A Shared Role for RBF1 and dCAP-D3 in the Regulation of Transcription with Consequences for Innate Immunity

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Abstract

Previously, we discovered a conserved interaction between RB proteins and the Condensin II protein CAP-D3 that is important for ensuring uniform chromatin condensation during mitotic prophase. The Drosophila melanogaster homologs RBF1 and dCAP-D3 co-localize on non-dividing polytene chromatin, suggesting the existence of a shared, non-mitotic role for these two proteins. Here, we show that the absence of RBF1 and dCAP-D3 alters the expression of many of the same genes in larvae and adult flies. Strikingly, most of the genes affected by the loss of RBF1 and dCAP-D3 are not classic cell cycle genes but are developmentally regulated genes with tissue-specific functions and these genes tend to be located in gene clusters. Our data reveal that RBF1 and dCAP-D3 are needed in fat body cells to activate transcription of clusters of antimicrobial peptide (AMP) genes. AMPs are important for innate immunity, and loss of either dCAP-D3 or RBF1 regulation results in a decrease in the ability to clear bacteria. Interestingly, in the adult fat body, RBF1 and dCAP-D3 bind to regions flanking an AMP gene cluster both prior to and following bacterial infection. These results describe a novel, non-mitotic role for the RBF1 and dCAP-D3 proteins in activation of the Drosophila immune system and suggest dCAP-D3 has an important role at specific subsets of RBF1-dependent genes.

Introduction

The RB family proteins (pRB, p130 and p107 in humans; RBF1 and RBF2 in Drosophila) co-ordinate changes in gene expression. Understanding the types of programs that these proteins regulate is important because of the unequivocal link between the inactivation of RB proteins and human cancer. Mutation of the retinoblastoma tumor susceptibility gene (RB1) is the rate-limiting step in the genesis of retinoblastoma and over 90% of human tumors exhibit reduced pRB function [1,2].

RB family members are best-known for their roles in the regulation of E2F-dependent transcription. E2F-controlled genes are needed for cell proliferation and RB proteins suppress the expression of these targets during G0 and G1 of the cell cycle [3]. In addition, RB proteins are also important for the regulation of genes that are not involved in cell cycle progression. For example, osteoblast differentiation is modulated by pRB through its interaction with Runx2 [4]; in muscle cells, pRB promotes the expression of muscle-specific differentiation markers, enabling these cells to irreversibly exit the cell cycle [5–7]; in Drosophila, RBF1 cooperates with the Hippo pathway to maintain photoreceptor differentiation, independent of dE2F1 activity [8]. Such E2F-independent functions may help to explain why the inactivation of RB proteins can have very different consequences in different cellular contexts. However, many of the E2F-independent activities of RB proteins are not well-understood. At present, it is unclear if pRB has different activities in different cell types, or whether there is a yet-to-be discovered, general process that allows RB proteins to activate or repress the expression of variable sets of genes in different cell types.

Recent studies have suggested that pRB family members may impact the organization of higher-order chromatin structures, in addition to their local effects on the promoters of individual genes [9]. Mutation of pRB causes defects in pericentric heterochromatin [10] and RBF1 is necessary for uniform chromatin condensation in proliferating tissues of Drosophila larvae [11]. Part of the explanation for these defects is that RBF1 and pRB promote the localization of the Condensin II complex protein, CAP-D3 to DNA both in Drosophila and human cells [11]. Depletion of pRB from human cells strongly reduces the level of CAP-D3 associated with centromeres during mitosis and causes centromere dysfunction [12].

Condensin complexes are necessary for the stable and uniform condensation of chromatin in early mitosis [13–16]. They are
Author Summary

The retinoblastoma protein (pRb) is a tumor suppressor protein known for its ability to repress transcription of E2F-dependent genes and induce cell cycle arrest. We have previously shown that Rb proteins in Drosophila and human cells interact with the Condensin II subunit, CAP-D3, in an E2F-independent manner. Condensins promote condensation of chromosomes in mitosis. Our previous studies suggested that the Drosophila pRB and CAP-D3 homologs, RBF1 and dCAP-D3, co-localize on DNA and may share a function in cells that never undergo mitosis. In this study, we show that one non-mitotic function shared between RBF1 and dCAP-D3 is the regulation of many non-cell-cycle-related, clustered, and cell-type-specific transcripts including a conserved family of genes that are important for the immune response in the fly. In fact, results show that normal levels of dCAP-D3 and RBF1 expression are necessary for the ability of the fly to clear infection with human bacterial pathogens. This work demonstrates that dCAP-D3 proteins can regulate a unique subset of RBF1-dependent transcripts in vivo and identifies a novel role for both RBF1 and dCAP-D3 protein in activation of innate immune genes, which may be conserved in human cells.

Conserved from bacteria to humans with at least two types of Condensin complexes (Condensin I and II) present in higher eukaryotes. Both Condensin I and II complexes contain heterodimers of SMC4 and SMC2 proteins that form an ATPase which acts to constrain positive supercoils [17, 18]. Each type of Condensin also contains three specific non-SMC proteins that, upon phosphorylation, stabilize the complex and promote ATPase activity [14, 19, 20]. The kleisin CAPH and two HEAT repeat containing subunits, CAP-G and CAP-D2 are components of Condensin I, while the kleisin CAP-H2 and two HEAT repeat containing subunits, CAP-G2 and CAP-D3, are constituents of Condensin II.

Given the well-established functions of Condensins during mitosis, and of RBF1 in G1 regulation, the convergence of these two proteins was unexpected. Nevertheless, mutant alleles in the non-SMC components of Condensin II suppress RBF1-induced phenotypes, and immunostaining experiments revealed that RBF1 displays an extensive co-localization with dCAP-D3 (but not with dCAP-D2) on the polytene chromatin of Drosophila salivary glands [11]. This co-localization occurs in cells that will never divide, suggesting that Condensin II subunits and RBF1 co-operate in an unidentified process in non-mitotic cells. In various model organisms, the mutation of non-SMC Condensin subunits has been associated with changes in gene expression [21–24] raising the possibility that dCAP-D3 may affect some aspect of transcriptional regulation by RBF1. However, the types of RBF1-regulated genes that might be affected by dCAP-D3, the contexts in which this regulation becomes important, and the consequences of losing this regulation are all unknown.

Here we identify sets of genes that are dependent on both rbf1 and dCap-D3. The majority of genes that show altered expression in both rbf1 and dCap-D3 mutants (larvae or adults) are not genes involved in the cell cycle, DNA repair, proliferation, but are genes with cell type-specific functions and many are spaced within 10 kb of one another in “gene clusters”. To better understand this mode of regulation we have investigated the effects of RBF1 and dCAP-D3 on one of the most highly misregulated clusters which includes genes coding for antimicrobial peptides (AMPs). AMPs are produced in many organs, and one of the major sites of production is in the fat body. Following production in the fat body, AMPs are subsequently dumped into the hemolymph where they act to destroy pathogens [25]. RBF1 and dCAP-D3 are required for the transcriptional activation of many AMPs in the adult fly. Analysis of one such gene cluster shows that RBF1 and dCAP-D3 bind directly to this region and that they bind, in the fat body, to sites flanking the locus. RBF1 and dCAP-D3 are both necessary in the fat body for maximal and sustained induction of AMPs following bacterial infection, and RBF1 and dCAP-D3 deficient flies have an impaired ability to respond efficiently to bacterial infection. These results identify dCAP-D3 as an important transcriptional regulator in the fly. Together, the findings suggest that RBF1 and dCAP-D3 regulate the expression of clusters of genes in post-mitotic cells, and this regulation has important consequences for the health of the organism.

