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Differential Gene Expression During Compensatory Sprouting of Dendrites in the Auditory System of the Cricket *Gryllus bimaculatus*

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Abstract

Neurons that lose their pre-synaptic partners due to injury usually retract or die. However, when the auditory interneurons of the cricket are denervated, dendrites respond by growing across the midline and forming novel synapses with the opposite auditory afferents. Suppression subtractive hybridization was used to detect transcriptional changes three days after denervation. This is a stage at which we demonstrate robust compensatory dendritic sprouting. While 49 unique candidates were downregulated, no sufficiently upregulated candidates were identified at this time point. Several candidates identified in this study are known to influence the translation and degradation of proteins in other systems. The potential role of these factors in the compensatory sprouting of cricket auditory interneurons in response to denervation is discussed.

Keywords

Suppression subtractive hybridization; Denervation; Invertebrate

INTRODUCTION

Within the nervous system, the shape and position of any neuron's dendritic arbor will influence its pool of potential synaptic partners. Historically, dendritic morphogenesis was thought to be predominantly determined by intrinsic genetic factors, and indeed, partial dendritic development has been shown to proceed in isolated neuronal cultures (Bartlett and Banker, 1984). However, experiments over the last two decades have shown that dendrites respond to a range of intrinsic and extrinsic factors (reviewed in McAllister, 2000; Scott and Luo, 2001; Kim and Chiba, 2004; Cline and Haas, 2008), and, importantly, that dendrites can be guided by the same proteins that influence axonal growth (Polleux et al., 2000; Whitford et al., 2002; Furrer et al., 2003). Furthermore, injury in mature neural systems appears to alter the expression of developmental guidance cues (Miranda et al., 1999; De Winter et al., 2002; Niclou et al., 2006), implying that the function of these cues may be recapitulated after injury.

One of the extrinsic factors that influence the maturation of dendritic form is pre-synaptic input. The synaptotrophic hypothesis states that synaptic inputs influence the elaboration of dendritic arbors (Vaughn, 1989), and there is good evidence that synaptic input is required for the normal development of dendritic structure in the mammalian brain (reviewed in Cline and Haas, 2008). The hypothesis further states that growing processes are stabilized by synaptic contacts. Consistent with this, removing pre-synaptic terminals usually destabilizes

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dendritic arbors, and a number of different types of post-synaptic responses have been reported (reviewed in Sherrard and Bower, 1998). The variety of observed responses is likely dependent on many factors such as age, cell type, and how profound the denervation is. However, it is clear that removing the predominant pre-synaptic input from developing neurons usually leads to negative effects on the post-synaptic neuron, including profound dendritic retraction (Benes et al., 1977; Deitch and Rubel, 1984) or even cell death (Parks, 1979; Born and Rubel, 1985; Sherrard and Bower, 1998; Baldi et al., 2000).

There are important exceptions to the typically negative response of developing dendrites to the removal of pre-synaptic input, or denervation, and studying them can inform our understanding of the factors that influence dendritic development, maintenance and plasticity (Hoy et al., 1985; Lakes et al., 1990; Pyapali and Turner, 1994). One of the more striking examples of a positive dendritic response to denervation is the compensatory growth of auditory interneuron dendrites after denervation in the cricket auditory system (Hoy et al., 1985; Schildberger et al., 1986). The auditory system of the cricket is crucial to its survival and reproduction. Crickets perform negative phonotaxis to the ultrasound pulses of predatory bats (>20 kHz), and female crickets perform positive phonotaxis to the calls of male conspecifics (5 kHz). The cricket auditory system consists of foreleg tympanal membranes which overlie the tympanal organ and whose auditory receptor neurons project *via* the tympanal nerve (nerve 5) into the first ganglion of the thorax, the prothoracic ganglion (reviewed in Ball et al., 1989). Auditory afferents convey acoustic information to several different types of interneurons (Fig 1A), most of which exist in mirror image pairs.

One auditory interneuron, ascending neuron-2 (AN-2) is used here to exemplify the denervation-induced changes in all auditory neurons examined (Schildberger et al., 1986). Normally, a majority of AN-2 dendrites grow up to but not over the midline of the prothoracic ganglia (arrow, Fig. 1A). Its dendrites receive auditory information from ipsilateral auditory afferents (gray “claw” in Fig 1A), which is then processed and relayed to the brain via an ascending axon (arrowhead, Fig. 1A). Denervation of the auditory interneurons can be achieved through unilateral removal of the prothoracic leg, which removes the auditory organ, and results in the degeneration of the auditory afferents (Fig 1B). Removal of the cricket ear in a first instar larval nymph induces denervated AN-2 dendrites to grow across the midline (arrow, Fig 1B), a boundary they usually observe, and form functional synaptic connections with the auditory afferents from the opposite ear by adulthood (Hoy et al., 1985; Schildberger et al., 1986). This compensatory synapse formation is remarkably precise, reinstating interneuron-specific threshold and intensity responses (Schildberger et al., 1986). This phenomenon may also explain how monaural females can recognize and roughly localize singing males (Huber et al., 1984). Since physiological recordings do not reliably detect auditory responses in the auditory interneurons of pre-adult nymphs, the rate of functional recovery can only be assessed in the adult. Acute denervation experiments in adults have indicated that deafferented auditory neurons also sprout new projections that are capable of forming new synaptic connections with the opposite afferents four to six days post-denervation (Brodfoehr and Hoy, 1988).

Given the robust nature of the compensatory growth of dendrites in the cricket auditory system, we have used suppression subtractive hybridization to ask which genes are differentially expressed after denervation. In the hopes of identifying candidates that might facilitate this positive growth response and synapse formation, we chose to investigate gene expression changes three days post-denervation in late-instar nymphs. Given that functional recovery has been documented in the adult as early as four days after denervation (Brodfoehr and Hoy, 1988), this three-day time-point was selected in order to correspond with the point at which dendrites were actively growing across the midline and perhaps beginning to form synapses. Semi-quantitative reverse-transcriptase-PCR was used to

independently confirm the differential expression of candidates after denervation. The role that candidate genes may play in the compensatory growth of cricket auditory interneurons is discussed.

