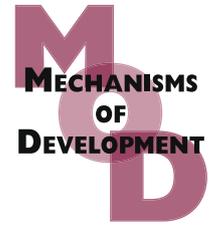


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## Pellino enhances innate immunity in *Drosophila*

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### ABSTRACT

The innate immune response is a defense mechanism against infectious agents in both vertebrates and invertebrates, and is in part mediated by the Toll pathway. Toll receptor activation upon exposure to bacteria causes stimulation of Pelle/IRAK kinase, eventually resulting in translocation of the transcription factor NF- $\kappa$ B to the nucleus. Here we show that Pellino, a highly conserved protein interacting with activated Pelle/IRAK, acts as a positive regulator of innate immunity in *Drosophila*.

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## 1. Introduction

The innate immune response is the first line of defense against infections in both vertebrates and invertebrates. In flies the Toll and IMD pathways mediate innate immunity. Gram-negative bacteria activate the IMD pathway resulting in Relish (a NF- $\kappa$ B homolog) translocation to the nucleus and induction of Diptericin and other antimicrobial peptides. Some Gram-positive bacteria and fungi activate the Toll pathway resulting in Dorsal or DIF (NF- $\kappa$ B homologs) translocation to the nucleus and activation of *Drosomycin* and other genes (Lemaitre and Hoffmann, 2007; Tanji and Ip, 2005). Exposure to bacteria results in proteolytic processing of Spätzle, which is the Toll receptor ligand. Activated Toll recruits three cytoplasmic proteins, dMyD88, Tube and Pelle, the serine/threonine kinase ortholog of IRAK. Recruitment causes phosphorylation and stimulation of Pelle/IRAK kinase. This

results, in an as yet unknown manner, in degradation of the I- $\kappa$ B ortholog Cactus, which allows Dorsal or DIF, to which Cactus is bound in the cytoplasm, to translocate to the nucleus, and activate gene transcription (Lemaitre and Hoffmann, 2007; Tanji and Ip, 2005).

Pellino is a highly conserved component of the Toll pathway, which binds phosphorylated Pelle/IRAK (Grosshans et al., 1999). The vertebrate homologs of the Toll pathway are the Toll-like receptor (TLR) and Interleukin-1 receptor (IL-1R) pathways, where mammalian Pellinos (Pellino-1, -2, and -3) have also been shown to bind phosphorylated IRAK (Lin et al., 2008; Moynagh, 2009). All Pellinos contain a CHC2CHC2 RING E3 ubiquitin ligase domain, and it was recently shown that all three human Pellinos mediate polyubiquitination of IRAK (Schauvliege et al., 2006). In vitro, Pellinos can mediate both lysine 48- and lysine 63-linked polyubiquitination of IRAK (Butler et al., 2007; Ordureau et al., 2008).

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However, in a tissue culture model, Pellinos mainly mediate lysine 63-linked polyubiquitination (Xiao et al., 2008). While lysine 48-linked polyubiquitination results in recognition by proteasomes and degradation, lysine 63 polyubiquitination is used for many purposes, among them protein kinase activation, which plays an important role in NF- $\kappa$ B regulation (Skaug et al., 2009). Functional studies on the role of Pellinos in TLR/IL-1R signaling were conducted in tissue culture cells using RNAi-mediated depletion of Pellino. In such assays Pellino-3b negatively regulates IL-1R signaling, whereas Pellino-2, the closest homolog of *Drosophila* Pellino, positively regulates TLR/IL-1R-dependent NF- $\kappa$ B activation (Xiao et al., 2008; Yu et al., 2002). Pellino-1 can act both positively and negatively on the TLR/IL-1R pathway (Choi et al., 2006; Jiang et al., 2003).

Here we identify a chemically induced mutation in *Drosophila* Pellino and show that *Drosomycin* induction and innate immunity is severely compromised in this mutant.