Results

RBF1 and dCAP-D3 regulate many of the same genes during the later stages of the D. melanogaster life cycle

Our previous data demonstrated that RBF1 co-localizes extensively with dCAP-D3 on polytene chromatin of non-dividing cells, leading us to hypothesize that the two proteins may cooperate to regulate transcription. To begin to test this idea, we first identified the stages of fly development where RBF1 and dCAP-D3 were most highly expressed. qRT-PCR using primers for dCap-D3 and rbf1 was performed on cDNA generated from various stages of the Drosophila life cycle (Figure 1A). The results demonstrate that both genes are transcribed at the highest levels in late third instar larval and adult stages. Concordantly, immunostaining for dCAP-D3 and RBF1 in cryosections of the abdomens of wild type flies confirmed that both proteins are highly expressed in the adult and that they are both present in the nuclei of many cells in normal adult tissues (Figure 1B).

Preliminary experiments showed that dCAP-D3 levels could influence the expression of very few of the previously identified RBF1-dependent transcripts. To gain a more complete understanding of the abundance and characteristics of RBF1/dCAP-D3 shared transcriptional targets, we carried out a microarray analysis of the entire Drosophila melanogaster genome and compared gene expression profiles of wild type, dCap-D3 and rbf1 mutant flies, at both the third instar larval and adult stages (Table S1). Since the null mutants are lethal, females expressing a transheterozygous combination of null and hypomorphic alleles were used for these experiments. The mutant flies used for microarray analysis expressed about 15% of wild type levels of each gene as judged by qRT-PCR and western blot (Figure S1). The microarray results revealed an extensive and highly significant overlap between RBF1 and dCAP-D3 regulated gene sets in both adults and larvae (Figure 2A and 2B). Shared target genes were evident in both upregulated and downregulated gene sets. Although some genes were mis-expressed in both larvae and adults, the majority of transcriptional changes were stage specific. The most highly significant p values for shared target gene sets were seen in upregulated larval genes (genes repressed by RBF1 and dCAP-D3 in the larvae, p≤6.3E-130) and downregulated adult genes (genes activated by RBF1 and dCAP-D3 in the adult, p≤9.8E-95) (Figure 2B). This suggests that RBF1 and dCAP-D3 may cooperate to repress specific programs during one stage of development and activate other programs in a later, more differentiated stage. Interestingly, at both stages, the genes dependent on both RBF1 and dCAP-D3 represented 15–17% of the total number of genes dependent on RBF1 in a given
developmental stage and 47–55% of the total number of genes dependent on dCAP-D3 in a given developmental stage. Thus RBF1 appears to be important at close to half of the transcriptional targets of dCAP-D3.

Characteristics of RBF1/dCAP-D3 shared target genes

We noticed that the lists of RBF1/dCAP-D3 shared target genes had two general properties. First, these genes are almost completely different from the lists of E2F-regulated genes that have been reported previously [26]. As expected, many of the targets that were upregulated in rbf1 mutant larvae could be categorized as E2F target genes involved in DNA repair, DNA replication and continuation of the cell cycle (comparison to microarray data from [26] and GO analyses of rbf1 mutant larvae-data not shown). However, few if any, of these cell cycle/proliferation related genes were altered in the dCap-D3 mutant flies (Figure 2C) suggesting that dCAP-D3 regulates a different subset of RBF1 dependent targets. In fact, less than 6% of dCAP-D3/RBF1 shared target genes in larvae were found to be bound by dE2F1 in dE2F1 ChIP-chip experiments (Korenjak et. al., unpublished data). Unexpectedly, many of the known E2F target genes did not show a significant increase in expression in rbf1 mutant adults (ie. genes that are apparently repressed both by RBF1 and dCAP-D3 are 25 times more likely to be clustered. Genes that were downregulated in rbf1 and dCap-D3 mutant adults (i.e. genes apparently activated by both RBF1 and dCAP-D3) are 15 times more likely to be clustered. Clustering of shared target genes was also seen in the larvae, although the fold difference was greatly diminished (5 fold) for the activated genes. Overall, the clustering effect was 3–7 fold more prevalent in dCAP-D3 regulated genes than in RBF-regulated genes. By way of comparison, RBF1/dCAP-D3 shared target genes in the larvae exhibited a much greater degree of clustering than the larval genes regulated by Hop or Nurf301, two other well-known chromatin remodeling proteins shown to regulate clusters of genes [27]. A list of the actual groupings of clustered genes is presented in Table S2.

Although proliferation-related genes were missing, gene ontology (GO) classification of the RBF1/dCAP-D3 shared target genes
revealed many significant categories in the lists of up- and downregulated genes in the adult, and for shared, repressed target genes in the larvae (Figure 2D, complete list for downregulated adult genes in Table S3). One of the most interesting GO categories represented in the adults were the defense response genes (GO:0050830). The fly relies on an innate immune system to defend against invading pathogens. This immune system is comprised of three major mechanisms: 1) phagocytosis, 2) induction of coagulation and melanization, and 3) production of Antimicrobial Peptides or AMPs.

Phagocytosis is a conserved mechanism that is often the primary cellular defense used by many organisms to engulf and destroy pathogens. In *Drosophila*, circulating blood cells called hemocytes phagocytose bacteria, fungi, and parasitic wasp eggs [28]. RBF1 and dCAP-D3 mutant adult microarray data was analyzed for changes in levels of 19 different genes reported to be involved in phagocytosis in *Drosophila* (Table S4). Of these 19 genes, 2 genes demonstrated significant changes in transcript levels in adults. *NimC1*, a gene expressed in plasmatocytes which make up 95% of *Drosophila* hemocytes, has been shown to be necessary for phagocytosis of bacteria [29], and was significantly upregulated in RBF1 and dCAP-D3 mutant adults. Embryonic and larval hematopoiesis depends on a number of transcription factors including Gcm [30,31]. *Gcm* transcripts were demonstrated to be downregulated in both RBF1 and dCAP-D3 adults (Table S4). While adult hemocytes do display phagocytic properties, they do not differentiate into specialized cells upon immune challenge [32,33], and it is therefore unlikely that misregulation of *gcm* in adults would affect phagocyte numbers.

In response to septic injury, proteolytic cascades are triggered which lead to coagulation and melanization. Reactive oxygen species formed during these processes, as well as the actual deposition of melanin, are thought to be toxic to microorganisms [34]. After scanning the literature for genes involved in coagulation and melanization, and then analyzing RBF1 and...
dCAP-D3 mutant adult microarray data for changes in transcript levels of these genes, it was determined that only one of the reported genes, CG8193, was significantly increased in both RBF1 and dCAP-D3 mutant adults (Table S5). CG8193/PPO2 is thought to encode a phenol-oxidase constitutively expressed in crystal cells, a type of hemocyte cell involved in melanization [35].

**Table 1.** RBF1 and dCAP-D3 tend to regulate clusters of genes.

<table>
<thead>
<tr>
<th>Gene Set</th>
<th>Ratio for upregulated⁎</th>
<th>Ratio for downregulated⁎</th>
</tr>
</thead>
<tbody>
<tr>
<td>Whole adult dCAP-D3 mut</td>
<td>12.42</td>
<td>11.68</td>
</tr>
<tr>
<td>Whole adult RBF1 mut</td>
<td>3.93</td>
<td>4.41</td>
</tr>
<tr>
<td>Whole adult shared targets</td>
<td>25.00</td>
<td>15.87</td>
</tr>
<tr>
<td>Whole larvae dCAP-D3 mut</td>
<td>14.2</td>
<td>15.9</td>
</tr>
<tr>
<td>Whole larvae RBF1 mut</td>
<td>2.60</td>
<td>2.03</td>
</tr>
<tr>
<td>Whole larvae shared targets</td>
<td>22.58</td>
<td>3.68</td>
</tr>
<tr>
<td>Whole larvae Hop mut**</td>
<td>1.91</td>
<td>1.30</td>
</tr>
<tr>
<td>Whole larvae Nurf301 mut**</td>
<td>1.55</td>
<td>1.30</td>
</tr>
</tbody>
</table>

*The ratio of observed clustering to expected clustering for the lists of differentially expressed genes between mutant and wild-type organisms (fdr < 0.15, log2 fc > 0.1) shows that RBF1 and dCAP-D3 shared target genes are 6–10 fold more likely to be present in clusters. Chromosomal clustering is calculated as the number of pairs of genes within 10,000 bp among the differentially expressed genes. The expected number is the average clustering of 500 random gene lists of the same length as the corresponding list of differentially expressed genes.