RESULTS

In designing the subtractive hybridization experiment, we needed to choose the best developmental stage and time post-denervation to investigate transcriptional changes. Though the most robust anatomical changes are evident in adults that have been chronically denervated throughout the approximately 40 days of nymphal development (as shown in Fig.1), we assumed that the relevant transcriptional changes involved in the compensatory sprouting would be rapid and possibly short-lived. Therefore, we wished to harvest tissue only a few days after denervation. Unfortunately, because we have been unable to explore the anatomical results of denervation in young nymphs, first or second instar nymphs were not appropriate for this experiment. Since little is known about the development of auditory interneurons, such as when the ascending neuron axons project to the brain, it was unclear whether our inability to backfill young nymphs was a technical or developmental limitation. However, since we could easily detect a robust response to denervation of the auditory interneurons in older nymphs, we chose to use these animals for the subtractive hybridization experiment.

Compensatory dendritic growth in the cricket auditory system

In the past, published backfills were performed using Lucifer yellow or cobalt and then photographed or traced (Hoy et al., 1985; Schildberger et al., 1986). Backfills of ascending neuron-2 (AN-2) can also be successfully performed using biocytin and confocal microscopy (Fig 2). Compensatory dendritic growth is anatomically evident by 3 days post-denervation in antepenultimate nymphal instars. While the majority of AN-2 dendrites from control animals ($n = 3$ backfills) respected the midline at this developmental stage (Fig. 2A, B), a number of long dendritic branches from the deafferented AN-2 ($n = 4$ backfills) were seen growing across the midline three days after denervation (Fig. 2C). While we did not quantify aspects of dendritic projections about the midline, there was little variability in the results, and the rapid morphological changes we saw here are consistent with previous work demonstrating that compensatory sprouting in adult animals restores auditory function within four to six days after denervation (Brodfuehrer and Hoy, 1988). Though compensatory dendritic growth is obvious in adult animals as well, it does not appear quite as robust as the reorganization seen in pre-adult animals. For this reason, we chose to use antepenultimate instars for suppression subtractive hybridization experiments since vigorous dendritic growth across the midline was obvious at this stage (Fig 2C).

Differential gene expression during compensatory dendritic growth

Suppression subtractive hybridization (SSH) was used to identify differentially expressed genes throughout the prothoracic ganglia three days after denervation. We chose to examine the expression in whole ganglia, as opposed to halves or quadrants, because we made no *a priori* assumptions as to where the transcriptional changes would take place. While transcriptional changes in the auditory interneurons themselves were likely, changes in the expression of genes at the midline might be equally important and would be lost if the ganglia were halved or quartered before proceeding. Therefore, the genes expressed in whole prothoracic ganglia of three-day denervated antepenultimate instars were compared with those expressed in ganglia from control animals, which had received a tibial amputation (sparing the ear) three days previously. Both forward and reverse subtraction was performed in order to identify up- and downregulated transcriptional changes after

denervation. For both libraries, the white to blue colony ratio was 65:35, and 95% of the white colonies contained plasmids with inserts.

Differential screening was performed in order to identify differentially expressed candidates. To identify genes downregulated after denervation, 288 control-enriched clones were selected and arrayed on nylon membranes in duplicate. A representative example (blot C1) is shown in Figure 3. The left membrane was hybridized with probes made from the denervate-enriched library (Fig 3A), and the right was hybridized with probes made from the control-enriched library (Fig 3B). Clones that hybridized at least two-fold more strongly with the control-enriched probes, such as B3 and C8 (arrows, Fig 3B) than to the denervate-enriched probes (arrowheads, Fig 3A) were defined as positive “hits”. Differential screening of 288 clones from the control-enriched library yielded a total of 120 clones defined as positive hits. Conversely, to identify genes upregulated after denervation, 288 denervate-enriched clones were similarly screened (Fig 4). Surprisingly, none of the denervate-enriched clones showed a two-fold enhancement of hybridization to the denervate probes (Fig 4A) as compared to the control probes (Fig 4B), meaning that none of the 288 clones screened were defined as upregulated. Some of the denervate-enriched clones, such as A12, B12, D4 or H11 appeared to hybridize slightly more to the denervate-enriched probes than the control-enriched probes (Fig 4). However, since they do not meet the two-fold criteria, they were not defined here as upregulated.

The 120 control-enriched clones identified through differential screening were sequenced, then translated and analyzed using the NCBI website. A total of 49 unique candidates were identified as downregulated three days after denervation (Tables 1 and 2). Candidates were named first by blot (i.e. C1) and then by row and column (i.e. B3), as in C1B3. An arbitrary cutoff of $E = 0.001$ (expectation value) was applied, which resulted in 27 candidates being defined as having no significant hits (NSH, Table 2). One of the candidates, C3F11, showed high homology to cytochrome oxidase, and was the only mitochondrial candidate identified through our screen. A number of the candidates were represented by multiple clones, for example, two of the unknown candidates, C1D12 and C3H7, appeared multiple times (Table 2). Clones matching alpha amylase, trehalase, salivary lysozyme, and regucalcin also appeared multiple times (Table 1). For the sake of comparison, those clones matching database entries were divided into categories (Table 1) including factors involved in general enzymatic function, stress response, protein degradation, and protein synthesis, and their relevant prevalence was calculated (Fig. 5).

Candidates known to be involved in the production of mature proteins included serine carboxypeptidase, translation initiation factor 3 subunit-8 (eIF-3-S8), and ribosomal protein S8. Two identified proteins, ubiquitin-specific protease and pushover, are involved in the process of protein degradation. Ubiquitin specific proteases cleave ubiquitins from peptides, and E3 ubiquitin ligases, such as pushover, attach ubiquitin to proteins destined for degradation (Varshavsky, 1997). Candidates possibly involved in stress response included pathogenesis-related protein-5 (PR-5)-like protein and regucalcin (also known as senescence-marker protein 30), a calcium regulatory protein that may protect against oxidative damage in the brain (Son et al., 2006). A large number of enzymes were also identified. Two of the enzymes, alpha-amylase and trehalase, metabolize carbohydrates (Coimbra, 1966; Clifford, 1980), and likely regulate the supply of metabolic energy in the animal. Alcohol dehydrogenase has been shown to be one of the enzymes involved in the production of retinoic acid, a hormone well known to regulate gene expression and neuronal development in mammals (Duester, 1994). Hydrolytic enzymes and lysozymes are known to play a role in immunological defense in insects (Adamo, 2004; Schmid-Hempel, 2005).