## 2. Materials and methods

### 2.1. Fly genetics

We used the following stocks: Df(3R)06624, TM3 Sb *twi-Gal4* UAS-2xEGFP, TM3 Sb *hs-hid*, *hs-Gal4*, *tubP-Gal4*, *arm-Gal4* UAS- $\alpha$ cateninGFP, *hs-Flp22*, *FRT82B ovo<sup>D1</sup>*, *FRT82B 7T2*, and TM3 *hb8-lacZ*. We made *Pli<sup>1</sup> hs-Gal4* and *Pli<sup>1</sup> UAS-Pli* recombinants by standard crosses.

We used viable molecularly mapped P elements carrying a mini-white marker that were evenly spaced on chromosome arm 3R for recombination mapping (Zhai et al., 2003). Briefly, we crossed P/7T2 virgin females to 7T2/TM3 Sb, *hs-hid* males. After heat shocking, the only survivors are red-eyed P/7T2 and white-eyed recombinants (+/7T2). Recombination frequency and projected molecular distance can then easily be calculated (Zhai et al., 2003).

To generate germ line clones, *hs-Flp22; FRT82B ovo<sup>D1</sup>* males were crossed to *FRT82B Pli<sup>1</sup>* females and heat-shocked at third instar for 2 h. *FRT82B ovo<sup>D1</sup>/FRT82B Pli<sup>1</sup>* females with germ line clones were then mated to either *Pli<sup>1</sup>/TM3, Sb twi-Gal4 UAS-2xEGFP* for the JNK experiments or to *Pli<sup>1</sup>/TM3, hb8-lacZ* stained with anti- $\beta$  galactosidase antibody for the Twist experiments to distinguish maternal and zygotic *Pli<sup>1</sup>* mutants from paternally rescued mutants.

### 2.2. Molecular biology

*Pellino* cDNAs were isolated from an ovarian cDNA library cloned in  $\lambda$  phages by hybridisation with the *Pellino* plasmid JG-Pli70 isolated in a two-hybrid screen for interactors of Pelle (Grosshans et al., 1999; Stroumbakis et al., 1994). The longest cDNA of 2900 nucleotides with the coding sequence at nucleotide 389–1663 was excised as an EcoRI–NotI fragment and cloned into pUAST. Transgenic flies were produced by injection into *y w* flies.

Genomic DNA preparation and PCR, as well as Western blotting were performed using standard protocols using the TM3, Sb *twi-Gal4 UAS-2xEGFP* balancer to select homozygously mutant embryos.

For RT-PCR, RNA was isolated from embryos using Trizol according to the manufacturer's instructions (Invitrogen). cDNAs were then synthesized using SuperScript II Reverse Transcriptase (Invitrogen). 1155 bp of the 3' end of *Pellino* cDNA was amplified with primers CGGAGTCACCCATT-GACTTT and GCAGCCAGAGACACAACAAA.

### 2.3. Histochemistry and antibodies

Cuticle preparations and antibody stainings were performed as previously described (Jani and Schöck, 2007; Schöck and Perrimon, 2002). The following primary antibodies were used: rabbit anti-Pellino (1:2000 (Grosshans et al., 1999)), goat anti-Pelle (1:500; sc-15769; Santa Cruz Biotechnology), rabbit anti-JNK1 (1:300; sc-571; Santa Cruz Biotechnology), rabbit anti-phospho-JNK (1:5000, Promega), rabbit anti-Twist (1:2500 (Thisse et al., 1988)), rabbit anti- $\beta$  galactosidase (1:2000; Cappel), mouse anti- $\alpha$  tubulin (1:10,000; DM1a; Sigma), and mouse anti-dJUN (1:1000 (Kockel et al., 1997)). As secondary antibody for Western blots we used horseradish peroxidase-linked IgG (1:2500; GE Healthcare), and for immunostainings antibodies of the AlexaFluor series (1:400; Invitrogen).

