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# Regenerating the central nervous system: how easy for planarians!

Francesc Cebrià

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**Abstract** The regenerative capabilities of freshwater planarians (Platyhelminthes) are very difficult to match. A fragment as tiny as 1/279th of the planarian body is able to regenerate a whole animal within very few days [Morgan. Arch Entw 7:364–397 (1898)]. Although the planarian central nervous system (CNS) may appear quite morphologically simple, recent studies have shown it to be more complex at the molecular level, revealing a high degree of molecular compartmentalization in planarian cephalic ganglia. Planarian neural genes include homologues of well-known transcription factors and genes involved in human diseases, neurotransmission, axon guidance, signaling pathways, and RNA metabolism. The availability of hundreds of genes expressed in planarian neurons coupled with the ability to silence them through the use of RNA interference makes it possible to start unraveling the molecular mechanisms underlying CNS regeneration. In this review, I discuss current knowledge on the planarian nervous system and the genes involved in its regeneration, and I discuss some of the important questions that remain to be answered.

**Keywords** Planarian · Central nervous system · Neural genes · Regeneration · Axon guidance · Neurotransmission

## Introduction

Freshwater planarians display a biological feature that has fascinated scientists since it was first reported (Pallas 1766): They can regenerate whole animals from tiny pieces of their bodies. Although the ability to regenerate is a phenomenon found to a greater or lesser extent in many metazoans (Sánchez Alvarado 2000), very few species can compete with planarians. Planarians were defined as “... almost immortal under the edge of the knife” (Dalyell 1814), and in the late 1890s, authors such as Randolph (1897) and Morgan (1898) published several papers describing the amazing regenerative abilities of these animals. In the first half of the twentieth century, several groups carried out experiments to address issues such as how the regenerative blastema is formed, the distribution of neoblasts (planarian totipotent stem cells) in intact and regenerating animals, whether inductive or inhibitory mechanisms are involved in regeneration, or the role of the nervous system in the regenerative process (for a review of the classical literature, see Brondsted 1969). However, some of these basic questions still remain to be satisfactorily answered.

Research on planarian regeneration has been revitalized in the last 10 years by the application of modern molecular tools (Agata et al. 2003; Agata and Watanabe 1999; Baguña 1998; Newmark and Sánchez Alvarado 2002; Reddien and Sanchez Alvarado 2004; Saló 2006; Sánchez Alvarado and Kang 2005). These new tools include whole-mount immunostaining and confocal microscopy (Cebrià et al. 1997; Reuter et al. 1995b; Reuter et al. 1996a), whole-mount in situ hybridization (Umesono et al. 1997), RNA interference (RNAi; Newmark et al. 2003; Reddien et al. 2005; Sánchez Alvarado and Newmark 1999), BrdU labeling of neoblasts (Newmark and Sánchez Alvarado 2000), expressed sequence tag (EST) collections (Ishizuka

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et al. 2007; Sánchez Alvarado et al. 2002; Zayas et al. 2005), and a genome sequencing project (further information on the white paper proposal can be obtained from <http://www.genome.gov/12512286>). The use of these tools should allow us to improve our understanding of the regenerative process in planarians.

Unlike most invertebrate and vertebrate animals, planarians can regenerate a complete, functional central nervous system (CNS) in only a few days. Although, at first sight, planarians and their nervous system may appear simple, a closer look reveals greater complexity. This complexity is found at many levels: (1) At the cellular level, we find unipolar, bipolar, and multipolar neurons; (2) at the structural level, different types of vesicles and release sites have been described along with a wide range of neuroactive substances, including serotonin, dopamine, noradrenaline, and several neuropeptides (McVeigh et al. 2005; Reuter and Gustafsson 1995; Ribeiro et al. 2005); and finally, (3) at the gene level, the first high throughput analyses of the planarian CNS have shown its complexity in the number and degree of conservation of neural specific genes (Mineta et al. 2003), as well as in the molecular compartmentalization of the planarian CNS (Cebrià et al. 2002b; Nakazawa et al. 2003; Umesono et al. 1999). Despite this weight of accumulated knowledge and the newly available molecular markers, we are still some way from fully understanding how the planarian CNS is regenerated. After cutting a planarian into, say, ten pieces, it is remarkable to see how, in only a few days, each of these fragments regenerates a new head, where the new photoreceptors are easily distinguished and in which a new brain differentiates. However, although this process seems very easy for a tiny planarian fragment, it involves many events that have yet to be fully elucidated, such as how neoblasts become committed to a neural fate, how the new nervous system is rewired, how the regenerated nervous system integrates with the preexisting CNS, and how the nervous system itself influences planarian regeneration.

In this review, I will first discuss previous research characterizing the planarian nervous system at different levels and recent studies that have identified numerous planarian neural genes. I will then describe what we have learned so far about planarian neural regeneration by using these new markers and modern methods. Finally, I will discuss the available data on the influence that the nervous system may have on planarian regeneration.

### Structure of the planarian nervous system

Freshwater planarians (Platyhelminthes) are among the simplest animals possessing a centralized nervous system. For a long time, Platyhelminthes were thought to occupy

a basal position in metazoan phylogeny, and that led many scientists to focus on the “primitive” CNS of these organisms. In recent years, however, the phylogenetic position of Platyhelminthes has been reconsidered, and it is now widely accepted that they occupy a less basal position and are included within the Lophotrochozoan clade (Baguña and Riutort 2004; Philippe et al. 2005; Ruiz-Trillo et al. 2002). However, the exact relationship of the Platyhelminthes with the other Lophotrochozoan phyla remains to be elucidated. Irrespective of the final phylogenetic position of Platyhelminthes, freshwater planarians display several features that make them interesting for scientists, the most popularly known being their remarkable regenerative capacity.