In order to verify the accuracy of the screen in detecting differences in the SSH samples, six randomly selected control-enriched clones were used to make probes for virtual northern blots. A portion of the original unsubtracted control and denervate cDNA was run on an agarose gel, blotted, and probed with these six probes (Fig 6). For example, lanes B3 and C8 were hybridized with probes made from the clones highlighted by arrows in Figure 3. In all six cases, strong bands were seen only in unsubtracted control cDNA and not in unsubtracted denervate cDNA, indicating that the identification of differentially expressed sequences from within the subtracted library was accurate.

Independent confirmation of downregulated clones

Though the virtual Northern blots indicated that we could have confidence in the accuracy of the screen of the original tissue samples, it did not independently verify changes in expression of any of these candidates in additional tissue. To validate the differential expression in an independent tissue sample, the relative expression levels of eight of the identified candidates were independently characterized using semi-quantitative reverse-transcriptase PCR (SQ-RT-PCR). These eight candidates were chosen to represent a range of identified and novel candidates (Fig 7). We purposefully chose several of the candidates that were represented by multiple clones. The gene-specific primers used in these experiments (Table 3) gave only a single band at the optimal cycle number. As described in the methods, multiplex reactions were run in triplicate (technical replicates) on a single control and denervate sample of pooled ganglia. The housekeeping gene, β -actin, was used for normalization. The normalized control bands were defined as 1, and normalized denervate values were expressed as a percent of control expression (black bars, Fig 7B). Chi-square analysis indicated that the resulting values were not randomly distributed about “1”, but instead confirmed that the denervate expression values were non-randomly distributed below “1” ($p=0.038$).

Though actin is routinely used as a housekeeping gene, its reliability has been questioned (Ruan and Lai, 2007). For example, actin has been shown to vary by gender, anatomical area, and type of experimental manipulation (Derks et al., 2008). Importantly, the small variation we saw from reaction to reaction was bidirectional, indicating that it was unlikely that actin was differentially regulated after denervation. In addition, calculating non-normalized results for each candidate (gray bars, Fig 7B) did not change our overall conclusion that the population of candidates showed a non-random distribution below “1”.

DISCUSSION

The anatomical changes involved in the compensatory sprouting of dendrites in the cricket were first described over 20 years ago (Hoy et al., 1985) and have been explored in a number of additional studies since that time (Pallas and Hoy, 1986; Schildberger et al., 1986; Brodfuehrer and Hoy, 1988; Schmitz, 1989). The experiments presented here document profound anatomical changes by three days after denervation in antepenultimate instar nymphs and represent the first reported attempt to understand the molecular basis of this compensatory sprouting phenomenon in the cricket. Our subtractive hybridization results indicate that while downregulated candidates were readily identified, the upregulation of gene transcription may occur rarely if at all at this time point and possibly only in the small number of sprouting neurons.

Rapidity of dendritic changes after denervation

Morphological changes in the denervated AN-2 were evident three days after denervation. At this time point, many dendrites had grown across the midline, whereas control AN-2 dendrites typically respected the midline. The earliest reported morphological changes

previously observed in the cricket are at six days post denervation (Brodfehrer and Hoy, 1988; Schmitz, 1989), though functional recovery has been reported as early as four days after denervation in the adult (Brodfehrer and Hoy, 1988). It is unclear whether the discrepancy between our results and the timing of the previously published morphological changes in adult crickets is simply due to differences in developmental stages or sensitivity of more modern techniques. We suspect that the sensitivity of confocal microscopy, combined with the enhanced fluorescence and reduced photobleaching of newer fluorophores, reveal a much more detailed anatomical picture.

Exploration of other denervation paradigms reveals a variety of morphological and molecular changes that occur over a range of time courses. For example, the rate of denervation-induced dendritic growth in the locust auditory system appears similar to the cricket, with sprouting obvious within five days of denervation (Lakes et al., 1990). In the chick auditory brainstem, denervation induces dendritic loss that is anatomically evident within an hour of denervation (Deitch and Rubel, 1984) and more pronounced within seven hours (Sorensen and Rubel, 2006). Microglial migration to the site of injury is evident in leeches within 24 hours (Morgese et al., 1983). Likewise, molecular changes in both invertebrates and vertebrates, such as alterations in the expression of tubulin, microtubule-associated proteins, and proteoglycans are often evident within 24 hours of denervation (Kwak and Matus, 1988; Mostafapour et al., 2002; Wang et al., 2005; Schafer et al., 2008; Wang and Rubel, 2008). Interestingly, time course experiments indicate that these mRNA and protein expression patterns usually persist for many days or even several weeks post-denervation (Kwak and Matus, 1988; Luthi, 1994; Schafer et al., 2008; Wang and Rubel, 2008).

Given these results, we chose to examine transcriptional changes in pre-adult crickets three days after denervation. The three-day time point seemed a best compromise that would allow us to identify early and maintained transcriptional changes induced by the denervation. In addition, we hoped to catch transcriptional changes responsible for the initial stages of synapse formation that would likely be occurring in anticipation of the functional recovery evident in adults by four days post denervation.

Deciding in which developmental stage to perform these studies was also a challenge. Crickets are considered to be paurometabolous insects, since they go through a gradual, simple metamorphosis (Borror et al., 1976). As such, the larval nymphs are typically very similar to adults, except adults have wings and are sexually mature, and nymphs go through a series of molts in order to increase body size. Though denervation-induced dendritic sprouting does occur in the adult auditory system, the morphological changes are less robust than in the late instar nymphs. Thus, we chose the time point with the most robust response in the hopes of identifying the most influential candidates. It is entirely possible that the transcriptional changes responsible for compensatory growth during development (nymphs) is distinct from that in adult. However, given the similarities in the central nervous systems of adults and nymphs, we have assumed that the changes we identify in the nymphs will be generally applicable to the adult.