### 2.4. Infections and mRNA analysis

For septic injury we used *Drosophila* adults. Homozygous *Pli<sup>1</sup>* adults were generated by heat shocking the progeny of *Pli<sup>1</sup> hs-Gal4/TM3* and *Pli<sup>1</sup> UAS-Pli/TM3* at 37 °C for 45 min for 3 d. These adults were aged between 2 and 4 d; one-half was heat-shocked again at 37 °C for 20 min for 4 consecutive days; the other half was aged without heat shocking. Adults were pricked on the lateral side of the thorax with a 0.2 mm diameter tungsten needle dipped into a 10 $\times$  concentrated culture of *Escherichia coli* or *Micrococcus luteus* bacterial LB cultures (Romeo and Lemaitre, 2008). Infected adults were incubated at 25 °C and allowed to recover for 24 and 12 h following *M. luteus* and *E. coli* infection, respectively; then they were used for RNA extraction using Trizol (Invitrogen) according to the manufacturer's instructions. We purified the extracted total RNA with DNase I (Invitrogen). We used SuperScript™ II Reverse Transcriptase (Invitrogen) for cDNA synthesis (Leulier et al., 2003; Romeo and Lemaitre, 2008).

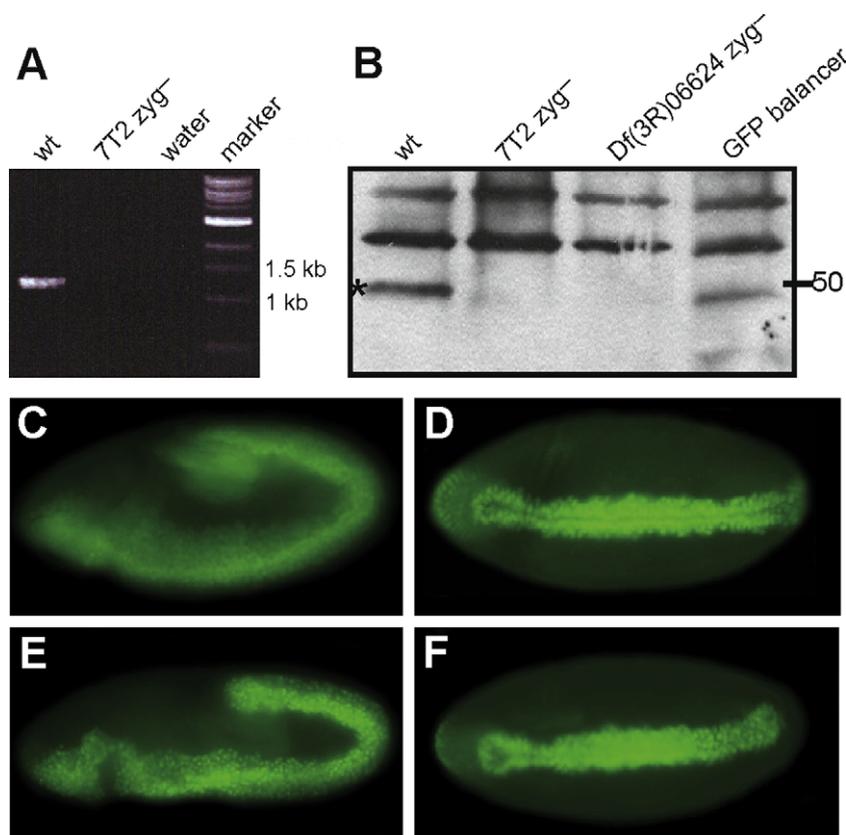
To monitor expression levels by quantitative real-time PCR we used the iCycler iQ system using 1 $\times$  iQ SYBR Green Supermix (Bio-Rad) with the following primers: *Drosomycin*, CGTGAGAACCCTTTCCAATATGATG and TCCCAGGACCAC CAGCAT; *Diptericin*, GCTGCGCAATCGCTTCTACT and TGGTGGAGTGGGCTTCATG. We normalized all values relative to *RpL32* expression levels as reference gene (primers GACGCTTCA AGGGACAGTATCTG and AAACGCGGTTCTGCATGAG) using the Q-Gen software package provided by Bio-Rad, which calculates normalized expression levels according to the formula  $NE = E_{reference} \exp(Ct_{reference}) / E_{target} \exp(Ct_{target})$ , where NE stands for normalized expression level, E for amplification efficiency and Ct for threshold cycle (Simon, 2003). We used the amplification efficiencies previously published for the primers and protocol employed by us (Romeo and Lemaitre, 2008). Afterwards we set wild type induction to 100%.

