RESEARCH ARTICLE

Hindsight/RREB-1 functions in both the specification and differentiation of stem cells in the adult midgut of Drosophila

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ABSTRACT

The adult Drosophila midgut is established during the larval/pupal transition from undifferentiated cells known as adult midgut precursors (AMPs). Four fundamental cell types are found in the adult midgut epithelium: undifferentiated intestinal stem cells (ISCs) and their committed daughter cells, enteroblasts (EBs), plus enterocytes (ECs) and enteroendocrine cells (EEs). Using the Drosophila posterior midgut as a model, we have studied the function of the transcription factor Hindsight (Hnt)/RREB-1 and its relationship to the Notch and Egfr signaling pathways. We show that hnt is required for EC differentiation in the context of ISC-to-EC differentiation, but not in the context of AMP-to-EC differentiation. In addition, we show that hnt is required for the establishment of viable or functional ISCs. Overall, our studies introduce hnt as a key factor in the regulation of both the developing and the mature adult midgut. We suggest that the nature of these contextual differences can be explained through the interaction of hnt with multiple signaling pathways.

KEY WORDS: Hindsight/RREB-1, Intestinal stem cells, Enterocyte, Differentiation

INTRODUCTION

Until relatively recently, it was a commonly held view that differentiated somatic tissues of Drosophila adults are static and non-proliferative. Lineage tracing techniques, however, have demonstrated the existence of stem cells within several tissues including intestinal stem cells (ISCs) within the posterior midgut (Michellchi and Perrimon, 2006; Ohlstein and Spradling, 2006; Singh et al., 2007). ISC regulation is remarkably conserved between mammals and Drosophila (Casali and Batlle, 2009; Hartenstein et al., 2010). Studies using Drosophila can, therefore, contribute to our understanding of stem cell biology and associated human diseases.

The adult Drosophila midgut arises from mitotically active cells of the embryonic endoderm (Hartenstein et al., 2010). These cells are marked by the expression of escargot (esg), which encodes a C2H2-type Zinc finger protein that is required for the maintenance of diploidy in several tissues (Hayashi et al., 1993; Korzelius et al., 2014). esg expression is maintained in cells that will become the adult midgut precursors (AMPs) (Takashima et al., 2011). During late stages of embryogenesis, the AMPs, which remain undifferentiated, migrate through the newly formed midgut to become situated along the basal surface of the epithelium (Jiang and Edgar, 2009; Takashima et al., 2011). During the third larval instar, AMPs are found as clusters in which 1-3 AMPs differentiate in a Notch-dependent manner to form a specialized cell type, the peripheral cell (PC), which enwraps the remaining eight or more undifferentiated AMPs at this stage (Mathur et al., 2010; Takashima et al., 2011).

During the larval/pupal transition, the differentiated larval enterocytes (ECs) and enteroendocrine cells (EEs) are eliminated by autophagic cell death (Denton et al., 2009). Most AMPs differentiate to form the adult ECs, while some remaining AMPs become ISCs (Takashima et al., 2011). The mechanism of AMP-to-ISC specification is not understood. AMP-to-EC differentiation, however, can occur through a pathway parallel to Notch signaling (see below) that requires ecdysone signaling and the transcriptional regulator Broad. Ecdysone signaling and Broad are also implicated in the differentiation of fully functional ISCs from AMPs (Zeng and Hou, 2012).

The hindsight (hnt) gene encodes a nuclear protein containing 14 C2H2-type Zinc fingers. The expression of hnt during development is complex and dynamic (Yip et al., 1997). In general, despite a wealth of information, a detailed understanding of how Hnt functions to regulate cellular and developmental processes has remained elusive (Oliva et al., 2015; Pickup et al., 2009; Sun and Deng, 2007; Wilk et al., 2000).

Ras responsive element binding protein-1 (RREB-1), the mammalian homologue of Hnt, can act as either a transcriptional repressor or activator, depending on the context and target gene (Liu et al., 2009; Thiagalingam et al., 1996). Recent studies suggest that Hnt and RREB-1 are functionally conserved (Ming et al., 2013). In humans, RREB-1 has been linked to pancreatic, thyroid, and colorectal cancer (Kent et al., 2013; Zhang et al., 2003).

In Drosophila, ISCs are marked by the expression of esg and can divide either symmetrically or asymmetrically (de Navascues et al., 2012). Asymmetric divisions typically produce one daughter cell that retains the ISC identity and a second committed daughter cell known as an enteroblast (EB) (Michellchi and Perrimon, 2006; Ohlstein and Spradling, 2006). EBs also express esg and differentiate without dividing to become either ECs or EEs; the former undergo endoreduplication and become polyploid, while the latter remain diploid (Strand and Michellchi, 2013; Zeng et al., 2013a). ISCs express the Notch ligand Delta, and EBs that receive a higher level of Notch activation differentiate as ECs, whereas EBs receiving a lower level of Notch activation differentiate as EEs (Ohlstein and Spradling, 2007). Reduced Notch signaling results in uncontrolled ISC division, decreased EC differentiation, and an increased number of EE-like cells (Michellchi and Perrimon, 2006; Ohlstein and Spradling, 2006, 2007), while overexpression of activated Notch promotes EC differentiation (Michellchi and Perrimon,
2006; Ohlstein and Spradling, 2007). Interestingly, hnt has been identified as a Notch-responsive gene and its expression has been shown to be Notch-dependent in some contexts (Krejci et al., 2009; Sun and Deng, 2007; Terriente-Felix et al., 2013).