Transcriptional changes after denervation

We performed a suppression subtractive hybridization (SSH) experiment to identify transcriptional changes three days after denervation. We used both a forward and a backward subtraction strategy in order to identify both up- and downregulated genes. While 120 clones were identified as downregulated by at least two-fold within three days after denervation, screening 288 clones in the opposite direction did not detect any candidates that were upregulated by at least two-fold. While the absence of any sufficiently upregulated candidates was unexpected, the downregulation was, in fact, consistent with another

denervation study which detected extremely rapid reductions in protein synthesis within 30 minutes of denervation in the chick auditory system (Steward and Rubel, 1985).

Though the cricket auditory interneurons respond to denervation by growing, perhaps the remaining denervated and axotomized neurons in the ganglion respond to denervation in a more typical or “negative” fashion. Since these non-auditory neurons represent the vast majority of cells in the ganglion, they may be responsible for some portion of the downregulated candidates detected. In fact, the concept that the auditory interneurons are responding differently from most other denervated neurons is consistent with past work in the cricket that examined the effects of cercal ablation on the giant interneurons in the terminal ganglia. Unlike the auditory interneurons, giant interneurons in the cricket do not respond to denervation by concerted sprouting across the midline, but instead typically show reduced dendritic length after denervation (Murphey et al., 1975).

If selective upregulation of transcription occurred only in the small number of auditory interneurons in the prothoracic ganglia, upregulated candidate mRNAs would likely be of low abundance in the pooled mRNA from the entire ganglion. It is important to note that several clones showed hybridization patterns that were consistent with upregulation, though at a subthreshold level. A different experimental design strategy, such as halving or quartering the ganglia before processing, might enhance the ability to detect small changes in a small number of neurons. However, this strategy would effectively eliminate the detection of any relevant changes that might be occurring at the midline or in an area remote to the auditory cell bodies. We chose to make no assumptions about the location of the transcriptional changes when designing this experiment and instead used whole ganglia for the experiment. However, re-evaluating our screen using a lower threshold might result in the identification of rare transcripts that are upregulated. This strategy would also likely increase the number of false positives identified.

SSH is, in fact, an ideal technique to employ when trying to detect low-abundance transcripts, due to the normalization step which equalizes the abundance of cDNAs within the target population (Diatchenko et al., 1996). However, it might be necessary to screen at least 5,000–10,000 clones isolated from the SSH cDNA libraries in order to detect a reasonable proportion of the low abundance transcripts (Cao et al., 2001). Therefore, our initial screen of 288 clones may not have been sufficient to identify changes in rare transcripts. Alternatively, perhaps three days post-denervation was not the optimal time at which to detect transcriptional upregulation.

Many of the candidates identified through this experiment matched nothing in the NCBI database (Table 2). Though it is exciting to contemplate the identification of novel factors that may be involved in this compensatory sprouting phenomenon, there are several reasons why known proteins could have appeared as “no significant hits” in this study. First, the sequenced portion of the gene may have been in part of the gene that isn't well conserved among species. Obviously more sequence information could be gathered from the cricket for each of these clones, which could help identify these candidates. In addition, the sequences may have represented non-coding RNAs whose regulatory function has not yet been identified (Genikhovich et al., 2006). Or, finally, they may have represented novel genes with no known homologues. Given that we are working in an organism with little published sequence information and that crickets are separated by millions of years of evolution from other species for which genome sequences are available (Willmann, 2004; Buschbeck and Friedrich, 2008), more 5' and 3' sequence information will help clarify if these are truly novel genes or not.

A large number of enzymes were identified through this screen. We were most intrigued by a potential role for alcohol dehydrogenase in post-injury sprouting, since this enzyme is part of the multi-step conversion of retinol into retinoic acid. Retinoic acid is well known to influence neuronal development and regeneration in mammals (Maden, 2001; Rawson and LaMantia, 2006), though its role in invertebrate nervous systems has been less clear. However, recent evidence indicates that retinoic acid induces neurite outgrowth and growth cone turning in invertebrate neurons (Dmetrichuk et al., 2006). It is difficult to theorize how a downregulation in alcohol dehydrogenase, which could presumably change the amount of retinoic acid available, would create an environment more permissible to dendritic growth. However, since retinoic acid is a transcription factor, one could imagine various scenarios in which decreases in retinoic acid levels reduce the transcription of growth inhibiting factors.

Many of the enzymes identified, such as alpha-amylase, trehalase, and lysozyme, may be involved in immune defense, stress response, and energy metabolism. Though it makes some sense that these enzymes might be modulated after injury, we wouldn't have predicted that these enzymes would be downregulated. Many of these enzymes are known to be components of hemolymph (Jahagirdar et al., 1984; Adamo, 2004; Schmid-Hempel, 2005) though not necessarily neuronal tissue, so it isn't clear why they were identified through this neuronal screen. The prothoracic ganglion is, of course, surrounded by hemolymph, and one possibility is that some of these enzyme candidates represent contaminants that were somehow processed along with the ganglia. This also implies that we consistently dissected denervated ganglia with less contamination than control ganglia in two separate experiments (SSH and SQ-RT-PCR), both of which consisted of pools of individual ganglia. Since we can think of no systematic reason why contaminants would be biased towards control tissue, we have assumed that the downregulation of these enzymes within neuronal tissue is a result of denervation. However, given the lack of known neuronal functions for many of these enzymes, it is difficult to speculate on their potential roles.

A selection of eight candidates used for SQ-RT-PCR independently confirmed the general validity of our SSH results (Fig 7). Because this SQ-RT-PCR experiment consisted of a single sample of pooled ganglia for each condition it was not appropriate to confirm the quantitative extent of downregulation for any individual candidate. Instead, examining the relative expression levels of the group as a whole indicated that our candidates were non-randomly distributed below "1." We assume that repeated independent confirmation of the differential expression of all our candidates would both verify downregulated candidates and identify several false positives. The false positive rate of SSH is generally accepted to be approximately 5 to 10% (cf. Cao et al., 2001; Jones et al., 2006). However, in practice, published results indicate a low rate of near 10% and a higher rate of 50 or even 60% (Qin et al., 2003; Jones et al., 2006; Pinter et al., 2006). The rigor of the verification process influences the number of false positives, and some of the variability in these false-positive rates across studies is likely due to choice of technique used to independently confirm differential regulation. It would appear that it would be most informative to utilize a functional test in order to independently confirm the involvement of an identified candidate. Thus, in our future characterization of the candidates identified in Tables 1 and 2, we will supplement *in situ* hybridization and quantitative-PCR experiments with more functionally relevant tests such as examining the effects of RNA interference on the compensatory growth of dendrites.

