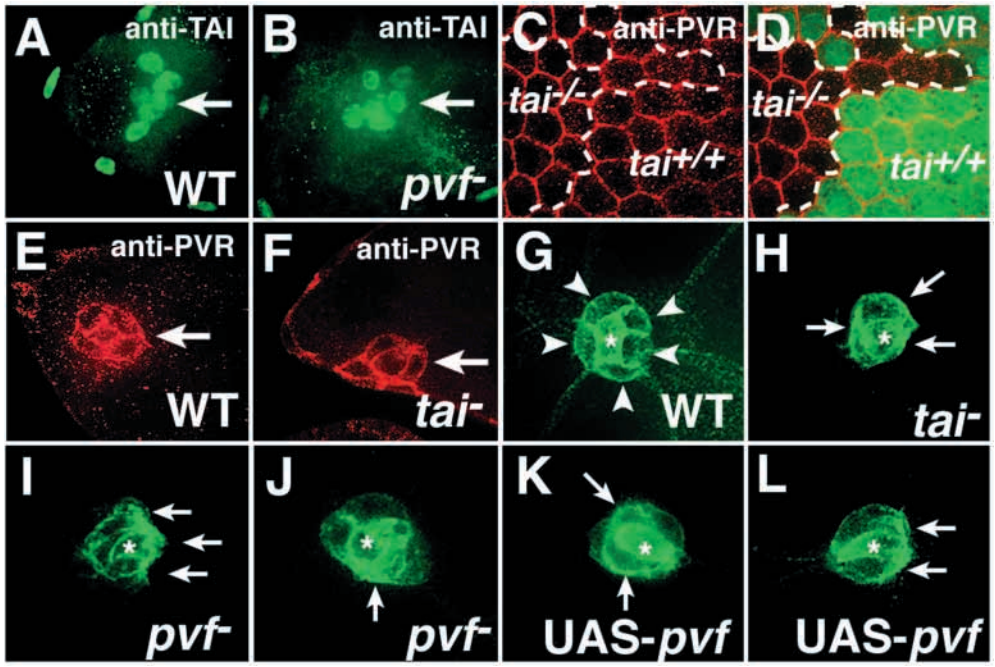

Fig. 4. E-cadherin distribution and TAI and PVR expression in mutant egg chambers. (A,B) Expression of TAI in wild-type (A) and *Pvf1*^{EP1624} (B) egg chambers. Border cells are indicated by the arrow. (C,D) PVR expression (red) in the follicle cells surrounding the oocyte in an egg chamber containing a large *tai* mutant follicle cell clone. Absence of GFP staining (green in D) marks the cells that are homozygous mutant for *tai*^{61G1} (*tai*$^{-/-}$; broken line indicates the clone border). (E,F) PVR expression in wild-type (E) and *tai* mutant (F) border cell clusters (arrows). (G-L) Merged confocal *z* sections showing DE-cadherin protein expression in border cell clusters. (G) An example of a stage 9 wild-type border cell cluster undergoing migration. The polar cells (*) express highest levels of DE-cadherin, whereas the border-cell/nurse-cell junctions exhibit lower, punctate staining for DE-cadherin (arrowheads). DE-cadherin levels are high at junctions between border cells. (H) Stage 10 *tai* mutant border cell cluster. DE-cadherin protein levels are high throughout the cluster (compare with polar cells, *), especially at several nurse-cell/border-cell boundaries (arrows). (I,J) Stage 10 *Pvf1* mutant egg chamber. DE-cadherin levels are high at a subset of border-cell/nurse-cell junctions (arrows). (J) DE-cadherin is high between border cells (compare with polar cells, *) and in one border-cell/nurse-cell junction. (K,L) Stage 10 *slbo*-GAL4/UAS-*Pvf1* (UAS-*Pvf1*) border cell clusters. DE-cadherin levels are high at border-cell/nurse-cell junctions (arrows); polar cells are marked with an asterisk. Anterior is towards the left in all panels.