The Egfr/Ras/MAPK signaling pathway (hereafter the Egfr pathway) is required for ISC proliferation (Biteau and Jasper, 2011; Buchon et al., 2010; Jiang and Edgar, 2009). Over-activation of Egfr signaling results in increased ISC proliferation and midgut hyperplasia (Biteau and Jasper, 2011; Buchon et al., 2010; Jiang and Edgar, 2009). While Egfr signaling promotes ISC proliferation, it does not influence subsequent differentiation events (Biteau and Jasper, 2011).

An additional pathway regulating ISC proliferation is the JAK/STAT pathway. Activation of this pathway in ISCs leads to increased ISC proliferation while reduced JAK/STAT signaling leads to an accumulation of EB-like cells, suggesting that this pathway is required for the competence of EB cells to undergo EC or EE differentiation (Beebe et al., 2010).

As summarized in several recent reviews, the list of signaling pathways and genes regulating midgut development, homeostasis, and regeneration has become extensive (Buchon et al., 2014; Kux and Pitsouli, 2014; Naszai et al., 2015; Tipping and Perrimon, 2014; Zeng et al., 2013a). Several studies have recently expanded our understanding of both EC and EE differentiation. Regarding the former, the expression of esg has been found to suppress EC differentiation through the repression of EC-specific genes such as Pdm1 (Korzelius et al., 2014). Additionally, BMP signaling (Dpp/Gbb) as well as the chromatin remodeling proteins Brahma and Osa have been shown to be required for proper EC differentiation (Jin et al., 2013; Zeng et al., 2013b; Zhou et al., 2015). EE differentiation is promoted by the proneural genes asense and scute, with the transcriptional regulation of asense being Osa-dependent (Bardin et al., 2010; Zeng et al., 2013b). More recently, robo/slit signaling has been found to regulate a negative feedback mechanism that limits EE regeneration (Beebe and Jasper, 2014).

This study represents the first detailed analysis of the expression and function of hnt in the adult midgut. We report that ISCs/EBs express hnt and that this expression is increased in differentiated ECs and is absent from EEs. We find hnt expression in ISCs/EBs to be independent of Notch signaling and Egfr-dependent. In addition, we show that hnt overexpression induced in ISCs/EBs results in EC differentiation and we conclude that hnt can promote, but is not sufficient, for EC differentiation. Qualitative and quantitative mosaic analysis of loss-of-function alleles demonstrates a requirement for hnt in ISC-to-EC differentiation, but not in AMP-to-EC differentiation. An additional and novel finding of our study is the requirement for hnt in the establishment of viable or functional ISCs. Overall, our work ascertains that the transcriptional regulator Hnt/RREB-1 is an important component of the developing and homeostatic adult midgut where it functions in the both the specification and subsequent differentiation of ISCs.

RESULTS
hnt is expressed in the adult intestinal epithelium

The Notch signaling pathway is required for the normal maintenance and regeneration of the adult midgut (Michelli and Perrimon, 2006; Ohlstein and Spradling, 2006). The gene hnt has been identified as a target of the Notch signaling pathway, but in contexts other than that of the adult midgut (Krejci et al., 2009; Sun and Deng, 2007; Terriente-Felix et al., 2013). To investigate the possible functions of Hnt in the adult midgut, and to determine if hnt is a target of Notch signaling in this context, we performed anti-Hnt immunostaining of adult midguts. Immunostaining of esgα midguts following shift to permissive conditions (see Materials and Methods) allowed unambiguous identification of ISCs/EBs as Hnt-positive. Large, polyploid, GFP-negative cells corresponding to ECs were also Hnt-positive (Fig. 1A). In general, the intensity of anti-Hnt signal in the esgα-marked ISCs/EBs was less than the signal observed in ECs. In addition, small GFP-negative cells were sometimes observed to be weakly Hnt-positive (data not shown), possibly representing EEs. Unfortunately, anti-Hnt and the EE marker anti-Prospero (Pros) are both mouse monoclonal antibodies, which precluded a double immunolabeling experiment. To circumvent this problem we used a GFP enhancer trap line, yet1, which we here report as a new EE marker. Anti-Pros immunostaining of yet1 adult midguts confirmed that yet1 expression and Pros co-localize (Fig. 1B). Anti-Armadillo (Arm) immunostaining also confirmed that yet1-expressing cells are single small cells associated with reduced Arm, consistent with EE morphology (Fig. S1). Anti-Hnt immunostaining of the yet1 line subsequently established that strong GFP-positive cells are Hnt-negative (Fig. 1C), while weakly GFP-positive cells are sometimes weakly Hnt-positive (arrows, Fig. 1C). We conclude that strong yet1 expression marks differentiated EEs and that this cell type does not express hnt. These observations also suggest that hnt is down-regulated in EEs that are specified to become EEs.