The planarian CNS consists mainly of an anterior brain or cephalic ganglia and a pair of ventral nerve cords (VNC) that run along the length of the animal (Fig. 1). Usually, the brain is bilaterally symmetrical, and its shape is frequently correlated with the shape of the head. The two halves of the brain are connected by one or more commissures, depending on the species (Agata et al. 1998; Cebrià et al. 2002c; Hyman 1951; Lentz 1968; Reuter et al. 1995b; Reuter et al. 1996a; Rieger et al. 1991). The brain is organized as a central neuropil surrounded by an outer layer of neuronal cell bodies (Morita and Best 1965; Morita and Best 1966; Oosaki and Ishii 1965), and it displays a typical spongy texture, as it is traversed by muscles and processes from secretory cells (Baguña and Ballester 1978). A large number of different sensory nerves leave the brain and connect with the margins and sensory organs of the head (Hyman 1951; Rieger et al. 1991). Thus, MacRae (1967) described sensory nerve endings within the epithelium of the auricles of *Dugesia tigrina*. Because those cells looked similar to vertebrate olfactory cells, it was suggested that they could function as chemoreceptors (MacRae 1967). The planarian brain lies on top of the VNC that run below it (Agata et al. 1998; Cebrià et al. 2002c; Okamoto et al. 2005). In some cases, these cords continue anterior to the brain (Hyman 1951). Both at the molecular and morphological level, the brain and VNC can be considered as independent structures (Agata et al. 1998; Cebrià et al. 2002c; Okamoto et al. 2005). Although several pairs of nerve cords are observed (including dorsal and lateral cords) in lower Platyhelminthes and marine planarians, in most freshwater planarians, only the ventral cords are present (Hyman 1951). Based on comparisons of the nervous system in different groups of Platyhelminthes, it has been suggested that there is an evolutionary tendency toward a reduction of the number of nerve cords (Reisinger 1972). Along the length of the planarian VNCs, small clusters of neurons are grouped in more or less regularly spaced ganglia that, similar to the brain, have a spongy structure (Baguña and Ballester 1978); from these ganglia,

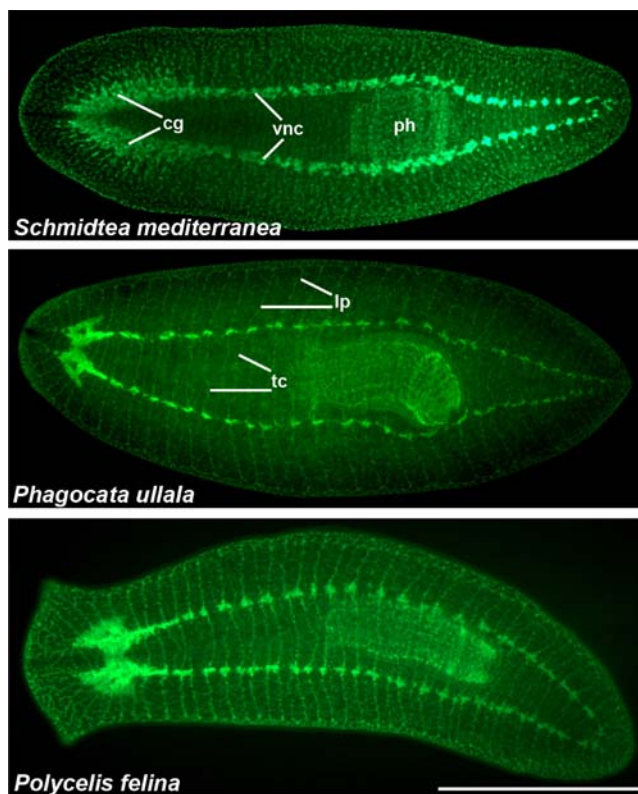
transverse commissures extend connecting both VNCs and forming an orthogon (Fig. 1). Also, lateral nerves extend from the VNC and form bundles that branch near the edge of the animal and are continuous with a fine marginal plexus representing the submuscular nerve plexus (Lentz 1968).

In addition to the CNS, several peripheral nerve plexuses have been described in contact with the main cords in planarians (Koopowitz and Chien 1974; Koopowitz and Chien 1975; Reuter and Gustafsson 1995). In triclads, a subepidermal plexus is generally found (Hyman 1951). This plexus appears as a diffuse network of very thin processes (Baguña and Ballester 1978); within it, the cells are sparse, bipolar, or multipolar, and consist of spindle-shaped ganglion and sensory cells (Lentz 1968). From this plexus, some nerve fibers penetrate the epithelium (Baguña and Ballester 1978; Reuter and Gustafsson 1995). Also, some nerve bundles connect this subepidermal plexus with the submuscular one, situated below the muscle layers of the body wall (Baguña and Ballester 1978; Lentz 1968). This submuscular plexus contains a fairly regular network of

fibers with a small number of nerve cell bodies observed within it (Baguña and Ballester 1978). Most cells in this plexus seem to be bipolar, although unipolar and multipolar cells can also be found (Lentz 1968). Other nerve plexuses are found around the gut diverticula, within the pharynx (one external and one internal), and around the testis and ovaries of mature sexual planarians (Baguña and Ballester 1978; Reuter and Gustafsson 1995).

### Types of planarian neurons

Together with unipolar neurons, similar to those found in invertebrates, freshwater planarians possess bipolar and multipolar neurons in their nervous system (Bullock and Horridge 1965; Lentz 1968; Rieger et al. 1991). Up to seven types of neurons besides glia-like cells were classically identified by cytological methods based on their size, number of processes, and properties of the nuclei (reviewed in Bullock and Horridge 1965). Golgi impregnation and methylene blue staining revealed the complexity of the branching pattern in the processes of different planarian neural cells (Bullock and Horridge 1965). In planarians, bipolar neurons are typically found in transverse commissures between the VNCs, where they can function as interneurons (Rieger et al. 1991). Also, sensory neurons are usually bipolar (Reuter and Gustafsson 1995). At the fine structural level, glia-like cells have been described between brain neurons and along the VNCs (Morita and Best 1966). These accessory or supporting cells lack vesicles and have very little cytoplasm with very few organelles (Golubev 1988; Reuter and Gustafsson 1995). Although glia-like cell bodies are difficult to distinguish (Rieger et al. 1991), sheathing of axons and commissural fibers has been described in the neuropil of planarians (Trawicki et al. 1988). However, the presence of glial cells in the planarian nervous system has yet to be convincingly shown by the use of specific molecular markers. Two novel genes named *1020HH* and *eye53*, with no similarity to sequences in current databases, are expressed in discrete cells in the brain and along or surrounding the VNCs; these genes could be associated with some kind of supportive role for neural cells (Cebrià et al. 2002b, c). *1020HH* and *eye53* are also expressed surrounding the axons of the photosensitive cells, and as they code for putative secreted molecules, it has been proposed that they could be neurotrophic factors required in the synapses between the photosensitive cells and their targets (Inoue et al. 2004). Recently, a planarian homologue of *slit* (an axon guidance molecule) has been shown to be expressed along the midline of *Schmidtea mediterranea* (Cebrià et al. 2007). In both vertebrates and invertebrates, *slit* is expressed in glial cells located along the midline, where it functions as a