4B). We conclude that ecdysone signaling does not affect PVF or PVR protein expression in follicle cells, nor does the *Pvf1* pathway regulate the expression of TAI in follicle cells.

Because *tai* has been shown to regulate the distribution of DE-cadherin in the border cells, we tested whether PVF1 might also regulate the distribution of DE-cadherin in border cells. In wild-type border cells undergoing migration, DE-cadherin is detected at high levels in the central, non-migratory polar cells and between border cells, whereas it is detected at lower levels at the interface between border cells and nurse cells (Fig. 4G) (Bai et al., 2000; Niewiadomska et al., 1999). In *tai* mutant border cells, the distribution of DE-cadherin is altered and variable, and the protein can accumulate abnormally at the interface between nurse cells and border cells (Fig. 4H) (Bai et al., 2000). In *Pvf1* mutant egg chambers, DE-cadherin distribution in the border cell cluster was disrupted to various degrees (Fig. 4I,J). In some *Pvf1* mutant egg chambers, we detected DE-cadherin mainly to one side of the cluster at junctions between nurse cells and border cells (Fig. 4I). We also observed *Pvf1* mutant egg chambers in which DE-cadherin was detected at high levels overall in the border cells and in a few junctions between border cells (Fig. 4J). Misexpression of PVF1 (*slbo*-GAL4/UAS-*Pvf1*) in the border cells altered DE-cadherin distribution in a manner similar to that of *Pvf1* mutant egg chambers (Fig. 4K,L). The distribution of Armadillo (Arm), the *Drosophila* homolog of β-catenin, is indistinguishable from that of DE-cadherin in wild-type border cells (Bai et al., 2000; Oda et al., 1997). We found that Arm

Table 2. Quantitation of phenotypic classes observed following misexpression of PVF1, PVF2 and GRK in anterior follicle cells

	Anterior follicle cell clones			
Genotype* (*n*)†	Class I (%)	Class II (%)	Class III (%)	Class IV (%)
UAS-*Pvf1*(1×)‡ (148)	87	5	8	0
Pvf1$^{-/-}$;UAS-*Pvf1* (124)	80	5	14	1
Pvr$^{-/+}$;UAS-*Pvf1* (128)	80	2	18	0
UAS-*Pvf2* (130)	100	0	0	0
UAS-*Pvf1* + UAS-*Pvf2* (94)	79	2	13	6
UAS-*Pvf1* (2×)‡ (95)	57	11	19	13
UAS-*s-grk* (138)	100	0	0	0
UAS-*Pvf1* + UAS-*s-grk* (112)	83	4	12	1

*Genotypes are *hsflp*/+; AyGAL4/*x*, where "*x*" is the indicated UAS-transgene.
†Total number of egg chambers examined for each genotype.
‡1× and 2× represent total number of copies of the transgene.
See Fig. 6 legend and text for description of classes.