ISC expression of hnt is not dependent on Notch signaling but is dependent on Egfr signaling

To address the expression of hnt in the context of reduced Notch signaling, anti-Hnt immunostaining was performed on midguts in which Notch was depleted by expression of UAS-Notch-RNAi using the esgα technique. Consistent with previous findings (Michelli and Perrimon, 2006; Ohlstein and Spradling, 2006), we found that midguts with reduced Notch signaling display an overproliferation of two cell types which we observed as small GFP-positive, Hnt-positive cells, as well as small GFP-negative, Hnt-positive cells (Fig. 2A). Our above finding that Hnt is not expressed in differentiated EEs supports the view that the small GFP-negative, Hnt-positive cells represent an intermediate cell type that is neither a fully differentiated EE nor an ISC. In the GFP-positive overproliferating ISC-like cells, however, we found no indication of reduced hnt expression. Taken together, these observations support the interpretation that ISCs do not express hnt in a Notch-dependent manner.

The mammalian homologue of hnt is RREB-1, and several lines of evidence suggest that RREB-1 functions in the regulation of Egfr signaling (Kent et al., 2013, 2014; Thiagalingam et al., 1996). Moreover, Egfr and hnt mutants share a number of phenotypes, including premature degeneration and death of the extra-embryonic tissue known as the amnioserosa (Frank and Rushlow, 1996; Shen et al., 2013). For these reasons we examined the expression of hnt in the context of reduced Egfr signaling. Midguts depleted of Egfr by expression of UAS-Egfr-RNAi were sparsely populated by GFP-positive cells (ISCs/EBs), and these were uniformly Hnt-negative (Fig. 2B). Thus, while we found no dependence on Notch signaling, we find that hnt expression in ISCs/EBs is dependent on Egfr signaling.

Increased hnt expression forces ISC to EC differentiation

Our initial observations suggested that hnt expression may increase in association with EC specification, and decrease during EE differentiation. We were initially interested in determining if hnt
overexpression in ISCs/EBs (using the esg" technique) could bias specification towards the EC fate. What we found, however, was a striking loss of all ISCs/EBs. As early as 14 h post shift, ISCs/EBs with high levels of Hnt and a slight increase in size were observed (Fig. 3A). At 4 days post shift no small GFP-positive cells remained, and large weakly GFP-positive cells were observed in the midgut (Fig. 3B), with the exception of the gastric region stem cells (data not shown). Since esg expression is lost in differentiating EEs and ECs, it remained possible that hnt overexpression did not result in ISC loss through EC differentiation, but that the observed ISC loss is the result of ISC/EB delamination or death. To address this possibility, we repeated hnt overexpression experiments using the esgF/O technique to facilitate ISC lineage tracing (see Materials and Methods). Using esgF/O to express UAS-GFP-hnt, most GFP-positive cells appeared as large differentiated ECs that were integrated into the midgut epithelium at 3 days post shift. The lack of co-localization of Pros and GFP also confirmed that hnt-overexpressing cells do not differentiate as EEs (Fig. 3D). Control esgF/O midguts at 5 days post shift were typically found to contain clusters of GFP-positive cells consisting of several large cells as well as one or two small cells (Fig. 3E). At the same time point (5 days post shift), hnt overexpression using hntEP55 resulted in esgF/O lineages of only one or two cells that were Pdm1-positive, consistent with EC differentiation (Fig. 3F). Overall, these results show that increased hnt expression can force ISC-to-EC differentiation.

The overexpression of hnt as ‘differentiation therapy’ in the fly

The successful treatment of some forms of cancer involves ‘differentiation therapy’, whereby treatment aims to force malignant cells to resume normal differentiation (Warrell et al., 1991). The adult Drosophila posterior midgut has emerged as a model for mammalian midgut homeostasis and displays remarkable parallels in terms of dysregulation and hyperplasia (Casali and Batlle, 2009; Hartenstein et al., 2010; Wang and Hou, 2010). As previously shown in the literature and repeated in this study, reduced Notch signaling in the Drosophila midgut results in overproliferation of ISC-like cells (Micchelli and Perrimon, 2006; Ohlstein and Spradling, 2006, 2007). The activation of Egfr signaling is also known to result in overproliferation (Biteau and Jasper, 2011; Buchon et al., 2010; Jiang and Edgar, 2009). Similar to differentiation therapy, we tested the ability of hnt overexpression to suppress each overproliferation background. Using the esg" technique, we found that expression of EgfrAC resulted in discernable hyperplasia in the posterior midgut region within 24 h of induction (Fig. 4A). Such hyperplasia was not evident in midguts co-expressing UAS-GFP-hnt (Fig. 4B). By 3 days post induction EgfrAC expression resulted in extensive hyperplasia (Fig. 4C) that was completely suppressed by UAS-GFP-hnt
co-expression (Fig. 4D). Similarly, the overproliferation of ISC-like cells associated with the expression of Notch-RNAi (Fig. 4E) was suppressed by UAS-GFP-hnt co-expression at 7 days post induction (Fig. 4F). Overall, these results suggest that increased hnt expression can abrogate overproliferation by forcing ISCs to differentiate as ECs.

Recent results have established that esg is required for ISC maintenance (Korzelius et al., 2014), and this prompted us to determine if co-expression of esg could suppress the forced differentiation associated with hnt overexpression. Using the esg FR T technique, and similar to results shown in Fig. 3D (but here shown 7 days post-induction), hnt EP55 overexpression resulted in the terminal differentiation of all ISCs as ECs, evident as large single or doublet GFP-positive cells (Fig. 4G). Co-expression of UAS-esg suppressed this effect, and no large, GFP-positive cells were observed (Fig. 4H). In summary, these results demonstrate that hnt overexpression is capable of promoting EC differentiation in a number of different contexts. The ability of esg overexpression to suppress EC differentiation, however, suggests that hnt overexpression alone is not sufficient for EC differentiation.