For survival experiments, embryos were collected from the cross of  $Pli^1$  *hs-Gal4/TM3* with  $Pli^1$  *UAS-Pli/TM3*; the embryos were then sterilized by dechoriation in 50% bleach for 3 min, and grown on regular fly food, or fly food autoclaved for 50 min, and dispensed into sterilized bottles (Tang et al., 2008). Adults were scored for the absence of *Stubble* marking the balancer chromosome. For survival curves, homozygous  $Pli^1$  mutant adults or wild type adults were pricked as described in the previous paragraph. Log-rank analysis was used to establish statistical significance between survival curves.

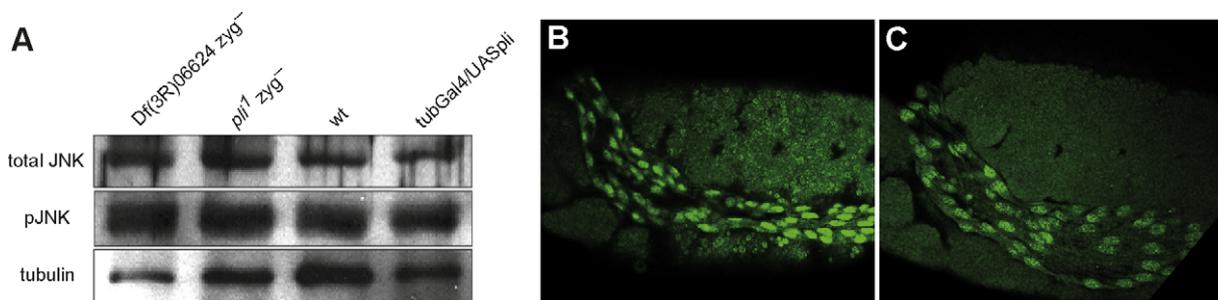
### 3. Results and discussion

We uncovered the mutant *7T2* in a collection of zygotic lethal mutations while screening for mutants with maternal-effect germ band retraction defects (Schöck and Perrimon, 2003). *7T2* zygotic mutants are pupal lethal, whereas *7T2* germ line clones have germ band retraction defects, but also twisted embryos and embryos with head involution defects (Fig. S1 and Table S1). We mapped *7T2* by recombination with molecularly mapped P elements (Zhai et al., 2003). The third round of P element-mediated recombination narrowed the area to a small region between 19675990 and 19756853 basepairs containing eight genes (Table S2). The small dele-

tion *Df(3R)06624* within that region did not complement *7T2*, and *7T2* as well as *7T2/Df(3R)06624* zygotic mutants are pupal lethal. Mapping this deficiency by PCR indicates that it only deletes *Pellino* (*Pli*) in addition to *TF-IIAS* (Grosshans et al., 1999; Zeidler et al., 1996) (Fig. S2). *7T2* germ line clones crossed to *Df(3R)06624* show the same frequency of defects as crossed to *7T2*. In contrast, *7T2* germ line clones crossed to paternally wild type flies show very few defects, indicating that the mutation causing the observed maternal and zygotic phenotypes lies within *Df(3R)06624* (Table S1). As lethal mutations in *TF-IIAS* complement *7T2*, we assayed by RT-PCR for the presence of *Pellino* mRNA and by Western blotting for the presence of *Pellino* protein in *7T2* mutants. Both *Pellino* mRNA and *Pellino* protein are absent in *7T2* and *Df(3R)06624* (Fig. 1A and B). We finally generated *UAS-Pli* transgenic flies to test for rescue of *7T2* by ubiquitous expression of *Pellino* using the *UAS/Gal4* system (Brand and Perrimon, 1993). Expressing *Pellino* with *hs-Gal4* using 1-h heat shocks every day from first-instar onwards rescues *7T2* homozygous mutants to viability (31% homozygous adults with heat-shock [ $n = 548$ ], compared to 3% homozygous adults without heat-shock [ $n = 491$ ]; see also Fig. 4A). We therefore conclude that *7T2* disrupts *Pli* and is a null allele we refer to as  $Pli^1$  from now on.