**Fig. 1** Planarian CNS. Whole-mount immunostaining with an anti-synapsin (3C11) antibody in three different species of freshwater planarians. Note the differences in the CNS between different planarian species. *Phagocata ullala* and *Polycelis felina* possess smaller and more compact brains. Also, their VNCs display a more defined orthogonal pattern than *Schmidtea mediterranea*. Anterior is shown to the left. *cg* Cephalic ganglia, *vnc* ventral nerve cord, *ph* pharynx, *tc* transverse commissure, *lp* lateral process. Scale bar, 1mm for *S. mediterranea*, 0.8 mm for *P. ullala* and 0.5 mm for *P. felina*



repulsive cue (reviewed in Dickson and Gilestro 2006). As planarian *slit* shows a conserved repulsive role at the midline (Cebrià et al. 2007), the possibility is raised that *slit*-positive cells could be some kind of planarian glial cells. Further characterization of these cells and detailed expression and functional analyses of planarian homologues of genes such as *gcm* (glial cells missing), glial maturation factor B, and glial factor-1, identified from an EST database (Zayas et al. 2005) should help to reveal the distribution of glia-like cells in the planarian nervous system.

Planarian neurons are characterized by a high content of secretory vesicles (Oosaki and Ishii 1965; Reuter and Gustafsson 1989). The different types of vesicles have been used to distinguish different types of neurons in the planarian brain. Thus, Oosaki and Ishii (1965) described three types of vesicles in the brain of *D. gonocephala*: small clear vesicles, dense vesicles, and neurosecretory vesicles, which apparently were not seen intermingled in the same nerve cells. This large number of vesicles indicates a secretory nature, and in fact, the term neurosecretory has long been used to describe the planarian nervous system (reviewed in Reuter and Gustafsson 1995; Rieger et al. 1991). Neurosecretory monopolar cells are numerous on the posteroventral surface of the brain of *Polycelis nigra* (Lender and Klein 1961). Neurons possessing dense vesicles were found to be associated with the photoreceptors of *D. dorotocephala*; their number changes with the circadian cycle, and they may secrete melatonin (Morita et al. 1987; Morita et al. 1988).

### Neuroactive molecules

The presence of various neuroactive substances has been observed in all groups of Platyhelminthes using a variety of approaches (reviewed in McVeigh et al. 2005; Reuter and Gustafsson 1995; Ribeiro et al. 2005; Rieger et al. 1991). As planarians lack a circulatory system, it is thought that neurosecretory substances are released close to the target cells. Immunoreactivity to serotonin (5-hydroxytryptamine [5-HT]) has been reported in a few species of freshwater planarians, including *Girardia tigrina* (Reuter et al. 1995b), *Dendrocoelum lacteum*, and *Polycelis tenui* (Reuter et al. 1996a), as well as in the terrestrial planarian *Bipalium kewense* (Fernandes et al. 2003). In most cases, serotonin-positive cells are found in the CNS, in both the brain and the VNCs, as well as in the peripheral nerve plexuses, such as the pharyngeal, submuscular, and subepithelial plexuses. Also, immunostaining against gamma-aminobutyric acid (GABA) has been shown in the CNS and the subepidermal plexus of *G. tigrina* (Eriksson and Panula 1994). Two families of neuropeptides, the FMRFamide-like peptides and the neuropeptide Fs, have been shown to be present in

planarians (McVeigh et al. 2005). An antiserum against neuropeptide F from *Moniezia expansa* (Maule et al. 1992) labels the CNS and peripheral plexuses (submuscular and pharyngeal) of freshwater (Reuter et al. 1995b) and marine (Reuter et al. 1995a) planarians. In addition, immunohistochemistry with antibodies against other invertebrate neuropeptides labels the nervous system of different groups of Platyhelminthes (reviewed in Reuter and Gustafsson 1995), for instance, enkephalin-positive neurons in planarians (Venturini et al. 1983).

In the various groups of Platyhelminthes (including planarians) analyzed, aminergic and peptidergic substances do not seem to colocalize, leading to an apparent compartmentalization of the different neuronal populations (Maule et al. 1990; Reuter et al. 1996a; Reuter and Palmberg 1989; Wikgren and Reuter 1985). Further analyses with additional markers against different neuroactive molecules should allow a fine map of the planarian nervous system to be developed and the different neuronal populations characterized.

### Gene expression in the planarian CNS

Umesono et al. (1997) reported the first whole-mount in situ hybridization of a planarian gene (an *orthopedia* homologue) expressed in the CNS. Later, the same authors showed how planarian homologues of the Otx family defined different compartments in the brain of *D. japonica* (Umesono et al. 1999). Thus, *Djotp* is expressed in the lateral branches of the brain, *DjotxB* is expressed in the spongy central region of the brain, and *DjotxA* is expressed in more medial regions. In an attempt to identify a large number of neural genes in planarians, the laboratory of Kiyokazu Agata constructed a complementary DNA (cDNA) library from the planarian head. From this library, 3101 non-redundant ESTs were reported; blast homology searches revealed that 116 of those clones showed significant similarity to genes related to the nervous system (Mineta et al. 2003). More than 95% of those planarian neural genes were found in *Drosophila*, *Caenorhabditis elegans*, and humans, indicating a high degree of conservation. Among them, 42 clones were associated with neurotransmission (choline transporter, acetylcholine receptor, and neuropeptide Y receptor), 33 clones were associated with axon guidance (N-CAM and netrin), 21 clones were categorized under brain morphogenesis/neural differentiation (frizzled, noggin, and the BMP receptor), and 21 clones showed homology to genes involved in sensory systems (arrestin, rhodopsin, and mechanosensory protein 2; Mineta et al. 2003). Interestingly, two of those clones showed homology to vertebrate genes such as sortilin1 and noggin that are not found in *Drosophila* or *C. elegans*.