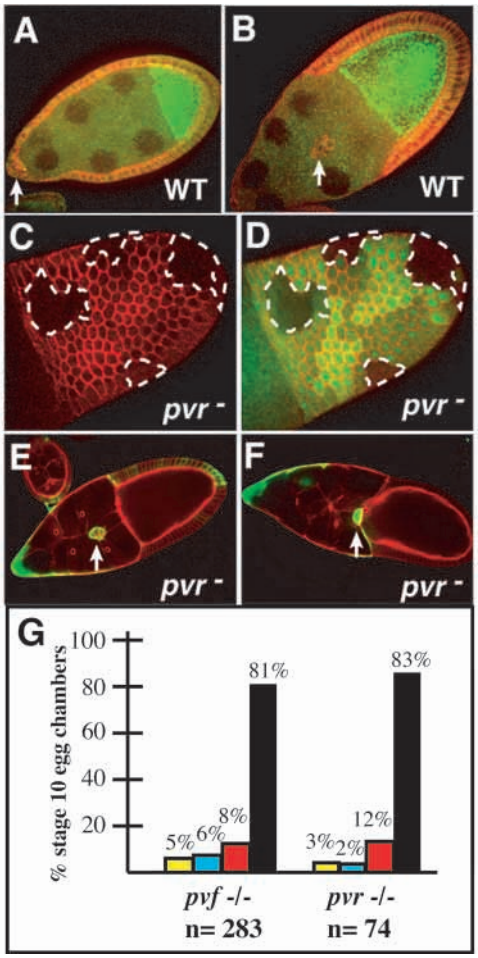

Fig. 5. PVR function in border cell migration. (A,B) Wild-type expression of PVF1 (green) in the oocyte and nurse cell cytoplasm and PVR (red) in follicle cells at stage 8 (A) and stage 9 (B). PVR is expressed in the border cells (arrows). (C,D) PVR expression (red) in the outer follicle cells of an egg chamber with several Pvr^{c2195} mosaic clones. Loss of GFP (green in D) marks cells homozygous mutant for *Pvr* (broken lines surround the mutant clones). (E,F) Egg chambers with border cells (arrows) mutant for *Pvr*. GFP (green) positively marks the homozygous mutant cells and filamentous actin (red) outlines all cells. (E) Egg chamber in which the mutant border cell cluster (arrow) exhibited delayed migration. (F) Egg chamber in which the mutant border cell cluster (arrow) migrated to the oocyte. (G) Quantitation of the *Pvr* mutant migration defect compared with the *Pvf1* migration defect. Quantitation of border cell migration shown as the proportion of egg chambers in which the border cells migrated 0-25% (yellow), 26-50% (blue), 51-75% (red) and 76-100% (black) of the normal distance. Anterior is towards the left in all panels.

localization was disrupted in a similar way to DE-cadherin in all the genotypes examined (data not shown). We conclude that both *tai* and *Pvf1* are required for the correct distribution of DE-cadherin and Arm in the border cells.

Loss of the PVF1 receptor disrupts border cell migration

In order to better understand the role of *Pvf1* in regulating border cell migration, we next examined the contribution of the PVF1 receptor, PVR (Cho et al., 2002; Duchek et al., 2001; Heino et al., 2001). A dominant-negative version of PVR causes an incompletely penetrant border cell migration defect (Duchek et al., 2001). It is not clear whether the mild phenotype actually represents the effect of a null mutation in the receptor or reflects a partial loss-of-function effect of the dominant negative mutation. Moreover, the *Drosophila* genome encodes two additional ligands related to PVF1, called PVF2 and PVF3 (or VEGF27Cb and VEGF27Ca), which are expressed in the ovary (Duchek et al., 2001) and could possibly contribute to border cell migration. However, there is only a single receptor, therefore we tested to what extent a *Pvr* mutation disrupted border cell migration (Fig. 5). An allele of *Pvr* (Pvr^{c2195}) was recently reported (Cho et al., 2002). We generated homozygous mutant clones in follicle cells using this allele. We found that PVR was undetectable in mutant cells (Fig. 5C,D) and so Pvr^{c2195} is a strong loss-of-function, and possibly null, allele. Border cell clusters in which all cells were homozygous for the mutation displayed delays in border cell migration, but the phenotype was incompletely penetrant (Fig. 5E,G) and many border cell clusters completed their migration to the oocyte (Fig. 5F). This phenotype is indistinguishable from the null phenotype for *Pvf1* (Fig. 5G).