Protein translation and degradation in compensatory dendritic growth

Several of the candidates identified in our SSH experiment could act to influence protein levels in a transcription-independent manner. These results hint that denervation may induce changes at the level of protein translation and degradation in addition to those seen at the transcriptional level. Exciting work over the last few years has elucidated an important role

for the proteasome system in synapse formation and synaptic plasticity (reviewed in Hegde and DiAntonio, 2002; DiAntonio and Hicke, 2004; Bingol and Schuman, 2005; Sutton and Schuman, 2005). The proteasome system has also been shown to influence the structure of developing neurons (Zhao et al., 2003). Though we had originally predicted that SSH would identify differentially regulated developmental guidance factors after denervation, transcriptional alterations in protein synthesis machinery or the ubiquitin proteasome system could specifically influence the levels of these types of proteins at the translational or post-translational level instead.

Our SSH identified two candidates, pushover and ubiquitin specific protease 14 (USP-14), that are involved in the process of protein degradation via the ubiquitin proteasome system (UPS). This system involves a series of enzymes that attach a small, highly conserved peptide called ubiquitin to the N-terminus of proteins (Varshavsky, 1997). Ubiquitinated proteins are then recognized by specific proteasomes and digested. Pushover is a large, highly conserved ubiquitin ligase with a calmodulin binding domain, suggesting that pushover function may be calcium sensitive (Xu et al., 1998). Interestingly, several E3 ligases have been shown to regulate the expression of molecules involved in midline patterning in developing neuronal systems, including the slit receptor, roundabout, and components of the netrin signaling pathway (Campbell and Holt, 2001; Myat et al., 2002; Ing et al., 2007). Also, examination of differential gene expression in the chick found that an E3 ubiquitin ligase, UBE3B, was strongly upregulated after noise trauma (Lomax et al., 2000). In light of our results, the UBE3B work suggests that regulation of UPS function via E3 ubiquitin ligase transcriptional changes may be an important regulator of injury response in auditory systems.

Translational control of proteins can be rapid and profoundly influential as well. For example, rapid and local protein synthesis is necessary for the proper directional growth of developing axons. Guidance factors expressed during development, such as netrins and semaphorins, have been shown to activate translation initiation factors, which result in a rapid increase in local protein synthesis levels which then influence axonal growth (Campbell and Holt, 2001). Our SSH screen identified several proteins that could influence protein translation, including a translation initiation factor, which could potentially alter the way growing dendrites respond to existing guidance factors. In fact, there is evidence that injured pheochromocytoma (PC12) cells regenerate rapidly in a transcription-independent manner (Twiss et al., 2000). These results underscore the fact that protein synthesis levels may be changing even though no alteration in transcription is detectable.

The SSH experiment presented here was a first step in understanding the transcriptional changes in individual genes or groups of genes that might influence the unusually robust compensatory sprouting seen in the cricket auditory system. Some of the transcriptional changes identified through this experiment indicate that more profound and specific changes may be occurring at the protein level. If the compensatory growth in this system were driven by posttranslational protein regulation or modification, a proteomics screen would be a more effective way of identifying specific changes. We are in the process of performing a two-dimensional differential gel electrophoresis experiment that is better suited to identify differentially regulated or modified proteins. It is our hope that what we learn about this unusual and robust injury response in the cricket will expand our understanding of the control of dendritic growth and plasticity, and that this information may be applicable to the growth of dendrites in other neuronal systems.

EXPERIMENTAL PROCEDURES

Animals

A colony of Mediterranean field crickets, *Gryllus bimaculatus* (originally supplied by Dr. Ron Hoy, Cornell University), was maintained on a 12:12 light/dark cycle at 28°C and 40–60% relative humidity. Crickets were fed commercial cat chow and drinking water *ad libitum*. Moist soil was offered for egg laying. Only crickets from this breeding colony were used for the described experiments.

Denervation and tissue collection

All crickets used in this study were treated identically throughout the experiment, with the exception of the type of surgery. Surgeries and tissue collections were performed side by side. Tissue was collected from crickets in the antepenultimate instar stage, which is the stage at which wing buds are first evident. Unilateral denervation of the central auditory neurons was accomplished by amputating the right prothoracic leg (foreleg) at or above the tibial femoral joint. Control crickets used for SSH were amputated at the right tarsal-tibial joint, leaving the developing auditory organ intact. All crickets used in this study were cooled to 4°C prior to amputation and tissue collection. After surgeries were performed, crickets were grouped by condition (control or denervate) and housed for three days in small, shoebox sized containers with adequate food, water and hiding places. Three days post-amputation, the prothoracic ganglia were dissected in RNase-free PBS, frozen immediately in liquid nitrogen, and stored at –80°C until processing. Control and denervated samples were amputated and dissected in parallel.

For backfill experiments, two types of denervations were performed. In the first, chronically amputated crickets were used to generate the schematic in Figure 1. These crickets had legs removed initially during the first nymphal instar. These crickets were checked every few days and any regenerating blastema were removed. Once these animals matured into adults, AN-2 was backfilled (see below). The second type of backfill experiment was used to demonstrate the anatomical changes three days after denervation in antepenultimate instar nymphs (Figure 2).