**hnt is required for EC differentiation in the adult midgut**

Having established that hnt overexpression can promote, but is not sufficient for EC differentiation, we wished to determine if hnt is necessary for this process. Our main approach for these experiments was to generate marked somatic clones within the ISC population of the adult midgut. Using a FLP/FRT-based twin spot technique, which permits analysis of all cell types, we first generated clones in which daughter cells either inherited two copies or no copy of an X-linked His2Av-GFP transgene marker in the background of a third chromosome carrying His2Av-RFP (see Materials and Methods). Following clone induction in mature adult females, twin spots composed of both small cells (presumptive ISCs/EBs or EEs) and large cells (presumptive ECs) were observed (Fig. 5A). Clones induced in hntXE81 heterozygotes, on the other hand, did not propagate the hntXE81 mutant side of the twin spot (RFP-only) and large hntXE81 mutant cells (presumptive ECs) were never observed (Fig. 5B). These observations suggested that hnt could be required for ISC
ability to express either ISC/EB or EC specific markers. While the
using a modified MARCM technique. Unlike the above GFP/RFP
between these two possibilities, a quantitative analysis was performed
maintenance and proliferation or EC differentiation. To distinguish
first proposed, is prone to hyperplasia (Biteau et al., 2008; Choi et al., 2008),
proliferation. In addition, even in the context of the aged midgut, which is prone to hyperplasia (Biteau et al., 2008; Choi et al., 2008), hnt mutant cells are incapable of EC differentiation.
Additional quantitative analysis compared hnt mutant ISC clones of the null allele hnt<sup>ES1</sup> to the hypomorphic allele hnt<sup>108</sup>. In this experiment, induced clones were marked by the expression of UAS-GFP<sup>pos</sup> under the control of both esg<sub>GAL4</sub> and NP6293 (see Materials and Methods). Using this technique we measured the percentage of large GFP-positive cells, presumably indicative of differentiated ECs, at various time points after clone induction. Overall, large cells (EC-like) were most frequent in controls, significantly less frequent in hnt<sup>108</sup> clones, and were negligible in hnt<sup>ES1</sup> clones (Fig. S2A-C). Interestingly, while hnt<sup>108</sup> mutant clones contained a small percentage of large GFP-positive cells, anti-Pdm1 immunostaining showed these cells to be Pdm1-negative, suggesting that these large cells are not fully differentiated ECs (Fig. S2D).
Finally, to rule out the possibility that hnt ISC mutant clones result in increased EE differentiation, we measured the average number of Pros-positive cells in midguts harboring control, hnt<sup>ES1</sup>, and hnt<sup>108</sup> mutant ISC clones. We found no significant difference in the frequency of Pros-positive cells among the three genotypes, suggesting that hnt mutant ISC clones do not result in increased EE differentiation (Fig. S2F).
Taken together, both qualitative and quantitative analysis of somatic clones using two different hnt loss-of-function alleles allows us to conclude that differentiated ECs are not found within hnt mutant clones induced in ISCs. Therefore, hnt function is necessary for EC differentiation from the ISC/EB state in the adult midgut.

hnt is not required for EC differentiation from the AMP state but is required for the establishment of ISCs from AMPs
Having established that hnt is required for EC differentiation from the ISC/EB state, we wished to determine if hnt is generally required for EC differentiation, or if this requirement is specific to the adult ISC/EB. To address this question we repeated clonal analysis experiments in which clone induction was performed on third instar larvae. In so doing, hnt loss-of-function clones were induced among the population of proliferating AMPs. Most AMPs differentiate directly to ECs in the formation of the adult midgut, without passing through the ISC/EB state (Jiang and Edgar, 2009; Micchelli et al., 2011). Using NP6293-MARC and clone induction by heat shocking third instar larvae produced ample NP6293>GFP-positive cells in both control and hnt<sup>ES1</sup> heterozygous (Fig. 7A,B; Fig. 6D).
Using esg-MARC under identical conditions resulted in
DISCUSSION

**hnt expression and Notch signaling**

Our results demonstrate that *hnt* expression is maintained in ISCs depleted of Notch. While this establishes that *hnt* expression in ISCs is Notch-independent, it does not rule out the possibility that EC differentiation could require Notch-dependent *hnt* expression. For example, it remains possible that Notch signaling from the ISC to the EB could augment *hnt* expression in the EB, thereby promoting EC fate. Consistent with this possibility, our anti-Hnt immunostaining results suggest that *hnt* expression is increased in ECs relative to ISCs. In addition, our finding that *hnt* is not expressed in mature EEs also suggests that *hnt* is down-regulated as EBs enter the EE differentiation pathway, possibly reflecting reduced Notch signaling associated with EE differentiation. Taken together, our results do not rule out the possibility that *hnt* expression is Notch-dependent during ISC-to-EC differentiation.