Ectopic expression of PVF1 is sufficient to misguide the border cells

PVF1 is expressed in the oocyte and its receptor is expressed in all follicle cells (Fig. 5A,B), and so it has been proposed to guide the border cells (Duchek et al., 2001). However, this has not been directly tested. We used the 'FLP-out' GAL4 system (Ito et al., 1997) to express PVF1 in random groups of follicle cells in order to test whether PVF1 was sufficient to guide the border cells to a new source of ligand (Fig. 6; Table 2). We scored border cell migration in egg chambers that expressed PVF1 in the anterior follicle cells that surround the nurse cells (squamous follicle cells) but not in border cells (Fig. 6). Antibody staining confirmed that PVF1 was actually expressed in the follicle cell clones (Fig. 6A-C). The levels of ectopic PVF1 expressed in clones of anterior follicle cells appeared to exceed the concentration of endogenous PVF1 in the nurse cells.

We observed four classes of phenotypes when PVF1 was ectopically expressed in clones of anterior follicle cells. In the class I phenotype, border cell clusters migrated normally to the oocyte (Fig. 6D); most of the egg chambers misexpressing PVF1 fell into this class (Table 2). The class II phenotype was characterized by border cells that did not migrate away from the anterior pole (Fig. 6E). In all examples of this class, we observed that the border cells were adjacent to a group of follicle cells expressing ectopic PVF1 (Fig. 6E); 5% of egg chambers misexpressing PVF1 fell into class II (Table 2). In class III egg chambers, border cells were located on the side of the egg chamber, not far from the anterior pole and adjacent to cells expressing ectopic PVF1 (Fig. 6F); we observed 8% class III phenotypes (Table 2). In the class IV phenotype, the border cells were found on the side of the egg chamber at least two nurse cells or more away from the anterior pole, adjacent to a clone of cells expressing ectopic PVF1 (Fig. 6G). Therefore it was possible for border cells to be guided to a source of PVF1, but this class was relatively rare (Table 2).