**Raw data for Hop and Nurf301 mutant larvae was obtained from supplemental data files found in [27].

False Discovery Rates for all ratios presented were <0.05.

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Figure 3. RBF1 and dCAP-D3 activate basal transcript levels of genes coding for Antimicrobial Peptides (AMPs). A) Graphic depictions of three separate AMP loci. The Attacin and Diptericin loci are located on Chromosome 2R at 51C1 and 55F8, respectively. The Cecropin locus is located on Chromosome 3R at 99E1. Genes within each locus are drawn in correct orientation to one another but are not drawn to scale. Genes colored in green are downregulated in dCAP-D3 mutant adult carcasses dissected of ovaries and most are also downregulated RBF1 mutants. Genes colored in blue remain unchanged in dCAP-D3 and RBF1 mutants. B) qRT-PCR analyses of transcript levels for 21 AMPs in female adult bodies (N = 10) with ovaries dissected shows that dCAP-D3 and RBF1 each regulate a much larger number of AMPs than originally indicated by the microarray results. Genes significantly upregulated in the mutants are highlighted in red and genes significantly downregulated in the mutants are highlighted in green. Transcript levels were normalized to tubulin 84B. All results had false discovery rates ≤ 0.05. C) qRT-PCR analysis of cDNA from wild type (WT/w1118/rbf1 mutant #1 (rbf1120a/rbf1120a)), dCAP-D3 mutant #1 (dCap-D3c07081/dCap-D3c07081) and dCAP-D3 mutant #2 (dCap-D3c07081/dCap-D3c07081) female adult whole flies confirms that two AMP target genes are regulated by both RBF1 and dCAP-D3, regardless of mutant genotype. Transcript levels were normalized to tubulin 84B mRNA levels.

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However, overexpression of CG8193/PP02 in cell lines or in flies does not induce constitutive melanization [36], nor did we see any evidence of melanotic lesions in RBF1 or dCAP-D3 mutant adults.

Several of the genes in the adult, downregulated GO category of “defense response to Gram positive bacteria” (Figure 2D and Table S3) fall into a family of proteins known as Antimicrobial Peptides or AMPs. In fact, two of these genes, *AtIA* and *AtIB*, represented some of the most highly deregulated targets in the mutant adults. Upon closer inspection of the microarray data, it was revealed that many other AMP genes were also deregulated in dCAP-D3 and/or RBF1 mutant adults, however their p-values were just below the confidence level. In addition, many of the AMP genes are present in clusters and located immediately next to one another in the genome (Figure 3A), making them an enticing group of genes for further study.

**AMPs are shared targets of RBF1 and dCAP-D3 in the adult fat body**

To confirm that the transcription of AMPs was indeed dependent on both RBF1 and dCAP-D3, qRT-PCR analysis was performed using cDNA generated from dCap-D3 or *rbf1* transheterozygotes (using whole female mutant flies whose ovaries had been dissected) (Figure 3B). Results showed that 17 of the 21 AMPs tested were downregulated in the *Cap-D3* mutants and 10 of those genes were similarly dependent on RBF1. qRT-PCR for AMPs performed on different allelic combinations of *rbf1* and *Cap-D3* mutants gave similar results (Figure 3C).

AMPs constitute one of the major defense mechanisms against bacterial and/or fungal infection in the fly [25,37,38]. They are produced in various adult tissues but one of the main organs responsible for their production is the fat body. Once produced in the fat body, AMPs are secreted into the hemolymph where they destroy or inhibit growth of pathogens [39].

We set out to test the hypothesis that RBF1 and dCAP-D3 regulate AMP genes in the adult fat body. First, we examined whether RBF1 and dCAP-D3 are expressed in this cell type. The *yolk-GAL4* driver was used to express GFP in adult fat body cells, effectively marking this cell type in green. Combined immunostaining for RBF1 and dCAP-D3 localization in crossections of adult wild type abdomens revealed a strong staining for both RBF1 and dCAP-D3 in the nuclei of adult fat body cells (Figure 4A, yellow arrows). *yolk-GAL4* has been characterized to drive expression in *Drosophila* at approximately 2–5 days post eclosion [40], making it possible to drive expression of transgenes after the majority of fly development has occurred. The staining for RBF1 and dCAP-D3 in the adult abdomens was specific, as *yolk-GAL4* driven expression of dsRNAs directed against RBF1 and dCAP-D3 specifically abrogated staining of their respective targets in fat body cells, without dramatically altering gross tissue morphology (Figure S3).

Next, we measured the changes in expression of AMPs in animals where *yolk-GAL4* driven expression of dsRNAs had reduced the expression of either RBF1 or dCAP-D3 in the fat body, qRT-PCR of cDNA from whole adult females showed a significant decrease in the expression of multiple AMP genes including *dipetecin, dipetecin B* and *Cecropin A2* (Figure 4B) in the knockdown flies. Interestingly, the fold change in transcript levels for *dipetecin* was comparable to the changes seen in dCap-D3 and *rbf1* mutant animals. These results suggest that the *yolk-GAL4*-expressing cells are a primary site of constitutive *dipetecin* expression in adult flies and that in these cells, RBF1 and dCAP-D3 are both needed to drive the basal expression levels of specific AMPs.

**Regulation of an AMP cluster by RBF1 and dCAP-D3 is direct and dynamically changes over the course of bacterial infection**

AMP genes can be regulated by multiple transcription factors [41–44]. We sought to determine, therefore, whether transcriptional regulation of these genes by RBF1 and dCAP-D3 was direct. For our ChIP analysis we focused on *dipetecin* and *dipetecin B*; two AMP genes that are situated within 1200 bp of one another (Figure 5B), that have well characterized promoters [45–47], and whose basal expression was dependent on both RBF1 and dCAP-D3 in the fat body (Figure 3B and Figure 4B). In addition, the basal transcript levels of at least one other gene in the region, *CG43070*, was found to be significantly activated by both RBF1 and dCAP-D3 (Figure S4).

To study the binding of RBF1 and dCAP-D3 at the *dipetecin* locus in vivo, transgenic fly lines were created which expressed N-terminally FLAG-HA tagged dCAP-D3 or N-terminally FLAG-HA tagged RBF1 under the control of the UAS promoter. These lines were then crossed to *yolk-GAL4/FM7* lines to create progeny in which the tagged protein was specifically expressed in the adult fat body. ChIP using FLAG antibody in FLAG-HA-dCAP-D3 expressing flies demonstrated that dCAP-D3 binds to two separate regions located approximately 3 kb upstream and 900 bp downstream of the *dipetecin* locus (Figure 5A and red bars in Figure 5B). Since *dipetecin* is strongly induced in response to bacterial infection, we examined the effect of infection with *S. aureus* on the binding of dCAP-D3 to the *dipetecin* locus. Strikingly, dCAP-D3 binding to the upstream site significantly increased after *S. aureus* infection (compare red bars to yellow bars, Figure 5B).

ChIP for FLAG in FLAG-HA-RBF1 expressing flies indicated that RBF1 binds to the identical upstream and downstream regions of the *dipetecin* locus as dCAP-D3 (red bars in Figure 5C). This binding was detected both before and after infection with *S. aureus* (blue and yellow bars in Figure 5C), but unlike the results for dCAP-D3 binding, RBF1 binding was most significant prior to infection. ChIP results show that 1) RBF1 and dCAP-D3 can bind directly to an AMP gene cluster at identical binding sites, 2) that the binding sites flank the *dipetecin* and *dipetecin B* genes, and 3) dCAP-D3 binding increases when gene expression is induced in response to bacterial infection.