(Mineta et al. 2003). A second approach that the laboratory of Kiyokazu Agata took to isolate neural-specific genes was to construct a microarray to compare head and trunk cDNAs on the basis that the cephalic ganglia occupy most of the head. The microarray contained 1640 non-redundant ESTs (Nakazawa et al. 2003). Whole-mount in situ hybridizations showed that, among the 30 genes with highest head/trunk expression ratio, 23 of them were expressed in the cephalic ganglia (Nakazawa et al. 2003). Those neural genes included planarian homologues of N-CAM, FGF receptor-like, acetylcholine receptor, and synaptotagmin; interestingly, 8 out of those 23 genes showed no sequence similarity to known genes (Nakazawa et al. 2003).

Whole-mount in situ hybridizations with some of the genes identified through the strategies described above, together with data from other laboratories, clearly show that, although the planarian brain may appear quite simple at the morphological level, at a molecular level, it is rather more compartmentalized. Although most genes that are expressed in the cephalic ganglia are also expressed in the VNCs, several examples of genes specifically expressed in the brain have been reported. Those examples include *nou-darake* (Cebrià et al. 2002a), *brain factor-1* (Koinuma et al. 2003), and *DSCAM* (Fusaoka et al. 2006). In contrast, to my knowledge, no gene expression specific to the VNCs has yet been described. The three molecular domains into which the planarian brain was first divided by the expression of homologues of the Otx family (Umesono et al. 1999) can be further subdivided (Cebrià et al. 2002b). Thus, some genes are specifically expressed in the lateral branches of the brain, which project to the head margins; those genes include homologues of *otp* (Umesono et al. 1997), *noggin* (Ogawa et al. 2002a), the *Six/so* family (Pineda and Salo 2002), a glutamate receptor (clone 1008HH), and a GTP-binding protein *Gi1* alpha subunit (Cebrià et al. 2002b). Even within the brain branches, some genes such as a *GTP-binding protein Gi1* alpha subunit and *synaptotagmin VII* are mainly expressed in the distal half of those lateral branches (Cebrià et al. 2002b). Other genes are expressed in the central spongy region of the brain but not in the lateral branches; among those genes, we find *Pax6* (Pineda et al. 2002), *wnt-5* (Marsal et al. 2003), a glutamate receptor (clone 1406), and novel genes *1020HH* and *Eye53* (Cebrià et al. 2002b; Inoue et al. 2004). Recently, it has been reported that planarian homologues of *Wnt* and *frizzled* genes show complementary expression patterns within the brain, as *DjWntA* is expressed in the posterior half of the brain, whereas *DjFzA* is detected in the anterior half (Kobayashi et al. 2007). Table 1 summarizes some of the neural genes characterized in freshwater planarians.

In summary, a large number of neural-specific genes defining different molecular domains in the planarian CNS

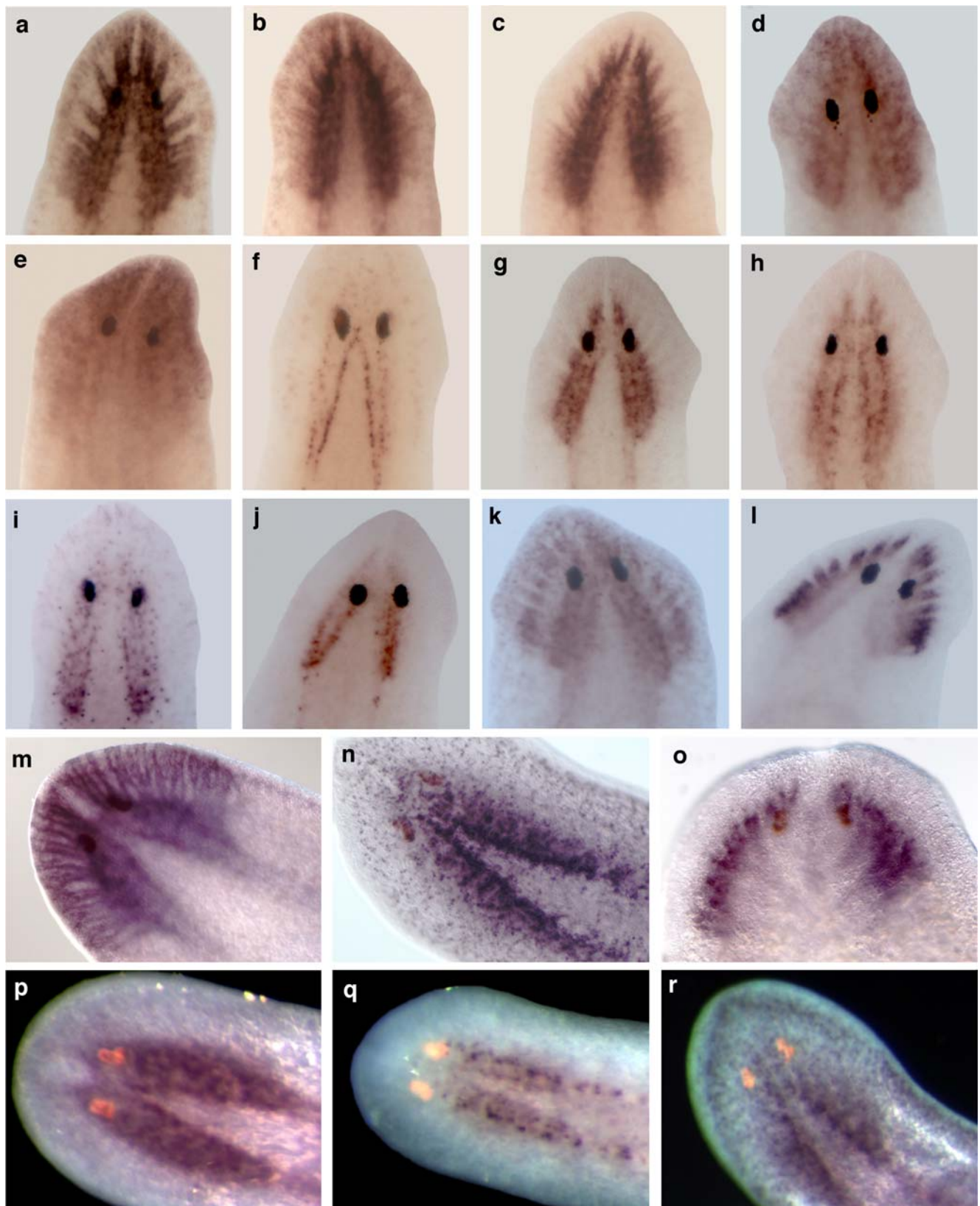
(Fig. 2) are now available and can be used to unravel the process of neural regeneration in these animals.