Although it appeared that the levels of ectopic PVF1 were

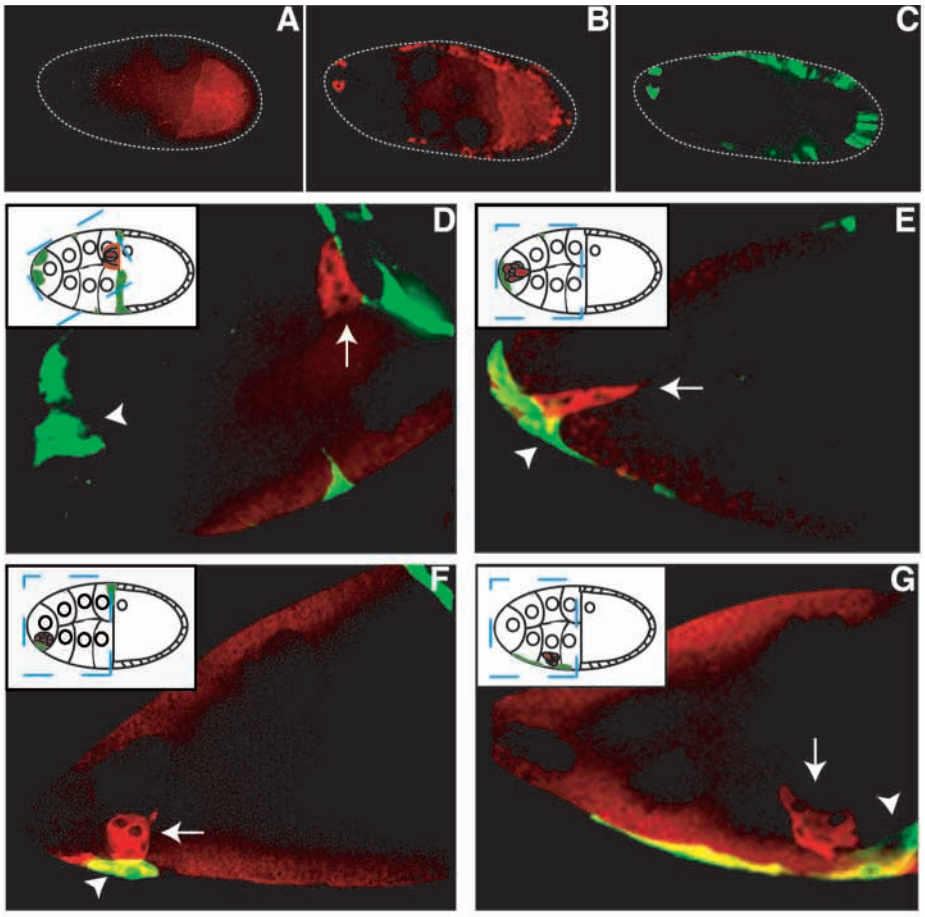

Fig. 6. (A) Wild-type expression of PVF1 (red) in the oocyte and nurse cell cytoplasm at stage 9. (B,C) Clones of ectopic PVF1 expression in follicle cells of a stage 9 egg chamber showing expression of PVF1 in red (B) co-expressed with β-galactosidase (green), which labels the clones (C). The broken lines show the outline of the egg chambers. (D-G) Classes of phenotypes observed after misexpression of PVF1, PVF2 or GRK. Egg chambers with clones of anterior follicle cells misexpressing one or more ligands (green, arrowheads). Singed staining labels the border cells (red, arrows). Representative examples of the four phenotypic classes are shown. (D) Class I: normal migration of the border cell cluster; an example of a UAS-*Pvf1* egg chamber is shown. (E) Class II: the border cells fail to migrate away from the anterior pole and are adjacent to a clone of follicle cells misexpressing ligand; an example of a UAS-*Pvf1* egg chamber is shown. (F) Class III: the border cells localize to the side of the egg chamber less than one nurse cell away from the anterior pole and adjacent to follicle cells misexpressing ligand; an example of a UAS-*Pvf1*;UAS-*grk* egg chamber is shown. (G) Class IV: the border cell cluster localizes to the side of the egg chamber at least two nurse cells away from the anterior pole, adjacent to a clone of cells misexpressing ligand; an example of a $Pvf1^{1624}$;UAS-*Pvf1* egg chamber is shown. (Insets) Schematics of the stage 10 egg chambers represented in the fluorescent images, depicting the position of the border cells (red) with respect to the cells misexpressing ligand (green). The area indicated by the blue dashed box in the schematic outlines the anterior half of the egg chamber, which is shown at high magnification in the fluorescent images. Anterior is towards the left in all panels.

higher than the local concentration of endogenous PVF1, it seemed possible that endogenous PVF1 was somehow more effective and therefore that the ectopic protein was not very active because of the presence of endogenous protein. Therefore, we induced clones of cells expressing ectopic PVF1 in a $Pvf1^{EP1624}$ mutant background, which lacks endogenous PVF1 protein (Duchek et al., 2001). Similar results were obtained whether or not endogenous PVF1 was present (Table 2), making it unlikely that endogenous PVF1 interfered with the ability of ectopic PVF1 to guide the border cells to new targets in the egg chamber. We also considered the possibility that PVF1 expressed in follicle cells might be sequestered by endogenous PVR, which is expressed in all follicle cells, such that little PVF1 ligand could be secreted by these follicle cells. However reducing by half the dose of PVR had little or no effect on the ability of ectopic PVF1 to redirect the migration (Table 2).

Most egg chambers expressing ectopic PVF1 exhibited normal border cell migration, so we tested whether other ligands could misguide the border cells, either alone or in combination with PVF1. PVF2 is a protein homologous to PVF1 that is capable of redirecting hemocyte migration in the *Drosophila* embryo, even though PVF1 cannot (Cho et al., 2002). We therefore tested whether PVF2 could misguide the border cells when ectopically expressed in follicle cells. PVF2 alone did not cause any border cell migration delays and did not guide the border cells to new targets (Table 2). Specific misexpression of PVF2 in the border cells using *slbo*-GAL4 did not affect their migration either (data not shown), therefore the border cells appeared to be unresponsive to PVF2 alone. The results of co-expressing PVF1 and PVF2 in follicle cell clones are shown in Table 2. There was a small increase in the proportion of egg chambers that fell into class IV, indicating that PVF2 might be more effective in combination with PVF1 than alone.