For comparison, we also performed ChIP for dCAP-D3 on the *CG3250* locus. *CG3250* was the one previously identified direct target of RBF1 [26] that we found to be repressed by RBF1 and dCAP-D3 and to be consistently upregulated in all tissues of *rbf1* and *dCAP-D3* mutant animals (Figures S2 and S5A). ChIP using FLAG antibody in FLAG-HA-dCAP-D3 expressing flies demonstrated a small amount of binding in the open reading frame of *CG3250* (Figure S5B and S5C). This binding pattern obtained with the FLAG antibody closely resembled the ChIP signal found when a dCAP-D3 antibody was used to immunoprecipitate the endogenous dCAP-D3 protein expressed everywhere in the adult fly (Figure S5D).

The ability of RBF1 and dCAP-D3 to regulate basal levels of AMP transcription prompted the question of whether these proteins were also necessary for the regulation of AMP transcription in response to bacterial infection. cDNA was generated from female adult flies expressing dCAP-D3 or RBF1 dsRNAs specifically in the fat body, at various time-points post-infection with *Staphylococcus aureus* (Figure 6). dsRNAs have been used successfully in the past to decrease in vivo expression levels of
proteins involved in innate immunity and to study their effects on responses to bacterial infection [48].

qRT-PCR for AMPs indicated two types of transcriptional defects in the RBF1 and dCAP-D3 deficient flies. In agreement with our earlier results, basal transcript levels of diptericin were reduced as a result of deficiency for either protein (Figure 6B, inset boxes). Following infection, diptericin transcripts remained very low in the dCAP-D3 deficient tissue and induction was minimal and severely delayed in comparison to GFP dsRNA expressing "wild type'' control flies. RBF1 deficiency, however, allowed normal induction of diptericin transcripts. Drosomycin is an AMP gene downstream of the Toll pathway, and it is strongly induced following infection with Gram positive bacteria or fungi [49]. qRT-PCR for levels of Drosomycin revealed a much different defect in expression. Neither dCAP-D3 nor RBF1 deficiency in the fat body had any effect on basal levels of Drosomycin, a result consistent with our microarray data from whole flies. However, both dCAP-D3 and RBF1 deficiency caused significant decreases in the maximal expression levels of drosomycin at 24 hours post-infection (Figure 6A).

The biological response to bacterial infection in the fly requires dCAP-D3 and RBF1

Next, we tested whether the inefficient transcription of AMPs that results from decreased expression of RBF1 or dCAP-D3 has a significant effect on the ability of the fly to recover from exposure to pathogenic bacteria. Survival rates after infection with the Gram positive bacterium, Staphylococcus aureus (Figure 7A, Figure 8A) or with the Gram negative bacterium, Pseudomonas aeruginosa (Figure 7B, Figure 8B) were measured in five different genotypes: females expressing GFP dsRNAs under the control of the yolk-GAL4 driver ("wild-type controls", yolk-GAL4 driving expression of dCAP-D3 dsRNA in the fat body, yolk-GAL4 driving expression of RBF1 dsRNA in the fat body, and positive control females which were either mutant for the Eater protein or expressing dsRNAs against the IMD protein. IMD is a major mediator of innate immune signaling in Drosophila [50]. Eater is a known phagocyctic receptor necessary for the response to infection with Gram positive bacteria [51]. We did not include data on flies expressing Eater dsRNAs under the control of yolk-GAL4, since Kocks et al [51] reported that Eater is not expressed in the fat body. In agreement with this, expression of Eater dsRNA in the fat body exhibited no changes in the ability of the fly to clear bacteria, while the Eater mutants described above showed a striking inability to phagocytize bacteria 5 hours following infection (data not shown and Figure 7). Following infection with S. aureus, both dCAP-D3 and RBF1 deficient flies were more susceptible to infection in comparison to flies expressing GFP dsRNAs (Figure 7A and Figure 8A). dCAP-D3 deficient flies were also more susceptible to infection with Gram negative bacteria, but this was not the case for RBF1 deficient flies, as their survival rates were not significantly decreased (Figure 7B and Figure 8B). These data demonstrate that acute knockdown of dCAP-D3 or RBF1 in the fat body of adult flies renders them more susceptible to bacterial infection, most likely due to inefficient transcription of AMP genes.

Recently, a number of reports have identified genes whose mutation can reduce the ability of the fly to survive bacterial...
infection, without influencing the ability of the fly to clear bacteria [52–54]. These genes have been described as having affects not on the resistance mechanisms which exist in the fly, but on the tolerance mechanisms of the fly. Tolerance mechanisms limit the damage caused to the host by the infection, but do not actually limit the pathogen burden [55]. To determine whether loss of dCAP-D3 and/or RBF1 expression in the fat body did indeed result in diminished capacity of the fly to clear bacteria, we performed bacterial clearance assays and measured the number of bacteria present in the fly from 0–20 hours post-infection (Figure 9). Results showed that flies deficient for RBF1 or dCAP-D3 behave more like positive control flies deficient for IMD or Eater proteins, and exhibit significant increases in bacterial numbers at 15 hours post-infection with *S. aureus*. This suggests that RBF1 and dCAP-D3 most likely affect the resistance mechanisms (i.e. AMP transcription), and not the tolerance mechanisms of the fly.

A second RBF family member, RBF2, regulates basal AMP transcription levels, but not induced levels, following infection

Since the observed defects in survival rates and AMP induction were not as severe for RBF1 deficient flies in comparison to dCAP-D3 deficient flies, we wondered whether the other *Drosophila* RBF member, RBF2, might compensate for loss of RBF1 activity. RBF2 has been shown to be upregulated upon depletion of RBF1, and co-regulates many genes with RBF1 as a part of the dREAM complex [26,56,57]. To address this question, we tested survival

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**Figure 5. RBF1 and dCAP-D3 bind to an AMP locus in vivo.** A) Graphic representation of the locus on which Chromatin Immunoprecipitation (ChIP) for RBF1 and dCAP-D3 in the adult fat body was performed. Genes highlighted in green are activated by both RBF1 and dCAP-D3 in the fat body. Positions of primer sets used are listed under the diagram of the locus. B) Chromatin immunoprecipitation for FLAG protein in female adult flies expressing FLAG-HA-dCAP-D3 in the fat body (*yolk-GAL4/+; UAS-FLAG-HA-dCap-D3/+*) demonstrates that the *diptericin* locus is a direct target of dCAP-D3. ChIP signal corresponding to FLAG-HA-dCAP-D3 binding in the absence of *Staphylococcus aureus* infection is colored in burgundy. ChIP signal corresponding to FLAG-HA-dCAP-D3 binding two and four hours after *S. aureus* infection is colored in blue and yellow, respectively. C) Chromatin immunoprecipitation for FLAG protein in female adult flies expressing FLAG-HA-RBF1 in the fat body (*yolk-GAL4/+; UAS-FLAG-HA-rbf1/+*) demonstrates that the locus is also a direct target of RBF1. Depiction of signal is as described in B. D) Chromatin immunoprecipitation for FLAG protein in female adult flies expressing FLAG-HA in the fat body (*yolk-GAL4/+; UAS-FLAG-HA/+*) demonstrates minimal non-specific binding of tag alone at the locus. Depiction of signal is as described in B. doi:10.1371/journal.pgen.1002618.g005
times and AMP induction in flies deficient for RBF2 in the fat body (yolk-GAL4, UAS-RBF2-dsRNA) or a combination of both RBF1 and RBF2 in the fat body (yolk-GAL4, UAS-RBF1 dsRNA, UAS-RBF2 dsRNA). The specific deficiencies in these flies were confirmed by qRT-PCR (Figure S6). qRT-PCR revealed that similar to the loss of RBF1 or dCAP-D3, loss of RBF2 or RBF1/RBF2 resulted in decreased basal transcript levels of diptericin but not drosomycin (Figure S7A and S7B, inset boxes). However, following infection with S. aureus, loss of RBF2 or RBF1/RBF2 did not cause decreased induction of either AMP transcript. In some cases, loss of both RBF1 and RBF2 actually resulted in an increase in diptericin transcription levels at 8 hours post infection. In response to infection with Gram positive bacteria (Figure S6A) or Gram negative bacteria (Figure S6B), RBF2 deficient or RBF1/RBF2 deficient flies did not exhibit any changes in survival rates that were significantly different from wild type control flies. These results demonstrate that RBF2 does regulate basal AMP transcript levels, but does not compensate for RBF1 in induction of AMP transcription in Drosophila following infection.