### The planarian CNS as a model to study neural regeneration

In contrast to most animals, freshwater planarians are a model in that we can study the regeneration of the CNS from a population of stem cells found in intact adult animals. Analysis of nervous system regeneration in planarians (Fig. 3) can provide us not only with valuable information to understand how stem cells are regulated, how they are determined in the neural lineage, and how they differentiate into new neural cells that integrate into the pre-existing CNS, but also information that may be of critical importance in enhancing the poor regenerative capacity of higher animals, including humans. This potential is important to be able to treat spinal cord injuries and neurodegenerative diseases such as Alzheimer's or Parkinson's disease. In vertebrates, for instance, one of the reasons that neural regeneration is blocked after axonal damage is the formation of a glial scar together with the presence of inhibitory molecules (Busch and Silver 2007; Galtrey and Fawcett 2007; Niclou et al. 2006). However, what happens in planarians? Do the glial-like cells described in some previous studies have a role on regeneration? Are inhibitory molecules upregulated after injury? Unfortunately, very little is known about the molecular and cellular events that take place just immediately after amputation of the planarian CNS.

#### Early stages of CNS regeneration

Based on immunostaining with an antiserum against 5-HT, Reuter et al. (1996b) suggested that the regeneration of the nervous system in the planarian *G. tigrina* is the result of two processes: (1) an initial outgrowth of the original main longitudinal nerve cords that consequently send processes transversely—these processes indicate the position of the developing anterior commissure, and (2) new nerve cells in front of the commissure differentiate from neoblasts and fasciculate with the fibers from the old VNCs, giving rise to the new brain. However, 5-HT is not the most appropriate marker for analysis of very early stages of regeneration. Whole-mount in situ hybridizations for a collection of neural-specific genes combined with the results of immunohistochemistry with an anti-synaptotagmin antibody in *D. japonica* showed that two small clusters of cells defining the new brain primordia appear within the blastema at day 1 of regeneration before any outgrowth from the truncated VNCs was observed with the available markers (Cebrià et al. 2002c). Those findings suggest that the brain





**Fig. 2** Molecular domains in the planarian brain. Whole-mount in situ hybridizations showing expression in the cephalic ganglia of two common species used in planarian regeneration research: *Dugesia japonica* (a–l) and *Schmidtea mediterranea* (m–r). **a** Clone 944HH, N-CAM; **b** clone 2814HH, synapsin; **c** clone 4307HH, nicotinic acetylcholine alpha receptor; **d** clone 721HH, FGF receptor-like; **e** 1993HH, unknown; **f** clone 639E, unknown; **g** clone 953HH, very low-density lipoprotein binding protein; **h** clone 793E, unknown; **i** clone 53E, unknown; **j** clone 1020HH, unknown; **k** clone 3491HH, synaptotagmin VII; **l** clone 1791HH, G protein alpha subunit; **m** clone H.10.2f, unknown; **n** clone H.117.5e, anosmin-1; **o** glutamate receptor; **p** Smed roboA; **q** Smed netrin2; **r** Smed netrin1. Clones **a–l** were described in Nakazawa et al. (2003) and Mineta et al. (2003). Clones **m–n** were reported in Sánchez Alvarado et al. (2002). Clone **o** has not been described previously (F. Cebrià and P. Newmark, unpublished data). Clone **p** was reported in Cebrià and Newmark (2007). Clones **q** and **r** were described in Cebrià and Newmark (2005)

primordia differentiate independently of the presence of processes from the preexisting nerve cords.

Morphological and molecular data suggest that the planarian brain and VNCs can be seen as distinct structures (Agata et al. 1998; Cebrià et al. 2002c). The challenge is, therefore, to understand how differentiation of the new

cephalic ganglia within the blastema is related to regeneration of the truncated nerve cords from the stump region. This will clearly require the use of new markers for those early stages and double labeling using available brain-specific genes and antibodies against neural processes from the VNC to clarify how the brain and nerve cords regenerate with respect to each other. It is interesting to notice that, in some cases, it is possible to regenerate more or less well-organized cephalic ganglia on top of completely disorganized VNCs. This is what happens after RNAi for netrin and a netrin receptor homologue (Cebrià and Newmark 2005). In those experiments, the silencing of either of the two genes resulted in the regeneration of morphologically abnormal cephalic ganglia that still retained their basic organization as the neuronal cell bodies were located at the periphery of a central neuropil. In contrast, the VNCs underneath this brain completely lost their organization and appeared as a disorganized meshwork of axonal processes and cell bodies (Cebrià and Newmark 2005). Thus, although it is obvious that the brain and the VNCs are intimately related in intact animals, several data suggest that