The most dramatic effects on border cell migration were observed when two copies of the UAS-Pvf1 transgene were included in the experiment, thus presumably doubling the concentration of ectopic PVF1. The proportion of class IV egg chambers jumped to 13% and that of egg chambers showing normal migration was reduced to 57% (Table 2).

EGFR and PVR might function redundantly to guide the border cells to the oocyte, because expression of dominant-negative EGFR and PVR together disrupt border cell migration more potently than either dominant-negative alone (Duchek et al., 2001). If these factors function redundantly to guide the border cells then either factor should be sufficient on its own to redirect the migration. We tested whether expression of a

secreted form of GRK (s-GRK) (Van Buskirk and Schupbach, 1999) was sufficient to attract the border cells. In all cases, we observed normal border cell migration following expression of s-GRK in follicle cell clones (class I; Table 2). To test whether expression of PVF1 and s-GRK together was a more effective guidance cue than either alone, we coexpressed them in follicle cell clones. We obtained similar results to ectopically expressing PVF1 alone (Table 2), indicating that ectopic s-GRK in anterior follicle cells did not affect border cell migration. Ectopic expression of GRK in border cells, in contrast to PVF2, was able to disrupt border cell migration to a small degree (data not shown) (Duchek and Rørth, 2001).

DISCUSSION

Genetic screen to identify genes that function with *tai* in border cell migration

We performed a screen to identify genomic regions that exhibit dominant genetic interactions with *tai* in order to identify new genes that are required for border cell migration and identified 14 different interacting genomic regions. We were able to identify *Pvf1* as the locus responsible for one of the deficiency interactions. The interaction of *tai* with *Pvf1* appears to be specific because *tai* did not interact with either loss-of-function mutations or deficiencies that remove other genes known to regulate border cell migration, such as *slbo* or *shotgun*/DE-cadherin (data not shown; Fig. 2). Mutations in *slbo* or *shotgun* reduce DE-cadherin levels in the border cells (Niewiadomska et al., 1999), so *tai* does not interact with every gene that regulates DE-cadherin, possibly because *tai* regulates the distribution rather than the levels of DE-cadherin in the border cells. Identification of *Pvf1* indicates that this screen provides a useful approach for identifying additional loci that affect border cell migration in general and regulated turnover of adhesion in particular.

Relationship between TAI and PVF1

The genetic interaction between *Pvf1* and *tai* indicates that the regulation of border cell migration timing and guidance might be linked. What is the nature of the interaction between *tai* and *Pvf1* during border cell migration? Ecdysone signaling did not regulate PVF1 or PVR expression nor did *Pvf1* regulate TAI expression, but the ecdysone and *Pvf1* pathways both affected the distribution of DE-cadherin and Arm. We favor a model whereby *tai* and *Pvf1* interact because they both regulate adhesion complex localization or turnover. The *tai* and *Pvf1* genes could act independently to regulate cadherin-dynamics. Alternatively, *tai* and *Pvf1* might function in a common pathway. TAI and PVR both function autonomously in the border cells, although they are unlikely to bind directly to each other because TAI localizes to the nucleus and PVR is a receptor tyrosine kinase localized to the membrane. One possibility is that PVR activates (or represses) the function of a protein whose expression is dependent on TAI, and that this protein in turn regulates cadherin dynamics in the border cells. Tyrosine phosphorylation of β-catenin, the Arm homolog, causes destabilization of adhesion complexes in other cell types (Lilien et al., 2002), so perhaps PVR activity destabilizes E-cadherin/Armadillo complexes specifically in the border cells. Identification of additional genes identified in this screen, in particular those that affect adhesion turnover in border cells, should help clarify the biochemical relationship between TAI and PVF1.