**Fig. 1 –  $Pli^1$  does not affect *Twist* expression in the ventral furrow. (A)** RT-PCR with primers amplifying exons 4, 5 and 6 of *Pellino* show amplification of 1155 basepair product only in mRNA from wild type, but not from late-stage homozygous *7T2* embryos. **(B)** Western blot with rabbit anti-*Pellino* antibody shows absence of a 47 kDa band corresponding to *Pellino* (marked with an asterisk) in late-stage homozygous *7T2* and *Df(3R)06624* embryos. Unspecific slower migrating bands serve as loading control. **(C and D)** Anti-*Twist* antibody staining of wild type embryos. A lateral view of a germ band-extending embryo, and a slightly earlier ventral view is shown. **(E and F)**  $Pli^1$  germ line clones at the same stage show no difference in width of the *Twist* expression domain.



**Fig. 2 – *Pli*<sup>1</sup> does not affect JNK signaling. (A) Comparison of total and phosphorylated JNK levels shows no difference between wild type and late-stage homozygous *Pli*<sup>1</sup>, *Df(3R)06624* or Pellino-overexpressing embryos. (B) Anti-dJUN antibody staining of wild type embryo at the onset of germ band retraction shows nuclear dJUN localization. (C) Anti-dJUN antibody staining of *Pli*<sup>1</sup> germ line clone at the same stage shows no difference in dJUN localization.**

Pellino was first identified as a biochemical interaction partner of Pelle in the Toll pathway (Grosshans et al., 1999). Pellino is a 424 amino acid protein, which shares 58% identical amino acids with human Pellino-2. As all Pellino proteins described to date interact with Pelle/IRAK, one may expect dorsal-ventral patterning defects. As mentioned previously, *Pli*<sup>1</sup> germ line clones exhibit 19% twisted embryos similar to phenotypes observed in *twi* and *sna* mutants. To determine if Twist expression, a read-out of dorsoventral signaling mediated by the Toll pathway, is reduced, we stained *Pli*<sup>1</sup> germ line clone and wild type embryos with anti-Twist antibody. We could not detect a difference in the width of the Twist expression domain, suggesting that *Pli*<sup>1</sup> either does not affect dorsoventral signaling or the phenotype and penetrance is too weak to be detected (Fig. 1C–F). Better quantitative methods for analyzing the Dorsal gradient or the Twist expression domain, which were recently established, may resolve this issue in the future (Kanodia et al., 2009).

We next wanted to know if *Pli* plays a role in germ band retraction. Vertebrate Pellino-2 and -3 have been implicated in JNK signaling (Schauvliege et al., 2007). Time-lapse analysis of *Pli*<sup>1</sup> mutants marked by *arm-Gal4 UAS- $\alpha$ cateninGFP* showed that *Pli*<sup>1</sup> mutants look very similar to  $\beta$ PS integrin (*mys*<sup>XG43</sup>) null mutant embryos (data not shown) (Schöck and Perrimon, 2003). It was recently shown that JNK signaling upregulates integrin expression at the leading edge during dorsal closure (Homsy et al., 2006). Furthermore, JNK signaling is active in the amnioserosa during germ band retraction, and is restricted to the leading edge later on during dorsal closure (Reed et al., 2001). Finally, strong mutants in the JNK pathway have also germ band retraction defects (Bellotto et al., 2002). We therefore, explored if *Pli*<sup>1</sup> can modulate the JNK pathway by testing for the presence of nuclear dJUN staining in the amnioserosa at the onset of germ band retraction. We first compared phospho-JNK to total JNK levels in late-stage *Pli*<sup>1</sup> mutants and wild type by Western blotting. We also compared nuclear localization of dJUN in the amnioserosa at the onset of germ band retraction in wild type and *Pli*<sup>1</sup> germ line clones (Fig. 2). We could not detect any differences in JNK signaling by these two readouts, suggesting that *Drosophila* Pellino does not modulate JNK signaling.