**Table 1** Some genes expressed within the planarian CNS

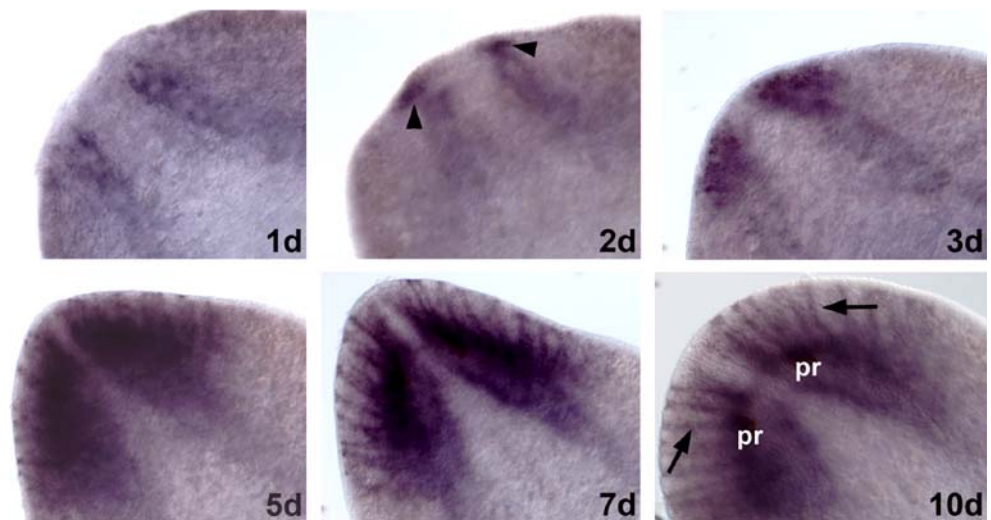
Gene	Homology	Expression pattern	Species	Reference
<i>Djotp</i>	Orthopedia	Brain lateral branches	Dj	Umesono et al. 1997
<i>PC2</i>	Pro-hormone convertase	General	Dj	Agata et al. 1998
<i>DjotxA</i>	Orthodenticle	Cephalic ganglia (medial region)	Dj	Umesono et al. 1999
<i>DjotxB</i>	Orthodenticle	Cephalic ganglia	Dj	Umesono et al. 1999
<i>GtPax6a</i>	Pax6	General	Gt	Pineda et al. 2002
<i>Djnlg</i>	Noggin-like	Brain lateral branches	Dj	Ogawa et al. 2002a
<i>nou-darake</i>	Fibroblast growth factor receptor-like	Cephalic ganglia	Dj	Cebrià et al. 2002a
<i>DjFGFR1 and 2</i>	Fibroblast growth factor receptor	Cephalic ganglia	Dj	Ogawa et al. 2002b
<i>1008HH</i>	Glutamate receptor	Brain lateral branches	Dj	Cebrià et al. 2002b
<i>4307HH</i>	Nicotinic acetylcholine receptor	General	Dj	Cebrià et al. 2002b
<i>Gtsix3</i>	Six/so	Brain lateral branches	Gt	Pineda and Saló 2002
<i>Gtwnt-5</i>	Wnt	General	Gt	Marsal et al. 2003
<i>DjXnp</i>	SNF2-like	Cephalic ganglia	Dj	Rossi et al. 2003
<i>DjFoxG</i>	Brain factor-1	Cephalic ganglia	Dj	Koinuma et al. 2003
<i>Djeya</i>	Eyes absent	Cephalic ganglia	Dj	Mannini et al. 2004
<i>DjPHM</i>	Peptidylglycine $\alpha$ -hydroxylating monooxygenase	General	Dj	Asada et al. 2005
<i>Inx3 and 4</i>	Innexins	General	Dj	Nogi et al. 2005
<i>Smed-netR</i>	Netrin receptor	General	Sm	Cebrià and Newmark 2005
<i>DjCAM</i>	N-CAM	General	Dj	Fusaoka et al. 2006
<i>DjDSCAM</i>	DSCAM	Cephalic ganglia	Dj	Fusaoka et al. 2006
<i>Smed-roboA</i>	Roundabout	General	Sm	Cebrià and Newmark 2007
<i>DjCHC</i>	Clathrin heavy chain	General	Dj	Inoue et al. 2007
<i>DjwntA</i>	Wnt	Posterior half of the brain	Dj	Kobayashi et al. 2007
<i>DjfrzA</i>	frizzled	Anterior half of the brain	Dj	Kobayashi et al. 2007
<i>DjTPH</i>	Tryptophan hydroxylase	Serotonergic neurons	Dj	Nishimura et al. 2007b
<i>DjTH</i>	Tyrosine hydroxylase	Dopaminergic neurons	Dj	Nishimura et al. 2007a

The term “general” is used for those genes that are broadly expressed in both the brain (cephalic ganglia) and the VNCs, independent of the number or subpopulations of neurons that they label.

Dj *Dugesia japonica*, Gt *Girardia tigrina*, Sm *Schmidtea mediterranea*



**Fig. 3** Central nervous system regeneration in *Schmidtea mediterranea*. Whole-mount in situ hybridization with EST clone H.10.2f (Sánchez Alvarado et al. 2002). With this marker, the brain primordia are first detected within the blastema at day 2 of regeneration (arrowheads). By day 10, a mature brain with well-differentiated lateral branches (arrows) is observed. Also, by this time, the new photoreceptors (*pr*) are completely differentiated



different specific factors might be responsible for the initial determination of the brain primordia and growth of the amputated nerve cords.

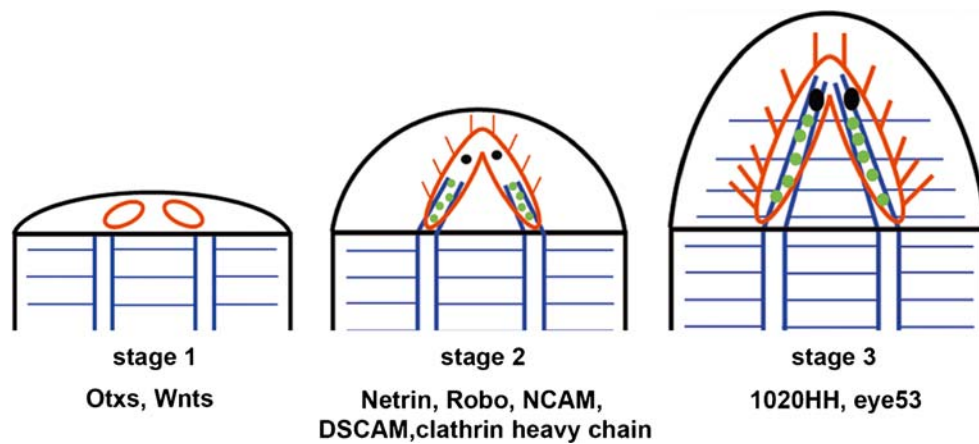
In recent years, a working model (Fig. 4) has been proposed for the regeneration of the planarian CNS (Cebrià et al. 2002c; Inoue et al. 2007; Kobayashi et al. 2007), where there would be an initial stage (24–36 h of regeneration; stage 1 in Fig. 4) in which the brain primordia form within the blastema and are then patterned to define different molecular domains. Next, an intermediate stage would be characterized by the growth of the primordia, regeneration of the VNCs in the blastema and formation of neural circuits (2–3 days of regeneration; stage 2). Finally, at later stages, from 4–5 days (stage 3 in Fig. 4), the regenerated CNS would recover most of its functionality.