**Hnt can promote but is not sufficient for ISC-to-EC differentiation**

We report that co-expression of *hnt* and *esg* suppresses ISC-to-EC differentiation (compare Fig. 4G with H). Combined expression of *Notch* and esg was reported to partially suppress ISC-to-EC differentiation associated with the over-activation of Notch signaling (Korzelius et al., 2014). Our co-expression experiment, however, used *hnt* and *esg* tagged with a lower level than *UAS-GFP-hnt*. This difference in the level of expression was apparent in our *esg* experiments where *hnt* was less effective than *UAS-GFP-hnt* in promoting ISC-to-EC differentiation (data not shown).

It remains possible that co-expression of *esg* and a higher level of *hnt* overexpression could force ISC-to-EC differentiation, and that there is a threshold effect with respect to the level of Hnt and EC differentiation. The question as to whether Hnt and Esg compete for target genes, or if expression of either of these genes affects the regulation of the other remains unexplored at this time.

The JAK/STAT signaling pathway has also been implicated in the specification of EC cell fate (Beebe et al., 2010). Although not a main focus of our study, we found that RNAi knockdown of Stat92E resulted in ISC-to-EC differentiation (data not shown). The JAK/STAT signaling pathway has also been implicated in the specification of EC cell fate (Beebe et al., 2010). Although not a main focus of our study, we found that RNAi knockdown of Stat92E had no effect on *hnt* expression. In addition, we found that co-expression of *UAS-GFP-hnt* with *UAS-Stat92E-RNAi* resulted in robust EC differentiation, suggesting that Hnt functions either in parallel or downstream of JAK/STAT signaling in EC differentiation (data not shown).

Overall, our analysis of *hnt* mutant clones supports the interpretation that *hnt* is necessary for ISC-to-EC differentiation. A recent genome-wide RNAi-based screen reported that depletion of Hnt using the *esg* technique results in ISC-to-EC differentiation.
This context is Egfr-dependent. In the scenario whereby hnt expression is positively regulated by Egfr signaling, we might expect similarities between Egfr and hnt mutant phenotypes. In support of this, we suggest that the phenotype of hnt mutant clones resembles Egfr mutant clones with respect to ISC proliferation and survival, and that these are dramatically different from the effects of reduced Notch signaling (Biteau and Jasper, 2011). The behavior of hnt and Egfr clones generated in the adult ISCs, however, differed with respect to cell differentiation. In mosaic analysis, and when using the MARCM technique, somatic recombination and subsequent mitotic division generate single cells that can be either mutant or wild type, presumably with equal probability. In the case of Egfr mutant clones, many newly formed single-cell clones can result in differentiated ECs or EEs, indicating that Egfr is not required for subsequent differentiation in the cases where the EB daughter cell is mutant (Biteau and Jasper, 2011). By contrast, hnt mutant ISC clones generated in the adult midgut fail to differentiate as ECs. We have established that Hnt is required for ISC-to-EC differentiation, and the above clonal analysis suggests that Egfr is not required for EC differentiation. From this, we speculate that any expression or upregulation of hnt required to promote EC differentiation is most likely independent of Egfr signaling. This interpretation further supports the notion of a separate induction of hnt expression that is independent of Egfr signaling.

**Hnt is not required for AMP-to-EC differentiation but is required in the establishment of ISCs from AMPs**

We show that Hnt is essential for ISC-to-EC differentiation, but not AMP-to-EC differentiation. As mentioned previously, Broad is known to play an important role in promoting AMP-to-EC differentiation, acting in parallel to the Notch signaling pathway. Additionally, Notch and Broad can effectively compensate for the loss of one another in allowing AMPs to differentiate as ECs (Zeng and Hou, 2012). We speculate that such AMP-to-EC differentiation in hnt mutant AMPs is occurring through the edcysone/Broad pathway and this possibility merits further investigation.

Interestingly, we find that hnt mutant clones induced in AMPs never result in small, ISC or EE-like cells. This is unlike either the broad or Notch mutants. broad mutant clones induced in AMPs generate non-functional ISCs, which are Delta-positive but fail to proliferate or differentiate (Zeng and Hou, 2012). Notch mutant AMP clones, on the other hand, differentiate as EEs (Zeng and Hou, 2012). The absence of ISC or EE-like cells in hnt mutant clones suggests that hnt may play a primary role in the establishment of the ISCs from the AMP state. It also remains possible, however, that hnt mutant AMPs are preferentially eliminated by programmed cell death specific to the period of the larval-to-pupal transition. Interestingly, recent work in ovarian follicle cell differentiation has suggested that Broad functions together with Hnt in regulating the Notch-dependent mitosis-to-endocycle transition and cell differentiation (Jia et al., 2014). Given that broad mutant AMPs fail to generate fully functional ISCs (Zeng and Hou, 2012), and the complete lack of ISCs in hnt mutant AMP clones, allows us to speculate that, like the follicle cell context, Hnt and Broad may function cooperatively to establish the ISCs of the adult midgut.