Biocytin backfills of AN-2 and microscopy

Anesthetized crickets were immobilized by pinning and their thoracic cavity was opened. Approximately half to three-quarters of the axons in the appropriate neck connective were removed, leaving intact the medial-ventral portion containing the axon for ascending-neuron 2 (AN-2). AN-2 was backfilled in the animal by retrograde uptake of 4% biocytin (Sigma) dissolved in 50 mM NaHCO₃. Animals were maintained at 4°C for 18–22 hours. Ganglia were dissected and fixed in 4% paraformaldehyde (Electron Microscopy Sciences, Hartfield, PA, USA), then treated with 0.5% triton and a 1:400 dilution of Alexafluor 488 streptavidin (Invitrogen). Tissue was rinsed, dehydrated, and mounted in methyl salicylate. Images were collected using a Zeiss LSM 510 META and a 40× Plan Neofluor objective (1.3 NA, Zeiss, Thornwood, NY, USA). All images shown are projections of multiple optical sections, and the number of sections for each presented image was included in the figure legends. The midline was determined using three criteria, low power images were first used to roughly find the midline as defined by the point between the anterior and posterior intraganglionic connectives. Then, this general location was influenced by the characteristic point between the major L-shaped dendrite and the connective leading to the soma. Finally, viewing images at high gain made the autofluorescent cells of the midline evident, and the midline location was confirmed.

Confocal images were also used to create the schematic in Figure 1. Briefly, one example of a control AN-2 and one example of a chronically denervated AN-2 were created from projections of multiple optical sections (151 and 141 optical sections respectively), printed, and placed on a light box. Individual processes were then traced and a rough schematic outline of the ganglia was placed appropriately around each traced neuron. A backfill of nerve 5 was imaged with the confocal microscope and, as above, used to trace the extent of the auditory neuropil. Though the individual (HWH) doing the tracing was not informed of the identity of each cell, the anatomical differences are such that the tracing could not realistically be performed blindly.

Suppression subtractive hybridization

Total RNA was purified, in parallel, from 10 control prothoracic ganglia (right tibia removed three days prior) and 11 denervated prothoracic ganglia (unilaterally amputated above tibial/femoral joint three days prior) using RNAPure Reagent (GenHunter, Nashville, TN, USA) according to the manufacturer's protocol, and the subtractive hybridization was performed (Clontech). Briefly, amplified double-stranded cDNA was prepared for each condition from 300 ng total RNA as described in the SMART PCR cDNA Synthesis Kit (Clontech). First strand cDNA was diluted five-fold, and 1 µl of the dilution was used for PCR amplification (18 cycles). SMART-amplified cDNA was digested by *RsaI* endonuclease. Suppression subtractive hybridization was performed in both directions (forward subtraction: 3-day denervate ganglia minus control ganglia, which will be referred to as denervate-enriched; and reverse subtraction: control ganglia minus 3-day denervate ganglia, which will be referred to as control-enriched). For each direction, two tester populations were created by ligating different suppression adaptors (Adaptor 1 or 2R). Each tester population was hybridized with 30-fold excess driver cDNA, and the two tester populations were hybridized together. Subtracted cDNA was amplified by primary PCR (25 cycles) and secondary (nested) PCR (10 cycles). The subtracted cDNA samples obtained by secondary PCR (control-enriched cDNA and 3-day denervate-enriched cDNA) were used for library construction. 40 ng of purified cDNA was cloned into the pAtlas vector and transformed into *E. coli*.

Differential screening of subtracted libraries

288 randomly picked white colonies from the control-enriched library and 288 randomly picked white colonies from the 3-day denervate-enriched library were used for differential screening. *E. coli* cultures were grown in 96-well format in 100 µl Luria broth with ampicillin (75 µg/ml) media for six hours at 37° C. Plasmid inserts were amplified with F1S and R1S primers (5'-AGTACGCTCAAGACGACAGAA-3' and 5'-AAAGCAGTGGTAACAACGCAG-3', respectively), and 100 ng of PCR-amplified insert was arrayed onto duplicate nylon membranes and hybridized with ³²P-labeled subtracted control and subtracted 3-day denervate cDNA probes. Blots were imaged with a phosphorimager, and clones were considered positive if there was at least a two-fold enhancement of probe binding as compared to its relevant duplicate.

Sequence analysis of candidates

Plasmids from 120 differentially expressed clones were purified and the inserts were sequenced using M13dir or M13rev plasmid primers. Sequence results were analyzed using BLAST web service at NCBI using the tblastx feature (<http://blast.ncbi.nlm.nih.gov/Blast.cgi> accessed November, 2008). A threshold E value of 0.001 was used to determine the identity. Those candidates with larger E values were labeled as “no significant hits” and listed separately (Table 2). When possible, a candidate's identity was defined as that hit with the lowest E-value, from the class insecta, and that was annotated (Table 1).

Virtual Northern blots

A portion of the original, unsubtracted SMART- control and denervate cDNAs (used above for SSH) were resolved on agarose gels and transferred to Hybond-N membranes (GE Healthcare Biosciences Corp, Piscataway, NJ, USA). Membranes were hybridized with ³²P-labeled probes prepared from six control-enriched clones randomly selected from the first blot (C1E9, C1F4, C1H1, C1B3, C1C8, C1E1).

Semi-quantitative RT-PCR

Tissue was dissected and pooled from an independent group of 33 control (tibia removed) and 32, 3-day denervate prothoracic ganglia (leg below tibial/femoral joint removed). Crickets for this experiment were handled in an identical manner as for the SSH experiments. RNA was purified using RNeasy Pure Reagent (Qiagen), DNaseI-treated with the MessageClean Kit (Qiagen), and quantified by an ND-1000 (nanodrop) Spectrophotometer (Thermo Fisher Scientific, Wilmington, DE, USA). All samples were processed in parallel. Single-stranded cDNA was made from 3 µg total RNA using the Superscript III First-Strand Synthesis System for RT-PCR (Invitrogen). To check for genomic contamination, a “no-RT” control was included for each sample. The first-strand synthesis reaction was diluted in order to allow reproducible and accurate aliquots (5 µl) to be removed for subsequent PCR reactions (Pernas-Alonso et al., 1999). Gene specific primers (Table 3) for eight candidates as well as for *Gryllus bimaculatus* β-actin (accession #DQ630919) were designed using Primer 3 (Rozen and Skaletsky, 2000). Pilot experiments indicated that these were good primer pairs to use because single well-defined bands were amplified. For each primer pair, a cycle series was run on control cDNA in order to determine the optimal cycle number, defined as producing a product strong enough to detect on an agarose gel, but still in the pre-plateau, exponential range. Multiplex PCR reactions, using candidate-specific primers and β-actin-specific primers, were run in triplicate at the optimal cycle number on four different cDNA templates: 1) control, 2) denervates, 3) control “no-RT,” and 4) denervate “no-RT.” Amplified products were run on a 2% agarose gel with ethidium bromide and digitally photographed using a Bio Doc-It Imaging System transilluminator (Ultra-violet Products, Upland, CA, USA). Digital images were saved for quantification.