To date, no factor has been clearly shown to be responsible for the initial formation of the brain primordia. However, as more genes are being isolated from different EST projects, as well as from “in silico” searches of the genome, candidate genes that may play a role in this early stage of CNS regeneration can be tested. Candidate genes for the patterning of the brain primordia between 1 and 2 days of regeneration have already been postulated in *D. japonica*. Otx-related genes have been found to define distinct mediolateral domains in the planarian brain (Umesono et al. 1997; Umesono et al. 1999). Unfortunately, however, no functional characterization of these genes has been reported, so further analysis will be required to confirm their proposed role in brain patterning. A recent study showed that a homologue of the Wnt family is required for the proper anteroposterior patterning of the planarian brain (Kobayashi et al. 2007). The authors showed that *DjwntA* and its putative frizzled receptor (*DjfrzA*) display complementary expression patterns in the brain; *DjwntA* is expressed in the posterior half of the brain, whereas *DjfrzA* is restricted in the anterior half (Kobayashi

et al. 2007). RNAi knockdowns of *DjwntA* resulted in posterior expansion of the brain, differentiation of ectopic eyes, and longer visual axons projecting to the expanded brain (Kobayashi et al. 2007), findings which clearly implicate the Wnt signaling pathway in brain patterning. Also, a different member of the Wnt family isolated in *G. tigrina*, *Gtwnt-5*, is expressed in a subpopulation of neurons in the CNS, and it has been suggested that it could have a role in mediolateral patterning of the CNS (Marsal et al. 2003), although support from functional analyses needs to be provided.

#### Genes required in intermediate and late stages of CNS regeneration

The intermediate stages of CNS regeneration would be characterized by the growth of the cephalic ganglia and the formation of proper neural networks. A clathrin heavy chain (CHC) homologue has recently been shown to be required at this stage (Inoue et al. 2007). After RNAi for *DjCHC*, the brain primordia seem to form normally; however, after that, the regenerated brain shows many morphological defects. In vitro cell cultures of neurons from *DjCHC*-knockdown animals showed that those neurons extended significantly fewer and shorter neurites as compared to the controls (Inoue et al. 2007), suggesting that this gene is important for axonal growth. Other neural genes that play an important role at this stage of regeneration are homologues of members of the immunoglobulin superfamily of neural cell adhesion molecules. Thus, *DjCAM* and *DjDSCAM* are expressed in the mature CNS and appear in the brain primordia within the regenerative blastema 2 days after amputation, whereas RNAi analyses suggest that they have a role in axonal development (Fusaoka et al. 2006). *DjCAM* knockdown results in impaired axon fasciculation in the lateral brain



**Fig. 4** Hypothetical model of planarian central nervous system (CNS) regeneration. Some of the genes postulated to have a function at each stage are indicated. At stage 1 (24–36 h of regeneration), the brain primordia (red circles) are determined within the blastema. Probably at this stage, the brain primordia are already be divided into different molecular domains along their anteroposterior and mediolateral axes (Kobayashi et al. 2007; Marsal et al. 2003; Umesonu et al. 1999). Stage 2 (2–3 days of regeneration) would be characterized by the outgrowth of the truncated ventral nerve cords (in blue) into the blastema

where they would reestablish proper connections with the growing cephalic ganglia (in red). The rewiring of the CNS and formation of new neural circuits would be mediated by factors such as homologues of axon guidance cues and cell-adhesion molecules (green circles; Cebrià and Newmark 2005; Cebrià and Newmark 2007; Fusaoka et al. 2006). A different factor recently shown to play a role at this stage is a planarian homologue of a clathrin heavy chain gene (Inoue et al. 2007). Finally, at stage 3 (from 4–5 days of regeneration), the newly regenerated CNS would recover all its functions (Inoue et al. 2004)

branches that project toward the head periphery (Fusaoka et al. 2006). A much more severe phenotype is obtained after *DjDSCAM* knockdown: The gross morphology of the regenerated brain is aberrant with a disorganized neuropil and a reduced number of abnormal lateral branches, along with disorganization of the axonal tracts in those branches (Fusaoka et al. 2006). Those results clearly suggest that *DjDSCAM* is required for proper regeneration of the neural network in the cephalic region.

To identify genes that might play a role in late stages of CNS regeneration, the laboratory of Kiyokazu Agata analyzed the function of two novel genes named *eye53* and *1020HH* (Inoue et al. 2004). Those two genes had been shown to be first expressed in the regenerating cephalic ganglia at day 5 after amputation (Cebrià et al. 2002c), suggesting that they could have a role in the final stage of neural regeneration at the time when the CNS would recover most of its functionality. The planarian visual system usually comprises a pair of photoreceptors in the anterior region; these photoreceptors contain pigmented and photosensitive cells, which have axonal processes that project in a very stereotypical pattern (Agata et al. 1998; Okamoto et al. 2005). During regeneration, the normal pattern of visual axon projections is reestablished after 5 days (Inoue et al. 2004). As *eye 53* and *1020HH* are expressed in the photosensitive cells and cells surrounding the visual axons, Inoue et al. (2004) established a behavioral assay to analyze the function of these genes in the photosensory system. Planarians typically display negative phototaxis, moving away from light. After RNAi for *eye53*

or *1020HH*, the animals regenerated a morphologically normal brain and visual system but did not show a normal photophobic response, suggesting that these two late-expressed genes are required for the functional recovery of the planarian visual system (Inoue et al. 2004).