The shared regulation of innate immune gene clusters by RBF1 and dCAP-D3 may be conserved in human cells

AMPs are conserved in many metazoans and play a very important role in fighting pathogens in barrier epithelial cells at mucosal surfaces [58]. pRB and CAP-D3 have been previously shown to interact physically and functionally in human cells [11]. Remarkably, and perhaps unexpectedly, the regulation of AMP genes by RB and CAP-D3 proteins may also be conserved in human cells. To determine whether pRB and CAP-D3 could regulate genes in human cells and, more specifically, whether the co-regulation of AMPs was conserved, siRNAs were used to decrease pRB and CAP-D3 expression in human Retinal Pigment Epithelial (RPE-1) cells and in premonocytic U937 cells. (Figure S9A and data not shown). qRT-PCR analyses of the levels of five different AMPs revealed that two AMPs (DEFB-3 and DEFA-1) were expressed in RPE-1 cells and both genes were significantly downregulated following the depletion of either pRB or CAP-D3 (Figure S9B). Interestingly, these genes are also located in a very large gene cluster, the Defensin locus, encompassing over 20 different AMPs. These data raise the possibility that the regulation of AMPs by CAP-D3 and pRB, and the ability of these proteins to regulate gene clusters, are properties that may be conserved in human cells.

Discussion

In Drosophila, RB-family proteins are best known as transcriptional repressors of cell cycle and proliferation genes. Here we describe a different aspect of RB function and show that, together with the Condensin II protein dCAP-D3, RBF1 functions to regulate the expression of a large number of genes during Drosophila development. A surprising characteristic of RBF1/
dCAP-D3 regulated genes is that they do not seem to be the classically repressed genes with functions in cell cycle progression, DNA damage and DNA replication. Instead, many RBF1/dCAP-D3-dependent genes are classified as being involved in cell-type specific functions and include genes that are involved in enzymatic cascades, organ development and cell fate commitment.

The idea that dCAP-D3 and RBF1 could cooperate to promote tissue development and differentiation is supported by the fact that both proteins are most highly expressed in the late stages of the fly life cycle, and accumulate at high levels in the nuclei of specific cell types in adult tissues. As an illustration of the cell-type specific nature of RBF1/dCAP-D3-regulation we show that dCAP-D3 and RBF1 are both required for the constitutive expression of a large set of AMP genes in fat body cells. The loss of this regulation compromises pathogen-induction of gene expression and has functional consequences for innate immunity. Interestingly, different sets of RBF1/dCAP-D3-dependent genes were evident in the gene expression profiles of mutant larvae and adults. Given this, and the fact that the gene ontology classification revealed multiple groups of genes, we suggest that the targets of RBF1/dCAP-D3-regulation do not represent a single transcriptional program, but diverse sets of cell-type specific programs that need to be activated (or repressed) in specific developmental contexts.

The changes in gene expression seen in the mutant flies suggest that RBF1 has a significant impact on the expression of nearly half of the dCAP-D3-dependent genes. This fraction is consistent with our previous data showing partial overlap between RBF1 and dCAP-D3 banding patterns on polytene chromatin, and the finding that chromatin-association by dCAP-D3 is reduced, but not eliminated, in rbf1 mutant animals and RBF1-depleted cells.

Although we have previously shown that RBF1 and dCAP-D3 physically associate with one another [11], and our current studies illustrate the fact that they each bind to similar sites at a direct target, the molecular events that mediate the co-operation between RBF1 and dCAP-D3 remain unknown.

These results represent the first published ChiP data for the CAP-D3 protein in any organism. Although we have only examined a small number of targets it is interesting to note that the dCAP-D3 binding patterns are different for activated and repressed genes (compare Figure 5 and Figure S5). More specifically, dCAP-D3 binds to an area within the open reading frame of a gene which it represses (Figure S5C and S5D). However, dCAP-D3 binds to regions which flank a cluster of genes that it activates (Figure 5). Whether or not this difference in binding is true for all dCAP-D3 regulated genes will require a more global analysis.

Figure 7. dCAP-D3 is necessary for a proper immune response to bacterial infection. Adult female flies expressing dCAP-D3 (red) dsRNAs under the control of yolk-GAL4 were infected with the Gram positive bacterium, Staphylococcus aureus (A) or the Gram negative bacterium, Pseudomonas aeruginosa (B). Flies expressing GFP dsRNAs under the control of yolk-GAL4 (green) were used as “wild-type” controls. Eater mutants which are defective in phagocytosis (blue) or flies expressing IMD dsRNAs which are compromised in a major innate immune signaling pathway (yellow) were used as positive controls. Results demonstrate that flies expressing reduced levels of dCAP-D3 in the fat body cells are more susceptible to either type of infection than wild type controls. Three independent experiments are depicted with results of each experiment shown as the average of three sets of 10 infected adults per genotype. These experiments were also performed using a sterile needle dipped in PBS to rule out death as a result of wounding and survival curves matched those of yolk-GAL4 expressing flies (data not shown). Results are presented as cox regression models with statistical significance (p<0.05) represented as shaded areas above and below the curves.

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Human Condensin non-SMC subunits are capable of forming subcomplexes in vitro that are separate from the SMC protein-containing holocomplex [59], but currently, the extent to which dCAP-D3 relies on the other members of the Condensin II complex remains unclear. We note that fat body cells contain polytene chromatin. Condensin II subunits have been shown to play a role in the organization of polytene chromatin in Drosophila nurse cells [60]. Given that RB proteins physically interact with other members of the Condensin II complex [11], it is possible that RBF1 and the entire Condensin II complex, including dCAP-D3, may be especially important for the regulation of transcription on this type of chromatin template.

A potentially significant insight is that the genes that are deregulated in both rbf1 and dCap-D3 mutants tend to be present in clusters located within 10 kb of one another. This clustering effect seems to be a more general feature of regulation by dCAP-D3, which is enhanced by RBF1, since clustering was far more prevalent in the list of dCAP-D3 target genes than in the list of RBF1 target genes.

We chose to focus our studies on one of the most functionally related families of clustered target genes that were co-dependent on RBF1/dCAP-D3 for activation in the adult fly: the AMP family of genes. AMP loci represent 20% of the gene clusters regulated by RBF1 and dCAP-D3 in adults. ChIP analysis of one such region, a cluster of AMP genes at the diptericin locus, showed this locus to be directly regulated by RBF1 and dCAP-D3 in the fat body and revealed a pattern of RBF1 and dCAP-D3-binding that was very different from the binding sites typically mapped at E2F targets. Unlike the promoter-proximal binding sites typically mapped at E2F-regulated promoters, RBF1 and dCAP-D3 bound to two distant regions, one upstream of the promoter and one downstream of the diptericin B translation termination codon, a pattern that is suggestive of an insulator function. We hypothesize that RBF1 and dCAP-D3 act to keep the region surrounding AMP loci insulated from chromatin modifiers and accessible to transcription factors needed for basal levels of transcription.