**MATERIALS AND METHODS**

**Drosophila stocks**

All cultures were raised on standard *Drosophila* medium at 25°C under a 12 h light/dark cycle, unless otherwise indicated. Unless otherwise stated, stocks were obtained from the Bloomington *Drosophila* Resource Center. Controls were performed using *yw*^1118^ or *yw*^1118^; P[ry^+t7.2^]=neoFRT
19A stocks. P[w[+mC]=neoFRT]19A is here abbreviated as FRT19A. The reporter line w^{118C}, P[w[+mC]=UAS-GFP,nls]14, abbreviated in this report as UAS-GFP\textsuperscript{w118C}, was used to characterize GAL4 expression patterns. The nuclear markers His2Av-GFP and His2Av-RFP are fully described as P[w[+mC]=His2Av-EGFP]C2 and P[w[+mC]=His2Av-mRFP]P1II.2 or P[w[+mC]=His2Av-mRFP]III.1, respectively. The UAS-Notch-RNAi line was used as P[w[+mC]=UAS-NdumRNAiP]14E. The UAS-EGR-RNAi line was used as P[G16154]v43267 and was obtained from the Vienna Drosophila RNAi Center. Most escargot GAL4 lines used (esg-GAL4 only, with UAS-GFP, and with both UAS-GFP and tub-GAL80\textsuperscript{ts}) have been described previously (Micchelli and Perrimon, 2006). The esg\textsuperscript{FRT19A} stock, described below, was provided by H. Jiang. The hnt\textsuperscript{hnt} and UAS-GFP-hnt lines have been described (Ming et al., 2013; Reed et al., 2001). A recombinant y w^{118C} hnt\textsuperscript{Xf81} FRT19A line was recovered in our lab. UAS-Esg\textsuperscript{GCT} was originally described as UAS-Atop4.2 (Queenan et al., 1997) and was obtained from T. Schüpbach. The NP6293 GAL4 line was obtained from the Kyoto Drosophila Resource Center. The Yet\textsuperscript{1 enhancer trap line is from A. Michelson (Mohseni et al., 2009). The UAS-esg line from S. Hayashi was provided by J. Korzelius (Korzelius et al., 2014). UAS-mCherry-moesin was provided by R. Jacobs (McMaster University, Canada). Stocks used for mosaic analysis included tub\textsuperscript{GAL80} hs\textsuperscript{FLP} FRT19A (full description: P[w[+mC]=ub\textsuperscript{P}GAL80\textsuperscript{L1.1} P[y[+t+7.2]=hs\textsuperscript{FLP}] P[y[+t+7.2]=neoFRT19A] as well as Dp(1;2)F4RDup originally from H. Salz (Case Western Reserve University, Ohio, USA).

The esg\textsuperscript{FRT19A} technique

A method for inducing gene expression within the ISCs/EBs of the adult midgut has been described (Micchelli and Perrimon, 2006) and is here abbreviated as the esg\textsuperscript{FRT19A} technique. Briefly, this method uses a chromosome that carries the esg\textsuperscript{GAL4} driver in addition to a UAS-GFP reporter and a tub\textsuperscript{GAL80\textsuperscript{FRT19A}} insertion. Rearing cultures at 18°C, which is permissive for GAL80\textsuperscript{ts}, prevents GAL4 activation and circumvents any effects associated with inducing gene expression during earlier stages of development. Shifting cultures to 29°C inactivates the GAL80\textsuperscript{ts} repressor, resulting in GAL4 activity and consequently UAS-reporter gene expression. To induce UAS-reporter gene expression in the ISCs, cultures were kept at 18°C and shifted to 29°C when adults were 3-5 days old. In all experiments midguts of females were analyzed. For co-expression esg\textsuperscript{FRT19A} experiments, virgin females carrying the X-linked UAS-N-RNAi or UAS-Esg\textsuperscript{GCT} insertions were crossed to males of the autosomal UAS-GFP-hnt stock. The male progeny of these crosses were subsequently crossed to esg\textsuperscript{FRT19A} virgin females.

The esg\textsuperscript{Xf81} technique

ISC lineages were marked using the esg\textsuperscript{Xf81} (flip-out) technique (Jiang et al., 2009). Briefly, the esg\textsuperscript{Xf81} stock carries the same elements as the esg\textsuperscript{FRT19A} stock (esg\textsuperscript{GAL4}, UAS-GFP, and tub\textsuperscript{GAL80\textsuperscript{ts}}) in addition to UAS-Flp (Fp recombinase) and a ubiquitous actin or tubulin based promoter designed to drive GAL4 expression but prevented from doing so by a CD2 cassette flanked by FRT sites (i.e. Act\textsuperscript{CD2}\textsuperscript{GAL4}). Shifting cultures from 18°C to 29°C is permissive to esg\textsuperscript{GAL4} expression of UAS-Flp, resulting in the removal or ‘flip-out’ of the CD2 cassette. This permanently activates Act\textsuperscript{CD2}\textsuperscript{GAL4} or tub\textsuperscript{GAL80\textsuperscript{ts}} within ISCs/EBs and their daughter cells. For hnt\textsuperscript{+} esg co-expression esg\textsuperscript{Xf81} experiments, virgin females carrying the X-linked hnt\textsuperscript{hnt} insertion were crossed to the autosomal UAS-esg line and resulting male progeny were crossed to esg\textsuperscript{Xf81} virgin females.