PVF1 functions as a concentration dependent guidance cue – evidence for additional guidance cues?

The results reported here demonstrate that ectopic expression of PVF1 is sufficient to redirect border cells even though, in *Pvf1* null mutants, border cell clusters migrate normally in the majority of egg chambers. When PVF1 was ectopically expressed in random follicle cells, the border cells were attracted to these sources of PVF1. The border cells were attracted more efficiently to sources of PVF1 signal close to the anterior pole, indicating that they respond better to high concentrations of the ligand. The finding that doubling the dose of ectopically expressed PVF1 dramatically increased the frequency with which the cells responded to the ectopic signal confirmed the idea of a concentration dependent effect.

The concentration of ectopic PVF1 at the anterior end of the egg chamber appeared to exceed the concentration of endogenous PVF1 at that position, even when only a single UAS-*Pvf1* transgene was included in the experiment. Consistent with that idea, elimination of endogenous PVF did not significantly alter the response of the border cells to ectopic ligand. The border cells still migrated normally in many cases, apparently ignoring ectopically expressed PVF1. The most likely explanation for this is that there are additional germ-line-derived attractive cues that instruct the cells to migrate correctly in the absence of endogenous PVF1 and in the presence of ectopic PVF1.

PVF2 does not seem to be a good candidate for a redundant guidance cue because loss of function of the PVR receptor produced a phenotype that was indistinguishable from loss of PVF1 alone. Moreover UAS-*Pvf2* was not able to redirect the border cells. This finding is surprising because PVF2 is thought to bind and activate the same receptor as PVF1. It is especially surprising because only PVF2 (expressed from the same UAS-PVF2 transgene) and not PVF1 is effective at misguiding hemocytes in the embryo (Cho et al., 2002). Together, these findings suggest a striking, and as-yet inexplicable, specificity of ligand action that will be interesting to study further.

We also found that GRK, the major EGFR ligand in the ovary, was not an effective guidance cue for the border cells, either when expressed alone or in combination with PVF1. The inability of GRK to affect border cells was striking because even class II and III phenotypes were absent, even though these were not uncommon following PVF misexpression. This is consistent with the observation that migration of the border cells to the oocyte is completely normal in *grk* mutant egg chambers and in mosaic egg chambers in which border cells lack EGF receptor function (Duchek and Rørth, 2001). GRK does, however, have a role in the dorsal migration of the border cells after they reach the oocyte (Duchek and Rørth, 2001). Currently, the evidence supporting a role for GRK in migration of the border cells to the oocyte is the combined effect of dominant-negative PVR and dominant-negative EGFR (Duchek et al., 2001). Taken together with the results supplied here, the evidence in favor of a role for EGFR is somewhat better than the evidence in favor of a role for GRK, possibly suggesting the involvement of other EGFR ligands.

In addition to ligands for PVR and EGFR, this study might imply the existence of other, as-yet-unidentified cues, that participate in the long-range guidance of the border cells. We propose that PVF1, and possibly additional unknown ligands, guide the border cells to the oocyte. Similarly, in the *Drosophila* central nervous system, multiple short-range and long-range cues are required to guide motor axons properly to their appropriate muscle targets (Winberg et al., 1998). Perhaps even a simple migration, such as that of the border cells, uses multiple cues, each of which might only have a small contribution. Screens such as the one reported here might help us to identify the full set of border cell migration cues as well as additional genes that function in adhesion complex turnover.

We would like to thank P. Rørth, the Developmental Studies Hybridoma Bank (University of Iowa, Iowa City), T. Schupbach, T. Hays, Exelixis and the Bloomington Stock Center for antibodies and fly stocks. Special thanks to T. M. Bridges, B. Hu and S. Misra for technical assistance, and to C. Montell for comments on the manuscript. This work was supported by grants from the National Institutes of Health (F32 GM20539) to J.A.M. and (GM46425) to D.J.M.

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