Figure 8. RBF1 is necessary for a proper immune response to Gram positive bacterial infection. Adult female flies expressing RBF1 (purple) dsRNAs under the control of yolk-GAL4 were infected with the Gram positive bacterium, Staphylococcus aureus (A) or the Gram negative bacterium, Pseudomonas aeruginosa (B). Flies expressing GFP dsRNAs under the control of yolk-GAL4 (green) were used as “wild-type” controls. Eater mutants which are defective in phagocytosis (blue) or flies expressing IMD dsRNAs which are compromised in a major innate immune signaling pathway (yellow) were used as positive controls. Results demonstrate that flies expressing reduced levels of RBF1 in the fat body cells are more susceptible to infection with Gram positive bacteria (A) than wild type controls. Three independent experiments are depicted with results of each experiment shown as the average of three sets of 10 infected adults per genotype. Results are presented as cox regression models with statistical significance (p≤0.05) represented as shaded areas above and below the curves. In the third experiment in (A), which is highlighted by a star, the survival endpoint becomes significant when the confidence level is changed to 90% (p≤0.10) instead of 95% (p≤0.05). These experiments were also performed using a sterile needle dipped in PBS to rule out death as a result of wounding and survival curves matched those of yolk-GAL4 expressing flies (data not shown). doi:10.1371/journal.pgen.1002618.g008

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The differences seen between RBF1 and dCAP-D3 deficient flies in diptericin induction cannot be attributed to functional compensation by the other Drosophila RB protein family member, RBF2, since results show that loss of RBF2 or both RBF1 and RBF2 do not decrease AMP levels following infection. Since results demonstrate that RBF1 binds most strongly to an AMP cluster prior to infection and regulates basal levels of almost all AMPs tested, we hypothesize that RBF1 (and possibly RBF2) may be more important for cooperating with dCAP-D3 to regulate basal levels of AMPs. Reports have shown that basal expression levels of various AMPs are regulated in a gene-, sex-, and tissue-specific manner, and it is thought that constitutive AMP expression may help to maintain a proper balance of microbial flora and/or help to prevent the onset of infections [37,68,69]. In support of this idea, one study in Drosophila which characterized loss of function mutants for a gene called caspar, showed that caspar mutants increased constitutive transcript levels of diptericin but not transcript levels following infection. This correlated with increased resistance to septic infection with Gram negative bacteria [70], proving that changes in basal levels of AMPs do have significant effects on the survival of infected flies. Additionally, disruption of Caudal expression, a protein which suppresses NF-κB mediated AMP expression following exposure to commensal bacteria, causes severe defects in the mutualistic interaction between gut and commensal bacteria [71]. It is therefore possible that RBF1 and dCAP-D3 may help to maintain the balance of microbial flora in specific organs of the adult fly and/or be involved in a surveillance-type mechanism to prevent the start of infection. RBF1 deficient flies also exhibit defects in Drosomycin induction following Gram positive bacterial infection. Mutation to Drosophila GNBP-1, an immune recognition protein required to activate the Toll pathway in response to infection with Gram positive bacteria has been show to result in decreased Drosomycin induction and decreased survival rates, without affecting expression of Diptericin [72,73]. Therefore, it is possible that inefficient levels of Drosomycin, a major downstream effector of the Toll receptor pathway, combined with decreased basal transcription levels of a majority of the other AMPs, would cause RBF1 deficient flies to die faster following infection with Gram positive S. aureus but not Gram negative P. aeruginosa.

Some dCAP-D3 remains localized to DNA in RBF1 deficient flies [11] and it is also possible that other proteins may help to promote the localization of dCAP-D3 to AMP gene clusters following infection. Given that dCAP-D3 regulates many AMPs including some that do not also depend on RBF1 for activation, and given that dCAP-D3 binding to an AMP locus increases with time after infection whereas RBF1 binding is at its highest levels at the start of infection, it may not be too surprising that dCAP-D3 showed a more pronounced biological role in pathogen assays involving two different species of bacteria.

Remarkably, and perhaps unexpectedly, the levels of both RBF1 and dCAP-D3 impact the basal levels of human AMP transcripts, as well. This indicates that the mechanism of RBF1/ dCAP-D3 regulation may not be unique to Drosophila. It is striking that many of the human AMP genes (namely, the defensins) are clustered together in a region that spans approximately 1 Mb of DNA. It seems telling that both the clustering of these genes, and a dependence on pRB and CAP-D3, is apparently conserved from flies to humans. The fact that dCAP-D3 and RBF1 dependent activation of Drosomycin was necessary for resistance to Gram positive bacterial infection in flies suggests the same could also be true for the human orthologs in human cells. Human AMPs expressed by epithelial cells, phagocytes and neutrophils are an important component of the human innate immune system.
Human AMPs are often downregulated by various microbial pathogenicity mechanisms upon infection [38,74–76]. They have also been reported to play roles in the suppression of various diseases and maladies including cancer and Inflammatory Bowel Disease [77]. We note that the chronic or acute loss of RB expression from MEFs resulted in an unexplained decrease in the expression of a large number of genes that are involved in the innate immune system [28]. In humans, the bacterium, *Shigella flexneri* was recently shown to down regulate the host innate immune response by specifically binding to the LXXCE lexot of pRB, the same site that we had previously shown to be necessary for CAP-D3 binding [11,79]. An improved understanding of how RB and CAP-D3 regulate AMPs in human cells may provide insight into how these proteins are able to regulate clusters of genes, and may also open up new avenues for therapeutic targeting of infection and disease. Further studies of in differentiated human cells may identify additional sets of genes that are regulated by pRB and CAP-D3.

**Materials and Methods**

**Fly strains**

W*1118* flies were used as “wild type” controls for microarray experiments. Unless otherwise noted, the genotype of RBF mutants was a transheterozygous combination of *rbf1* / *rbf2* , GFP virgins to *mwm7* / *M7* , GFP males at 18°C. Similarly, the genotype of CAP-D3 mutants was a transheterozygous combination of *dCAP-D3* / *dCAP-D3* which was obtained by mating *dCAP-D3* / *CyO* , GFP virgins to *dCAP-D3* / *CyO* , GFP males at 25°C, yolk- *GAL4* / *FM7* flies were a kind gift of M. Birnbaum and the timing of expression driven by yolk- *GAL4* has been previously characterized in [40]. The RBF1, dCAP-D3, RBF2, and IMD dsRNA expressing strains were obtained from the VDRC and their transformant IDs were 10696, 11573, and 101384 respectively. UAS-FLAG-HA tagged strains were created by first amplifying the ORF from either the CAP-D3 *RE18364* cDNA clone (DGRC) or the RBF1 *LD02906* cDNA clone (DGRC) using Pfx polymerase (Invitrogen). The pENTR/D-TOPO Cloning Kit (Invitrogen) was used to clone the ORF into a Gateway entry vector as described in the manufacturer’s protocol and at http://www.cwiemb.hu/labs/murphy/Gateway%20vectors.html. The LR Clonase kit (Invitrogen) was then used to recombine the ORF into the pUAS-FLAG-HA vector (DGRC) described in detail at the website mentioned above. pUAS-FLAG-HA-RBF1 and pUAS-FLAG-HA-dCAP-D3 vectors were then injected into embryos to create transgenic fly lines expressing the tagged proteins. Mutant flies used as positive controls in infection experiments included the *imd* mutant strain [51]. All flies were maintained at 25°C and placed in vials containing standard dextrose medium.

**Cell culture and RNAi**

HTERT-RPE-1 cells were grown in Dulbecco’s Modified Essential Medium (DMEM) supplemented with 10% fetal bovine serum (FBS) and 1% penicillin/streptomycin. RNAiMax (Invitrogen) was used, according to the manufacturer’s protocol, to transfect non-targeting, RB, and CAP-D3 specific siRNAs (described in [12]) at final concentrations of 100 nM. Total RNA was harvested 48 hours post transfection and reverse transcribed into cDNA, as described below.