Mosaic analysis: His\textsuperscript{2Av-GFP}/His\textsuperscript{2Av-RFP} twin spots

Experiments involving His\textsuperscript{2Av-GFP}/His\textsuperscript{2Av-RFP} twin spots used Bloomington stock 30563, fully described as y w P[w[+mC]=His\textsuperscript{2Av-HT} AicGFP\textsuperscript{G-565T}\textsuperscript{1} P[y[+t+7.2]=hs\textsuperscript{FLP}] P[y[+t+7.2]=neo\textsuperscript{FRT19A}] P[w[+mC]=His\textsuperscript{2Av-mRFP}\textsuperscript{P1LL.1}/TM6B, Tb. For the generation of control and hnt\textsuperscript{hnt} mutant clones, males of the above stock were crossed to virgin females of y w hnt\textsuperscript{hnt} FRT19A; Dp(1;2)F4RDup\textsuperscript{+}. Tb\textsuperscript{+} female progeny of this cross that carry Dp(1;2)F4RDup\textsuperscript{+}, which includes wild-type copies of both the white (w) and hnt genes, were used as controls. Sibling progeny lacking the duplication were used to generate hnt\textsuperscript{hnt} mutant clones. For adult ISC clone induction, 3-5 day old adult female progeny were heat shocked twice for 40 min in a 37°C water bath, separated by a 1 h interval at room temperature. For larval AMP clone induction, progeny were heat shocked as described above when cultures contained wandering third instar larvae. For analysis of clones induced during larval stages (AMP clones), progeny eclosing either 5 or 6 days following heat shock treatment were dissected 1-2 days post-eclosion (cultures were maintained at 25°C following heat shock).

Mosaic analysis: esg\textsuperscript{MARCM} and NP6293\textsuperscript{MARCM} techniques

Somatic clones were recovered using modified MARCM techniques (Lee and Luo, 2001). Rather than using a ubiquitous GAL4 driver, esg\textsuperscript{GAL4} and NP6293\textsuperscript{GAL4} drivers were used to positively mark clones as either ISCs/EBs or ECs, respectively. For esg\textsuperscript{MARCM} experiments tub\textsuperscript{GAL80\textsuperscript{ts}}
hs-FLP FRT19A; esgGAL4 UAS-GFPnls/Cyo males were crossed to either
virgin females of the y w hntX831 FRT19A; Dp(1;2)4FRDup/+ or w y
hntX831 FRT19A; FRT19A/FM7 and y w FRT19A stocks. For NP6293-MARC
quantitative experiments tubGAL80+ hs-FLP FRT19A; NP6293 UAS-
GFPpos His2Av-RFP/Cyo males were crossed to the same y w hntX831
FRT19A; Dp(1;2)4FRDup/+ (ISC esg-MARC and AMP NP6293-
MARC) or y w hntX831 FRT19A/FM7 and y w FRT19A stocks (ISC
NP6293-MARC and AMP esg-MARC). For anti-Hnt NP6293-
MARC immunostaining experiment tubGAL80+ hs-FLP FRT19A;
NP6293 UAS-GFPpos/Cyo females were crossed to y w hntX831
FRT19A; Dp(1;2)4FRDup/+ males. All esg-MARC and NP6293-MARC
experiments used the heat shock induction regimes as described above for
His2Av-GFP/ His2Av-RFP twin spots, with the exception that adult heat
shock treatment was repeated for 3-5 consecutive days and midguts were
dissected 7 days following the final heat shock treatment.

Experiments comparing the behavior of hntX831 and hntlopos clones (Fig. S2) combined both esgGAL4 and NP6293-MARC techniques. Here
GFP-positive clones indicate either ISCs/EBs due to esgGAL4 expression
(small GFP-positive cells) or ECs due to GFP-positive clones indicate either ISCs/EBs due to
His2Av-GFPpos/Cyo cells were scored as large if the nuclear diameter was greater
than approximately 7 μm. The recovery of adult females carrying both esg-
and NP6293-MARC was achieved by crossing y w hntX831 (or hntlopos)
FRT19A; Dp(1;2)4FRDup/+ females to NP6293 UAS-GFPpos His2Av-
RFP/ Cyo males to recover y w hntX831 (or hntlopos) FRT19A/Y; Dp(1;2)
4FRDup/ NP6293 UAS-GFPpos His2Av-RFP males. These male
were subsequently crossed to tubGAL80 hsFLP FRT19A; esgGAL4 UAS-GFPpos
females. Clones were induced as described for the GFP/RFP twin spot
analysis. Following heat shock, flies were maintained at 25°C and
transferred onto fresh food every 2-3 days. Adult females of the desired
genotype y w hntX831 FRT19A/tubGAL80 hsFLP FRT19A; His2Av-RFP
NP6293 UAS-GFPpos esgGAL4 UAS-GFPpos were identified by the absence of the
Confusus phenotype associated with Dp(1;2)4FRDup in addition to using
His2Av-RFP as a marker post-dissection. Females were
dissected and midguts examined by live imaging confocal microscopy on
days 3, 7, and 14 after clone induction. Control clones were similarly
recovered by crossing y w FRT19A/Y; His2Av-RFP NP6293 UAS-GFPpos/+ males to
tubGAL80 hsFLP FRT19A; esgGAL4 UAS-GFPpos females.

Immunostaining
Immunostaining of adult midguts was carried out as described (Singh et al.,
2012). The following primary antibodies were used at the indicated
dilutions: mouse monoclonal anti-Hindsight (Hnt) 27B8 1G9 (1:25; from
H. Lipshitz, University of Toronto, Canada); mouse monoclonal anti-
Prospero (Pros) MR1A 1:100; DSHB); rabbit anti-Pdm1 1:1000; from
X. Yang, Zhejiang University, China); mouse monoclonal anti-Armadillo
(Arm) N2 7A1 1:100; DSHB); TRITC-conjugated goat anti-mouse and
TRITC-conjugated donkey anti-rabbit secondary antibodies (1:500; Jackson
Immunoresearch).