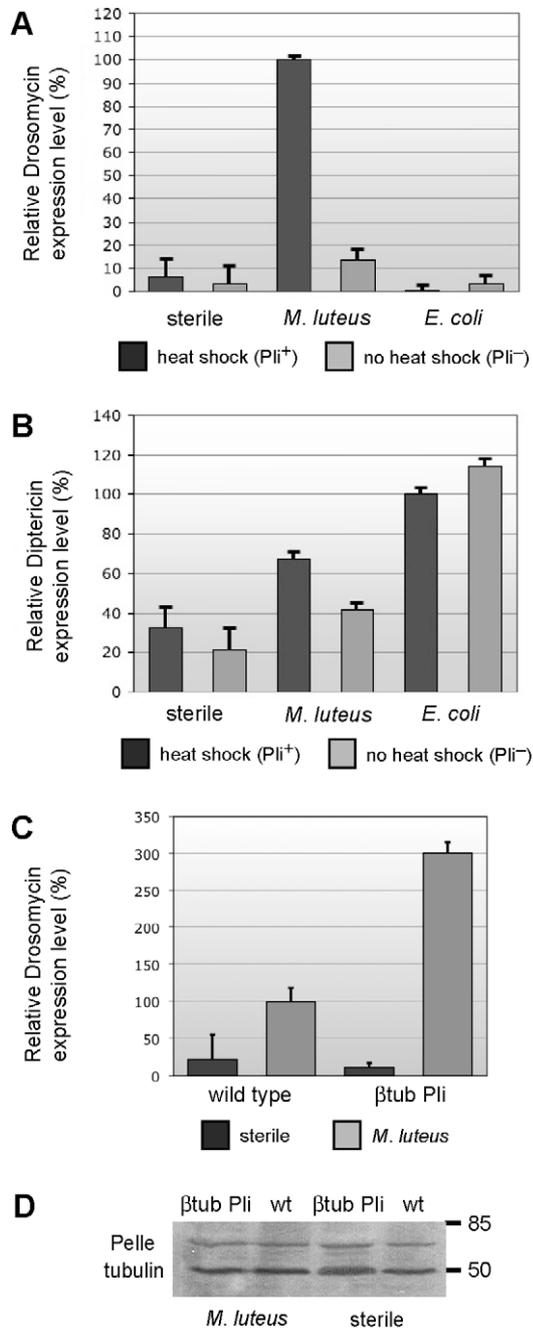
Another important function of the Toll pathway lies in innate immunity. We analyzed the induction of *Drosomycin*, a Toll pathway target gene, and *Diptericin*, an IMD pathway tar-

get gene, 24 h after pricking adults with *M. luteus* or 12 h after pricking adults with *E. coli*, respectively. We employed quantitative real-time RT-PCR (qPCR) to compare induction levels in *Pli*<sup>1</sup> mutant flies rescued to adulthood and continuously expressing Pellino (*Pli*<sup>+</sup>) with *Pli*<sup>1</sup> mutant flies rescued to adulthood without any further Pellino expression (*Pli*<sup>-</sup>). *Drosomycin* expression levels are strongly reduced in *Pli*<sup>-</sup> flies (Fig. 3A), whereas *Diptericin* induction is largely unaffected (Fig. 3B), demonstrating that Pellino is required for *Drosomycin* induction in *Pli*<sup>1</sup> mutant *Drosophila*. We also observe a reduction of *Drosomycin* induction in *Pli*<sup>1</sup> mutant larvae assayed by semiquantitative RT-PCR (Fig. S3). We did not observe a difference in Pelle/IRAK protein levels in *Pli*<sup>1</sup> mutants compared to wild type (Fig. S3). If Pellino functions mostly to modulate Toll signaling by enhancing it, this could explain why we did not observe a phenotype in dorsoventral patterning. Toll pathway signaling in innate immunity is more sensitive to perturbations than in dorsoventral patterning, which can be observed for example in hypomorphic mutations of *dMyd88*, which show a strong phenotype in innate immunity but no phenotype in dorsoventral patterning (Tauszig-Delamasure et al., 2002).