**qRT–PCR**

TRIZol (Invitrogen) was used to harvest total RNA from whole flies/species tissues according to the manufacturer’s protocol. After RNA was purified using the Qiagen RNAeasy kit, the Taqman Reverse Transcription kit (Applied Biosystems) was used to reverse transcribe 1.5 μg of RNA into cDNA. qRT-PCR was performed using the Roche Lightcycler 480 to amplify 15 μL reactions containing .5 μL of cDNA, .5 μL of a 10 μM primer mix and 7.5 μL of SYBR Green Master Mix (Roche). All qRT-PCR experiments were performed using three groups of 5 flies per genotype and three independent experiments were performed. Primer sequences are as follows: Rbf1qPCR F1-CTGACGAGGCTAC, Rbf2qPCR R1- GTTGTGCTGTGTCCTCCGGCA, Dro2qPCR R1- GGACTGCAGTGGCCACTGA, Dro7qPCR F1- GGCT-, Dro4qPCR R1- GCCCAGCAAGG-, CecqPCR Dro3qPCR R1- GTCCCTCCTCAATGCA-, Rbf2qPCR F1-CGTGAACGCCTTAGAGGTGCC, AttDqPCR F1- CCAAGGGAGTTTAT-, CecBqPCR R1-, orc1qPCR F1- CATCATCCTCAAA-, hRBqPCR R1- CAACCTCAAGAGCGCACGCC, tub84BqPCR F1- GGCA-, IMDqPCR Dro7qPCR R1- CACATGCC-, hCAP-D3qPCR F1- TCCGGAAG-, hCAP-D3qPCR R1- GGACCTGGCTG-, AndqPCR R1- GGGC-, MtkqPCR R1- GGTGTTTAGGATTGA-, AttBqPCR F1- CTCAAA-, Dro5qPCR F1- CAAGTTCCTGTACCTCTTCCTGGC, hGAPDHqPCR R1- CCAGGC-, DptqPCR R1-GTGACCCTG-, DptBqPCR F1- GGACTGGCTTGTGCCTTCTCG, CecA1qPCR R1- GGCGGCTTGTTGAGCGATTCC, dCAP-D3c07081/CyO males at 25°C and placed in vials containing standard dextrose medium.
CAGCGGCTGC, orc1qPCR R1- CCCTCGACGAGGCGTAAGGC, cg5250qPCR F1- CAATTTGACTATGGTGGTGACGCTG, dnapolalpha50qPCR R1- GGTTGGCCGATTITTTTGTGGAGA, dnapolalpha50qPCR R1- CAGAGGAAACCTCGGCGAAGC, mus209qPCR R1- CCCTCCAGCGTATTGTACATGCCC, dcap-D3 (YZ384), and anti-GFP (Jackson Immunoresearch).

**Chromatin immunoprecipitation**

40 flies per IP were used in all ChIP experiments. Flies were homogenized with a KONTES pestle pestle grinder (Kimble Chase) in 1 mL of buffer A (60 mM KCl, 15 mM NaCl, 4 mM MgCl2, 15 mM HEPES pH 7.6, .5% Triton X-100, 5 mM EDTA, free protease inhibitors cocktail (Roche)) containing 1.8% formaldehyde. Homogenized flies were incubated at RT for 15 minutes, at which point glycerine was added to a concentration of 225 mM. 2–4 mL of homogenized flies were transferred to 15 mL conical tubes and centrifuged at 4°C for 5 min at 4000 g. Supernatant was discarded and pellets were washed with 3 mL of buffer A. Tubes were centrifuged as described above, supernatant was discarded, and pellets were washed with 3 mL of buffer B (140 mM NaCl, 15 mM HEPES pH 7.6, 1 mL of new PBS was added to each tube. Tubes were rotated at 4°C for 20 min. Samples were then sonicated using the Branson sonifier at a setting of 3, with 8 sonication intervals of 20 seconds interspersed by 10 second breaks. Tubes were centrifuged at 4°C for 5 min at 2000 RPM and 500 μL supernatant was used for each IP. 50 μL of Dynal Protein A beads (Invitrogen) per IP were prepared according to the manufacturer’s recommendations. Beads were incubated with anti-FLAG M2 antibody (Sigma) or dCAP-D3 antibody (YZ384) for 2 hours at RT with rotation. Beads were washed according to manufacturer’s protocol and added to the diluted chromatin samples which were then incubated at 4°C overnight, with rotation. Samples were centrifuged at 3000 RPM, 4°C for 1 min and washed three times with buffer B+0.5% SDS and once with TE. Bound protein was eluted by adding 125 μL of Buffer C (1% SDS, 2% NaCl, TE) to the beads for 30 min at 65°C. Samples were again centrifuged and eluates were harvested and incubated for 4 hours at 65°C to reverse crosslinks. Samples were digested with Proteinase K and RNase A (Sigma), phenol-chloroform extracted, and counted as clustered if they overlapped, or if the genes lay within 10 000 base pairs of each other. Overall chromosomal clustering for a list of genes was quantified as the number of genes that co-localize according to this criterion. Significance of co-localization was evaluated by comparing to lists of randomly selected genes from the same chromosome.

**Generation of anti-dCAP-D3 antibody**

The rabbit anti-dCAP-D3 YZ834 antibody was generated by Zymenze Corporation. The antibody was purified using the BIO-RAD Affi-Gel 10 Gel according to manufacturer’s protocol.

**Immunofluorescence analysis of cryosections**

Adult female flies were cryosectioned (10 μm) and stained as previously described [80]. Primary antibodies included RBF1 (DX2), dCAP-D3 (YZ394), and anti-GFP (Jackson Immunoresearch). Images were obtained using a Zeiss LSM510 Confocal microscope.

**Preprocessing of array data**

Nimblegen microarray data were pretreated according to the manufacturer’s recommendation and replicate probes were averaged. Affymetrix microarray data was downloaded from array express as raw .CEL files and normalized by robust multi array averaged. Affymetrix microarray data was pretreated according to the manufacturer’s recommendations and replicate probes were averaged. Nimblegen microarray data were pretreated according to the manufacturer’s recommendations and replicate probes were averaged.

**Hypothesis testing**

Differentially expressed genes were identified using a linear model with a moderated T-test [82]. P values were corrected for multiple testing by calculating false discovery rates using the method of Benjamini and Hochberg [83]. Genes with a false discovery rate (FDR)<0.15 and a log2 fold change >0.1 were taken as significant. Gene ontology (GO) annotations were overrepresented on the lists of differentially expressed genes and GO-categories with hypergeometric test were corrected for multiple testing using the Benjamini-Hochberg method [83]. Genes with a false discovery rate (FDR)<0.05 were taken as significant.

**Gene clustering analysis**

Chromosomal positions of transcription start and stop sites for all genes on the chip were taken from FLYBASE. Genes were taken as clustered if they overlapped, or if the genes lay within 10 000 base pairs of each other. Overall chromosomal clustering for a list of genes was quantified as the number of genes that co-localize according to this criterion. Significance of co-localization was evaluated by comparing to lists of randomly selected genes from the same chromosome.

**Infection of flies with pathogenic bacteria**

*S. aureus* and *P. aeruginosa* bacteria were gifts from L. Stuart. *S. aureus* was grown in a shaking incubator at 37°C, in DIFCO Columbia broth (BD Biosciences) supplemented with 2% NaCl and *P. aeruginosa* was grown in a shaking incubator at 37°C in DIFCO Luria broth (BD Biosciences). Bacteria were inoculated in 10 mL cultures grown overnight. 10⁴ bacterial cells were then inoculated into a new 10 mL culture and this was grown to an OD₆₀₀ₙ₉ of 0.5. These cultures were then centrifuged at 3000 rpm in a 1.5 mL eppendorf tube for 5 minutes at 4°C and subsequently washed twice with PBS. After a third centrifugation, PBS was washed from the pellet and 25 μL of new PBS was used to resuspend the pellet. Infections were performed as previously described [85]. Specifically, a 25 mm diameter straight stainless steel needle and pin vise (Ted Pella Inc, Redding, CA) were used to infect adult flies. The needle was dipped into the resuspended bacterial pellet and used to prick the thorax of a CO₂-anesthetized adult fly in a region just underneath where the wing connects to the thorax. Flies were then separated from the needle using a brush and put into fresh vials containing standard dextrose medium with no more than 10 flies per vial.
extracted, and ethanol precipitated. DNA pellets were dissolved in 105 μL of ddH2O and .5 μL was used per qRT-PCR reaction.

Survival curves

Flies were collected approximately 5–8 days after eclosure and were infected as described above. Following infection, each group of flies was placed in a new vial of food and monitored for the number of surviving flies at each timepoint. Three experiments were performed, with each experiment including 3 groups of 10 flies per genotype per timepoint. Survival statistics were calculated using a cox proportional hazard model, and hazard ratios with a two sided p-value less than 0.05 were taken as significant.