Quantification of SQ-RT-PCR

Band intensity was measured using LabWorks software (Ultra-Violet Products). Background-subtracted intensity values were obtained for each band, and either used as is, or were then normalized based on the measured β-actin band background-subtracted intensities for each lane. The normalized control values were defined as one, and the denervate values were expressed as a proportion of control for each primer set. The non-normalized data are included and are presented in the same manner. Percent error was calculated for each triplicate by dividing the SEM by the average. Standard error propagation was applied. A one-sided Fisher's exact test was used to assess significance.

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Figure 1. Chronic denervation results in profound reorganization of auditory interneuron dendrites in the cricket

A) Traced reproduction of a confocal image of a control AN-2 backfilled with biocytin in the adult cricket prothoracic ganglion. Bilateral auditory afferents are shown in light gray and arborize in a “claw-shaped” end. The soma is contralateral to the main dendritic arbor and relevant auditory afferents, and a majority of the AN-2 dendrites respect the midline (arrow). The axon carries auditory information to the brain (arrowhead). B) Auditory interneurons can be denervated by amputation of the leg, which leads to degeneration of the auditory afferents (X). Denervation throughout the nymphal instars of the animal results in a profound reorganization of AN-2 dendrites in the adult. A large proportion of the dendrites have crossed the midline and arborize in the contralateral auditory neuropil. Scale bars approximately 100 μm .

Figure 2. Dendritic reorganization is evident three days after denervation in antepenultimate instars

Confocal images of biocytin-filled AN-2. A) Biocytin backfill of a control AN-2 (projection of 73 optical sections) reveals typical dendritic morphology. Midline is to the right of the image. B and C are images of the midline region of AN-2 and, for clarity, are presented as a projected subset of the sections that make up the whole volume of each cell. B) Biocytin backfill of control AN-2 (40 optical sections) shows dendrites growing up to (arrows), but not over the midline (dotted line). C) Biocytin backfill of AN-2 denervated on the left side (70 optical sections) shows obvious midline crossing of dendrites towards the right side (arrows). Scale bar = 20 μm for all images.

Figure 3. Example of the differential screening of the control-enriched library

Plasmid inserts from the control-enriched library were amplified and arrayed on duplicate nylon membranes (A and B). A) The left membrane was hybridized with radiolabeled probes made from the denervate-enriched cDNA pool. B) The right membrane was hybridized with radiolabeled probe made from the control-enriched cDNA pool. Arrows in B indicate two examples of clones for which the control-enriched probes hybridized more strongly than did the denervate-enriched probes (arrowheads in A) indicating downregulated candidates.

Figure 4. Example of the differential screening of the denervate-enriched library

Plasmid inserts from the denervate-enriched library were amplified and arrayed on duplicate nylon membranes (A and B). A) The left membrane was hybridized with radiolabeled probes made from the denervate-enriched cDNA pool. B) The right membrane was hybridized with radiolabeled probe made from the control-enriched cDNA pool. There were no examples of probes made from the denervate-enriched cDNA pool (A) hybridizing at least two-fold more than did the control-enriched probes (B).

Figure 5. Distribution of the candidates according to their putative function

Functions were assigned, as detailed in Tables 1 and 2, based on the results of BLAST searches. 55% of candidates had no match in the database below $E = 0.001$ and were defined as no significant hits. 31% of the candidates encoded enzymes of a variety of functions. The remaining 14% of candidates fell into three categories: stress response, protein synthesis, and protein degradation.

Figure 6. Virtual northern blots were used to confirm the validity of the screen process

Of the control-enriched clones determined to be differentially expressed, six were randomly selected from the first differential screen and used to make ^{32}P -labeled probes. The original unsubtracted control (C) and denervate (3D) cDNAs were resolved on agarose gels and blotted onto nylon membranes. The binding of specific probes (labeled at the top of each blot) to the control but not denervate lanes is an indication of the accuracy of the original subtraction.

Figure 7. Semi-quantitative RT-PCR analysis exploring expression in an independent sample
 A) Example agarose gel of SQ-RT-PCR experiment. Pairs of primers for candidate C2A4 and actin were combined in multiplex reactions. Each reaction was set up in triplicate, and lanes are labeled with the template used: “C” control, “D” denervate, “no-RT C,” control RNA to which no RT was added, and “no-RT D,” denervate RNA to which no RT was added. B) The expression level of the denervate lanes are expressed as a proportion of the normalized control expression and averaged for each triplicate. Black bars represent values normalized by the within-reaction actin, and gray bars represent non-normalized values. The error bars are the % error (SEM as a percent of the average). Chi-square analysis confirms that these values are non-randomly distributed below one ($p=0.038$).

Table 1
Twenty-two candidates identified as downregulated three days after denervation were homologous to genes in other species and can be broadly grouped

Candidates are listed in groups, which are identified on the left. The clone number for each candidate identified is given (second column). In cases where the sequences of multiple clones overlapped, a representative clone number was listed and the number of matching clones was included in parentheses. Candidates in bold were used in the semi-quantitative RT-PCR experiment (Fig 7). The *Gryllus bimaculatus* sequences we identified have been submitted to GenBank, and their accession numbers are listed in the “Gb Accession #” column. In order to identify each of these candidates, the full sequences were blasted using the “tblastx” feature of the NCBI database against the nucleotide collection (nr/nt) database, and the best annotated insecta match was identified when possible. Thus, for each candidate the “description” of the best match, the E-value for the best match, the accession number of the best match, the predicted percent identity (identical amino acids) and predicted percent similarity (similar amino acids) to the best match, and the species of the best match are given. The only mitochondrial match was C3F11 (cytochrome oxidase) and this is indicated with a “(mit)”. Candidates whose E-values were greater than 0.001 were defined as “NSH” (no significant hits) and included in Table 2.