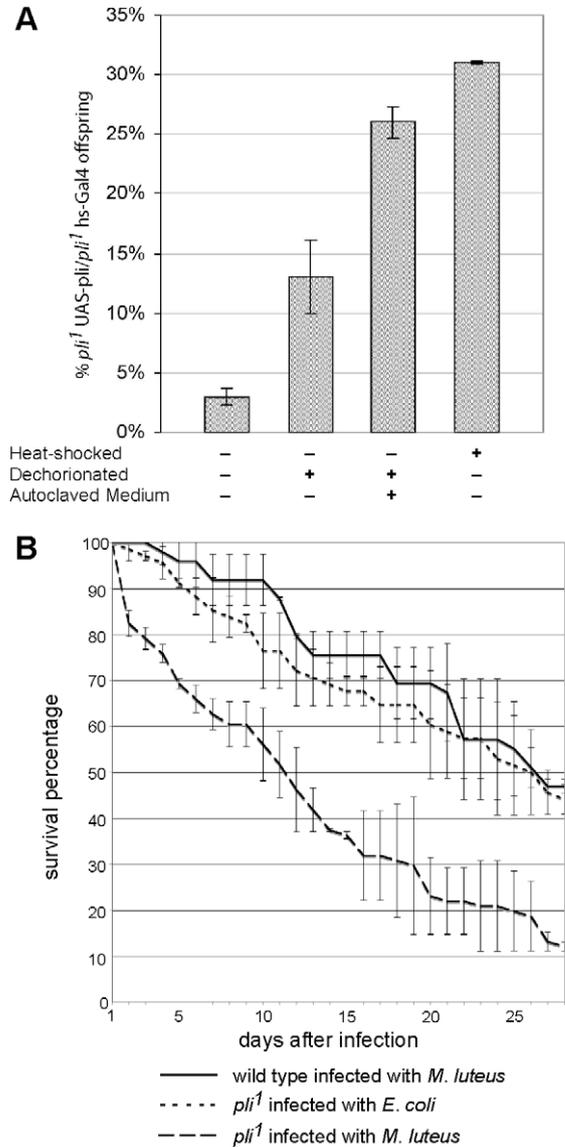
We then asked if overexpression of Pellino causes a stronger induction of *Drosomycin*. We therefore, overexpressed UAS-*Pli* with the strong and ubiquitous  $\beta$ tub-Gal4 driver and analyzed adult flies by qPCR. *M. luteus* infection of flies overexpressing Pellino results in a threefold stronger induction of *Drosomycin* compared to wild type flies. Importantly, Pellino overexpression cannot induce *Drosomycin* expression on its own, it can only enhance expression already induced by *M. luteus* infection (Fig. 3C). These data indicate that Pellino is a limiting factor in Toll signaling, but that it cannot activate the pathway by itself as for example *dMyd88* (Tauszig-Delamasure et al., 2002).

We also tested if Pellino overexpression affects Pelle/IRAK stability upon *M. luteus* infection, but we could not detect any differences in the level of Pelle protein (Fig. 3D). This is consistent with recent data on mammalian Pellino suggesting a role in regulating Pelle/IRAK activity rather than stability (Xiao et al., 2008).