Bacterial clearance assays

Flies were anesthetized by CO2 inhalation and infected as described above. Following infection, flies were dipped in 95% Ethanol, air dried, and placed into 1.5 mL Eppendorf tubes containing 300 μL of PBS. Flies were homogenized with a Kontes battery powered homogenizer and plastic pestle (USA scientific). The tubes were centrifuged for 2 min at 3000 rpm. Various dilutions were plated onto Columbia CNA with 5% Sheep’s Blood Agar (Becton Dickinson and Company). This type of agar contains antibiotics to inhibit growth of organisms other than Staphylococcus aureus.

Supporting Information

Figure S1 dCAP-D3 and RBF1 mutants expressing a transheterozygous combination of alleles retain approximately 15% of wild type protein expression. qRT-PCR (A) and Immunoblots (B) for rbf1 transcript levels/protein levels and dCAP-D3 transcript levels/protein in wild type (yolk-GAL4/w1118) and dCAP-D3 transheterozygous mutant (dCAP-D3/yolk-GAL4/+; rbf1120a/+/f e m a l e ) or RBF1 transheterozygous mutant (rbf1120a/+/f e m a l e ) female flies indicates that mutants retain 10–15% of wild-type protein expression levels. Transcript levels were normalized to tubulin 4β mRNA levels and α-tubulin was used as a loading control in B. (TIF)

Figure S2 RBF1 regulates E2F targets in specific tissues of the adult fly. Ovaries were dissected from female adult flies and cDNA was made from either carcass or ovaries. Top table: qRT-PCR analyses performed on cDNA from ovaries shows that decreased RBF1 expression results in the upregulation of a few E2F targets while decreased dCAP-D3 expression largely has no effect. Bottom table: qRT-PCR analyses performed on cDNA from carcass without ovaries shows that decreased RBF1 expression in the carcass does result in upregulation of many E2F targets, however, dCAP-D3 does not share regulation of these genes with RBF1. Transcript levels were normalized to tubulin 4β mRNA levels. All results were significant with p-values≤0.05. (TIF)

Figure S3 RBF1 and dCAP-D3 antibodies are specific. Immunostaining for dCAP-D3 (A) and RBF1 (B) in cryosections of abdomens of adult female flies expressing dCAP-D3 (A) or RBF1 (B) dsRNA in combination with GFP protein in fat body cells shows the antibodies recognize protein where dsRNAs are not expressed. Flies used in A were of the genotype yolk-GAL4, UAS-GFP/+; yolk-GAL4/d; dCAP-D3 d; RNA, and flies used in B were of the genotype yolk-GAL4, UAS-GFP/+; yolk-GAL4/d; dCAP-D3 d; RNA. (TIF)

Figure S4 qRT-PCR analysis of genes adjacent to the diptericin locus. qRT-PCR analysis of cDNA from 1) flies expressing driver alone (yolk-GAL4/+; +/+), 2) flies expressing rbf1 dsRNA (yolk-GAL4/+; UAS-rbf1) d; RNA in the fat body cells and 3) flies expressing dCAP-D3 d; RNA (yolk-GAL4/+; UAS-dCAP-D3 d; RNA) in the fat body cells demonstrates that CG43070 is also activated by RBF1 and dCAP-D3. (TIF)

Figure S5 Endogenous dCAP-D3 binds to CG3250 in a similar pattern as FLAG-HA-dCAP-D3. A) qRT-PCR was performed on cDNA generated from whole female flies (1) expressing yolk-GAL4 driver alone (yolk-GAL4/+; +/+ or (2) exhibiting acute, fat body specific knockdown of dCAP-D3 (yolk-GAL4/+; +; UAS-dCAP-D3 d; RNA/) or mutant flies expressing RBF2 (turquoise) dsRNAs or a combination of RBF1 and RBF2 dsRNAs (black) under the control of yolk-GAL4. (TIF)

Figure S6 Confirmation of rbf1 and rbf2 transcript knockdown in flies expressing RBF2 or RBF1 and RBF2 dsRNAs. qRT-PCR was performed on cDNAs from flies deficient for RBF2 alone or deficient for a combination of both RBF1 and RBF2. (TIF)

Figure S7 RBF2 does not regulate AMP induction following bacterial infection. Adult female flies expressing RBF2 (turquoise) or a combination of RBF1 and RBF2 (black) dsRNAs under the control of yolk-GAL4 were infected with the Gram positive bacteria, Staphylococcus aureus. A) qRT-PCR analyses for transcript levels of the Diptericin AMP gene in these flies show that control flies expressing GFP dsRNAs under the control of yolk-GAL4 (green) undergo a large induction of AMPs at 8-24 hours post-infection. Flies expressing RBF2 dsRNA or a combination of RBF1 and RBF2 dsRNAs show no significant, repeated changes in transcript levels upon comparison to control flies. B) qRT-PCR analyses for transcript levels of the Diptericin AMP gene in these flies show that control flies expressing GFP dsRNAs under the control of yolk-GAL4 (green) undergo a large induction of AMPs at 8-24 hours post-infection. Flies expressing RBF2 dsRNA or a combination of RBF1 and RBF2 dsRNAs exhibit a significant decrease in basal transcript levels in the majority of experiments, but do not exhibit significant changes in transcript levels following infection. Three independent experiments are shown and results for each experiment are the average of three sets of five infected adults. The inset boxes in the upper right corner of each graph are a larger representation of the 0 hour timepoint and therefore depict basal transcription levels. Asterisks emphasize statistical significance (p≤0.05) as determined by a students paired t-test. (TIF)

Figure S8 RBF2 deficiency in the fat body does not significantly affect survival following bacterial infection. Adult female flies expressing RBF2 (turquoise) dsRNAs or a combination of RBF1 and RBF2 dsRNAs (black) under the control of yolk-GAL4 were infected with the Gram positive bacterium, Staphylococcus aureus (A) or
the Gram negative bacterium, *Pseudomonas aeruginosa* (B). Flies expressing GFP dsRNAs under the control of *yolk-GAL4* (green) were used as “wild-type” controls. Eater mutants which are defective in phagocytosis (blue) or flies expressing IMD dsRNAs which are compromised in the Gram negative arm of the innate immune signaling pathway (yellow) were used as positive controls. Results demonstrate that flies expressing reduced levels of RBF2 or reduced levels of both RBF1 and RBF2 in the fat body cells do not significantly and repeatedly affect survival times in response to either type of infection upon comparison to wild type controls. Three independent experiments are depicted with results of each experiment shown as the average of three sets of 10 infected adults per genotype. Results are presented as cox regression models with statistical significance (p<0.05) represented as shaded areas above and below the curves. These experiments were also performed using a sterile needle dipped in PBS to rule out death as a result of wounding and survival curves matched those of *yolk-GAL4* expressing flies (data not shown).

**Figure S9** Regulation of AMP genes by RB and CAP-D3 is conserved in human cells. A) RPE-1 cells were transfected with (1) non-targeting Control siRNA, (2) pRB siRNA or (3) CAP-D3 siRNAs. qRT-PCR analyses were performed on cDNAs generated from cellular RNA collected 48 hours post transfection and results show that Rb and CAP-D3 are significantly decreased. B) qRT-PCR for AMPs in cells described in A shows that pRB or dCAP-D3 deficiency results in significant decreases in basal levels of two human AMP genes.

**Table S1** Microarray data from multiple samples of wild type cDNA, dCAP-D3 mutant cDNA, and RBF1 mutant cDNA. Experiments were performed using Nimblegen 385 k whole genome arrays. A detailed description of the information found in each column is provided to the right of the table.

**Table S2** Analysis of clustering frequencies among dCAP-D3 and/or RBF1 regulated target genes. A detailed description of the information found in each column is provided to the right of the table. Numbers within individual columns are arbitrary and designate genes present within the same cluster; they do not indicate any information about the strength of their misregulation in mutant flies.

**References**