Microscopy
For experiments that did not require immunolabeling, midguts were
dissected in a drop of halocarbon oil (1:1 mixture of series 56 and series
700, Halocarbon Products Corp.), covered with a coverslip and imaged live.
Immunostained midguts were mounted in 70% glycerol in PBS containing
2.5% DABCO (Sigma-Aldrich). Confocal microscopy and image
processing were performed as previously described (Cormier et al., 2012).

Quantitative analysis
To quantify the esg-MARC and NP6293-MARC results shown in
Fig. 6 GFP-positive cells were counted for the entire length of each midgut.
Box plot diagrams were configured using Microsoft Excel, with whiskers
indicating the minimum and maximum values of the data set. To quantify
the percentage of large GFP-positive cells shown in Fig. S2, the large
GFP-positive cells and total GFP-positive cells were counted along the top
surface for the entire length of each midgut. To quantify EE frequency in
midguts of control and midguts containing hntlopos or hntX831 mutant clones
(shown in Fig. S2F) Pros-positive midgut cells within one field of view
(20× objective) of the midgut/hindgut junction were counted. A minimum of
five midguts was scored for each genotype. Standard deviation and P
values were calculated using Microsoft Excel.

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Competing interests
The authors declare no competing or financial interests.

Author contributions
B.L.B. and B.H.R. designed the experiments. B.L.B. performed live imaging,
immunostaining experiments, and quantitative analysis. C.M. performed live
imaging and immunostaining experiments. P.G.P. performed quantitative analysis
and assisted in preparation of the manuscript. N.A.B. performed immunostaining
experiments and assisted in experimental designs. All other live imaging and
immunostaining experiments were performed by B.H.R. B.L.B. and B.H.R. wrote
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Supplementary information
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Fig. S1. *Yet1* is preferentially expressed in mature EEs.
Anti-Arm immunostaining (blue) of the *Yet1* enhancer trap line showing GFP-positive (yellow) cells that are found as individual cells associated with reduced Arm relative to surrounding GFP-negative small cells. This serves as additional evidence that *Yet1* expression is specific to EEs. Scale bar represents 20 µm.
Supplementary information

Figure A-C: Images of control, hnt[308], and hnt[XE81] cells stained with large GFP+ and control cells.

Figure D-D’: Images of control, hnt[308], and hnt[XE81] cells stained with GFPnls and Pdm1.

Figure E: Bar chart showing the percentage of large GFP+ cells at 3 d ACI, 7 d ACI, and 14 d ACI for control, hnt[308], and hnt[XE81].

Figure F: Bar chart showing the number of Pros+ cells for control, hnt[308], and hnt[XE81].

Fig. S2. Quantitation of hntXE81 and hnt308 mutant clones generated in adult ISCs.

(A-C) GFP expression (yellow) under the control the ISC driver esgGAL4 as well as the EC driver NP6293 showing somatic clones generated within the ISC lineage. His2Av-RFP expression (blue) marks all cells. Shown are representative examples of EC differentiation (asterisks) as seen in control clones (A), clones of the hypomorphic allele hnt308 (B), and clones of hntXE81(C). Scale bars represent 20 µm.

(D) Anti-Pdm1 immunostaining of hnt308 midgut esg-MARCM clones (arrows, yellow) showing GFP-positive hnt308 mutant cells to be Pdm1-negative.

(E) The percentage of GFP-positive cells scored as large cells (ECs) up to 14 days after clone induction (ACI) remained constant for control clones, was reduced for hnt308 clones, and was negligible throughout the time course for hntXE81 clones (**P < 0.01).

(F) The average number of Prospero-positive cells per midgut in control midguts relative to midguts harbouring hnt308 or hntXE81 mutant clones shows no significant difference (P > 0.8).
Fig. S3. The NP6293 GAL4 driver is specifically expressed in ECs within the adult midgut.

(A, B) Confocal images of the adult midgut showing UAS-GFP\textsuperscript{nls} (yellow) expression under the control of GAL4-NP6293 with ubiquitous His2Av-RFP (blue) expression. The basal surface of the adult midgut (A) shows the lack of GFP\textsuperscript{nls} in all small cells, which correspond to ISCs/EBs and EEs. The medial region of the same midgut epithelium (B) shows strong GFP\textsuperscript{nls} in all large ECs, but also shows the lack of GFP in EEs – which can be identified morphologically as they, unlike ISCs/EBs, extend through the midgut epithelium to the lumenal surface (arrow).

(C, D) Shown are confocal images of the adult midgut with UAS-GFP\textsuperscript{nls} (yellow) and UAS-mCherry-moesin (blue) expression under the control of GAL4-NP6293 (C, merged image; D, single channel showing mCherry-moesin expression alone). This cross section view demonstrates that NP6293 expressing cells have greatly enriched actin at their apical (lumenal) surface, consistent with the brush border of differentiated ECs. These observations establish that NP6293 is a marker of ECs in the adult midgut. Scale bars represent 20 μm.