Lastly, we asked if Pellino is required for innate immunity in vivo. We therefore, tested survival of *Pli*<sup>1</sup> UAS-*Pli*/*Pli*<sup>1</sup> *hs-Gal4* flies in a germ-free environment. These flies have some baseline survival presumably owing to leaky expression of



**Fig. 3 – Drosomycin induction is reduced in *Pli*<sup>1</sup>.** (A–C) Quantitative real-time RT-PCR (qPCR) was used to determine expression levels of innate immunity target genes. All values are normalized to *RpL32*. Error bars represent standard error of the mean of two independent experiments each done in triplicate. (A) qPCR of *Drosomycin* expression levels in *Pli*<sup>1</sup> mutant and rescued flies. (B) qPCR of *Diptericin* expression levels in *Pli*<sup>1</sup> mutant and rescued flies. (C) qPCR of *Drosomycin* expression levels in wild type flies and flies overexpressing Pellino. (D) Western blot with anti-Pelle antibody of flies from (C) shows that levels of Pelle/IRAK protein are unchanged. Anti- $\alpha$  tubulin antibody detects tubulin as a loading control. Two molecular weight markers are indicated on the right in kDa.



**Fig. 4 – Innate immunity is severely compromised in *Pli*<sup>1</sup>.** (A) Percent homozygous survivors of *Pli*<sup>1</sup> UAS-*Pli*/*Pli*<sup>1</sup> hs-Gal4/TM3 flies. 33% corresponds to the Mendelian ratio expected for full viability. Dechoronation with bleach removes germs from the egg, medium was sterilized by autoclaving. (B) Survival curves of non-heat-shocked *Pli*<sup>1</sup> UAS-*Pli*/*Pli*<sup>1</sup> hs-Gal4 flies infected with *M. luteus* (total  $n = 91$ ) or *E. coli* (total  $n = 68$ ) or wild type flies infected with *M. luteus* (total  $n = 49$ ). Log-rank analysis was used to compare controls (wild type infected with *M. luteus* and *Pli*<sup>1</sup> infected with *E. coli*) to *Pli*<sup>1</sup> infected with *M. luteus*. Statistical significance between combined control curves and *Pli*<sup>1</sup> infected with *M. luteus* is  $p < 0.0001$ . We also performed log-rank analysis to compare the two controls, and found no statistical significance ( $p = 0.58$ ). Error bars, standard deviation of three experiments.

UAS-*Pli* in the absence of heat-shock. We can increase the survival of “hypomorphic” *Pli*<sup>1</sup> flies (*Pli*<sup>1</sup> null plus potentially leaky transgene) to wild type levels by removing infectious

agents from their environment (Fig. 4A). We finally determined if these *Pli<sup>1</sup>* mutant adults are more susceptible to *M. luteus* infection. Infection of *Pli<sup>1</sup>* mutants with *M. luteus* strongly reduces viability, resulting in 50% lethality approximately 15 days earlier than in wild type flies infected with *M. luteus* or in *Pli<sup>1</sup>* mutant flies infected with *E. coli* (Fig. 4B).

Toll pathway mutants are typically female sterile (Charatsi et al., 2003), therefore, the zygotic lethality of *Pli<sup>1</sup>* is surprising. Pellino may either act in an additional pathway, or *Pli<sup>1</sup>* still carries a second-site mutation that reduces its viability. The baseline survival of *Pli<sup>1</sup>* UAS-*Pli* recombinants points in that direction, as well as the occasional adult escapers we observe in *7T2/Df(3R)06624*. Importantly, this possibility does not affect our conclusions, because we demonstrate germ line clone defects with *7T2/Df(3R)06624* (Table S1), and we observe normal *Drosomycin* induction upon expression of UAS-*Pli* in *Pli<sup>1</sup>* mutants (Fig. 3).

Overall our data indicate that Pellino is required to ensure survival in the presence of certain Gram-positive infectious agents, and that postembryonic Pellino functions predominantly as a positive regulator of innate immunity. In mammals Pellino-1 and -3 play a predominantly negative role in innate immunity, whereas there is evidence for a positive role for Pellino-2 (Moynagh, 2009; Yu et al., 2002). The evolutionarily conserved role of Pellino therefore, may be that of a positive regulator of innate immunity.

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## Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.mod.2010.01.004.

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