Category	Representative Clone (#seq)	<i>bimaculatus</i> Accession #	size (bp)	Best Match Description	E-value	Best Match Accession #	% Identity % Similarity	Species of Best Match
Enzyme	C2A4	GE653135	334	alcohol dehydrogenase	4.00E-24	NM_001101887.1	53/75	<i>Bos Taurus</i>
	C1B3 (14)	GE653162	633	alpha-amylase	1.00E-33	AF527876.1	78/89	<i>Anthonous grandis</i>
	C1H8	GE653138	128	alpha-amylase	1.00E-08	AF208002	56/75	<i>Diabrotica virgifera virgifera</i>
	C2A12 (8)	GE653128	332	alpha-amylase	4.00E-33	AF467104.2	57/72	<i>Megaselia scalaris</i>
	C2A7 (2)	GE653152	418	alpha-amylase	3.00E-38	DQ355516	68/79	<i>Blattella germanica</i>
	C3C12 (2)	GE653137	246	alpha-amylase	7.00E-26	EF600049.1	71/76	<i>Helicoverpa armigera</i>
	C3F10 (9)	GE653155	549	alpha-amylase	7.00E-62	DQ355516.1	74/84	<i>Blattella germanica</i>
	C3C10	GE653136	247	beta-1,4-endoglucanase	7.00E-14	AJ511343.1	69/81	<i>Mastotermes darwinensis</i>
	C1F1 (6)	GE653141	175	<i>bimac.</i> EST: lysozyme	3.00E-52	AY226458	63/78	<i>Gryllus bimaculatus</i>
	C3F11	GE653156	543	cytochrome oxidase I (mit)	6.00E-75	GPU88332	91/93	<i>Gryllus pennsylvanicus</i>
	C2B8	GE653134	272	oxidoreductase	5.00E-05	XM_001844134.1	55/78	<i>Culex quinquefasciatus</i>
	C1A6 (10)	GE653118	461	salivary lysozyme	2.00E-35	AY226458.1	63/76	<i>Anopheles stephensi</i>
	C1A5 (2)	GE653117	442	trehalase	6.00E-4	AJ512337	47/67	<i>Caenorhabditis elegans</i>
	C2H7 (2)	GE653127	368	trehalase	3.00E-27	NM_001112671.1	47/67	<i>Apis mellifera</i>
	C3H9	GE653149	284	trehalase	3.00E-20	D11338	59/75	<i>Tenebrio molitor</i>
Protein Degradation	C2F2	GE653126	505	pushover	3.00E-46	AF096896	53/74	<i>Drosophila melanogaster</i>
	C1H4	GE653145	290	ubiquitin specific protease	2.00E-26	XM_001897165	76/88	<i>Brugia malayi</i>
Protein Synthesis	C3D1	GH160416	222	ribosomal protein S8	6.00E-23	EF638994.1	86/92	<i>Triatoma infestans</i>
	C1G9	GE653143	311	serine carboxypeptidase	9.00E-33	AY962406	65/78	<i>Sitodiplosis mosellana</i>
	C3C5	GE653131	335	translation initiation factor 3	9.00E-40	XM_001842255	71/89	<i>Culex quinquefasciatus</i>
Stress Response	C1A9	GE653119	284	Pr-5-like protein	2.00E-23	AY863030	77/82	<i>Lysiphlebus testaceipes</i>
	C3F3 (4)	GE653160	413	regucalcin	3.00E-31	NM_205746	53/71	<i>Danio rerio</i>

Table 2
Twenty-seven candidates did not match any database entries and are defined here as “no significant hits.”

Those candidates whose E-values were greater than 0.001 were labeled as “NSH” (no significant hits) and are listed here. The clone number for each candidate identified is given (first column). In cases where the sequences of multiple clones overlapped, a representative clone number was listed and the number of matching clones was included in parentheses. Candidates in bold were used in the semi-quantitative RT-PCR experiment (Fig 7). The *Gryllus bimaculatus* sequences we identified have been submitted to GenBank, and their accession numbers are listed in the “Gb Accession #” column. The size of each clone is given.

Representative Clone (# seq)	Gb Accession #	size (bp)
C1C6	GE653142	322
C1C12 (3)	GE653150	209
C1D1	GE653166	195
C1D12 (8)	GE653120	565
C1D9	GE653158	433
C1G3	GE653129	465
C1G5	GE653132	441
C1H1	GE653122	155
C2A8	GE653121	233
C2B6	GH160417	521
C2C2	GE653157	188
C2C5	GE653133	220
C2D1 (2)	GE653154	586
C2D5	GE653123	372
C2D9	GE653153	291
C2E3	GE653124	319
C2F6	GE653140	330
C3A9	GE653159	277
C3B2	GE653139	199
C3B6 (2)	GE653144	535
C3C4 (5)	GE653130	308
C3D6	GE653165	372
C3E8	GE653163	340
C3F1	GE653164	275
C3F6	GE653161	250
C3H1	GE653146	278
C3H7 (8)	GE653148	317

Table 3
Gene-specific primers used for SQ-RT-PCR experiment

Pairs of gene specific primers for each of eight candidates tested amplified single bands at the optimal cycle number. Primers against *Gryllus bimaculatus* β -actin were used in each reaction for normalization.

	Left Primer	Right Primer
C1A9	AGAGTGCCTG TCTTGCCTTC	TTCCAGAAAA AGAGGTGCA G
C1B3	GGAGCTCTTC ACACCCTCAG	TACCCGGCTG TGTCTACTC
C1G5	TGCCCAAAT TATACTTAAC AAAGA	TGTGTGTTAT TAGACGTGTT CGTG
C1H4	TACAGCCCCG CTGCTTTTAC	GGGACGGTCT AGCTCTAGTG G
C2A4	AGGTACGAGC GCCCTAGATG	GGCAAATTTT GTAGCTGCTT G
C2D5	ATCTTCTCTT TGGCGCATGT	CCATTGGTGA TATTCTTGT GC
C2F2	CTGCGCTTTG CCCAGGAGAA	CGAGGCCCTG ATCTTGTCGT GTT
C3E8	TGCTCACTCC AGTTTGGTTT C	GCAGGTACCC ATTTTGTTGA C
β -Actin	CCTGGCATTG CTGATAGGAT	CCTGCTTGGA GATCCACATT