### The role of axon guidance cues during planarian CNS regeneration

When seeing the complexity of the neural networks in the CNS of both vertebrates and invertebrates, one cannot avoid wondering how axons find their proper targets, in many cases, after navigating a considerable distance through complex extracellular environments. It was Ramón y Cajal who already suggested in his neurotropic theory that some unknown forces guided the axons to their targets (reviewed in Ramón y Cajal 1928). Today, it is known that the proper wiring of the nervous system depends on several families of well-conserved axon guidance cues such as netrins, slit, ephrins, and semaphorins, which regulate not only axonal growth but also other aspects such as neural cell migration (for reviews, see Araújo and Tear 2003, Chilton 2006, and Guan and Rao 2003). Some of these factors act as repulsive cues for the growing axons, whereas others serve as attractants, and still, others may function as either repulsive or attractive cues depending on the context.

During regeneration of the CNS, damaged axons need to regrow and project toward their original targets, reestablish-

ing proper functional connections. However, in most animals, axonal projections in the CNS do not usually regenerate after injury because of intrinsic and environmental factors (for reviews, see [Goldberg 2003](#); [Selzer 2003](#)).

Planarians provide a good model in which to analyze the function of these guidance cues during the regeneration and maintenance of the CNS. Recent studies have addressed the function of planarian homologs of *netrin* (Cebrià and Newmark 2005), *robo* (Cebrià and Newmark 2007), and *slit* (Cebrià et al. 2007) during neural regeneration. In all cases, those genes have been shown to be essential for the proper regeneration of the CNS. However, for some of the abnormal phenotypes obtained, it is not yet clear if they are caused by direct axon-guidance defects or abnormal fasciculation or cell migration. For example, planarian netrins are expressed not at the midline but bilaterally along the VNCs or along the medial region of the cephalic ganglia (Cebrià and Newmark 2005). After silencing either *Smed\_netrin2* or *Smed\_netR*, commissural axons still cross the midline. In fact, the anterior commissure connecting the two cephalic ganglia appears much wider, although that could be the result of either more axonal projections crossing the midline in that region or defasciculation of a normal number of projections (Cebrià and Newmark 2005). On the other hand, silencing of *Smed\_roboA* results in a thinner anterior commissure, and in some cases, a complete loss of the commissure (Cebrià and Newmark 2007). Thus, planarian *netrin/netR* and *robo* could be seen as having opposing effects; however, it is noticeable that the effects seen in planarians seem to be the opposite of what has been observed in other systems, where netrins attract commissural axons toward the midline (*netrin* and *netrin receptor* mutants show fewer or no axonal projections crossing the midline) and *robo* mediates the repulsive role of midline slit (in *slit* and *robo* mutants commissural axons get trapped at the midline). *Smed-slit* seems to display a more conserved function in planarians as a midline repellent. This gene is expressed at the midline, and its silencing results in collapse of the whole regenerated CNS at the midline (Cebrià et al. 2007), a situation that resembles what happens to commissural axons in *Drosophila* and vertebrate *slit* mutants.

Unexpectedly, silencing of these cues in planarians also causes defects that go beyond axon guidance. Thus, after silencing *Smed\_slit*, ectopic neural tissue and eyes differentiate around the midline, suggesting that this gene could somehow regulate the behavior of neural precursors at the planarian midline (Cebrià et al. 2007); however, further data will be necessary to clarify the origin of those ectopic neural cells. Finally, differentiation of ectopic pharynges and dorsal outgrowths with a cephalic identity is observed after *Smed\_roboA* RNAi (Cebrià and Newmark 2007). Those defects seem to correlate with the failure of the

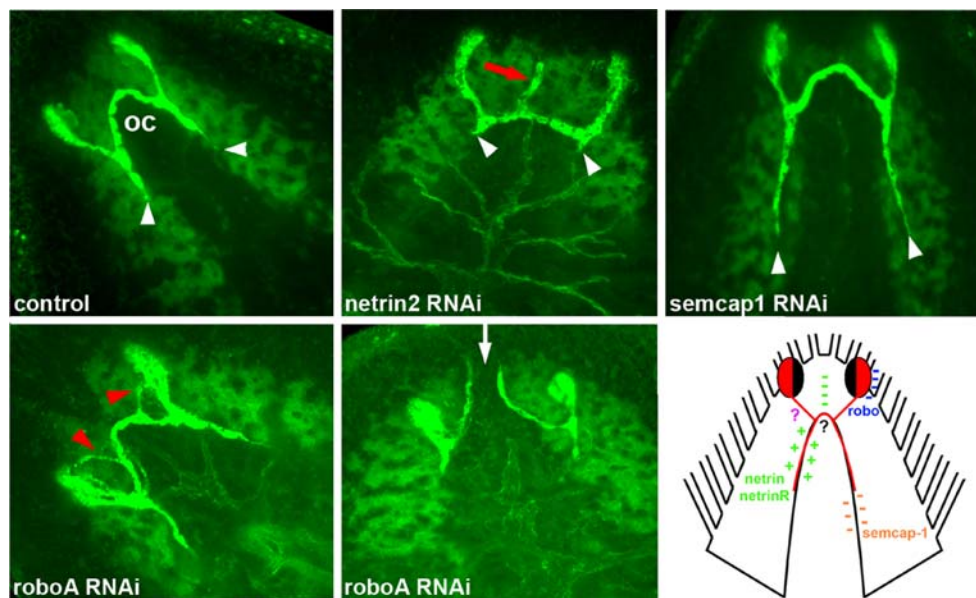
newly differentiated cephalic ganglia to reestablish proper connections with the regenerating VNCs, suggesting that, in the absence of a proper brain/VNC connection, a neurally derived signal would change some positional information and trigger the differentiation of those ectopic structures (Cebrià and Newmark 2007).

### Proper targeting of visual axons depends on multiple guidance cues

The axonal projections of planarian photosensitive cells display a highly stereotypical pattern in which some axons project ipsilaterally and others project contralaterally to form an optic chiasm (Fig. 5; [Okamoto et al. 2005](#)). Given this highly stereotypical pattern of visual projections and the fact that, in higher invertebrates and vertebrates, different cues are essential for guiding the retinal axons, planarians are an attractive model in which to study the function of these axon guidance cues during the regeneration of the visual system.

Similar to the situation described in vertebrates (reviewed in [Inatani 2005](#)), several studies have shown that different cues seem to control different stages of the development and guidance of planarian visual axons (Fig. 5). For instance, *Smed\_netrin2* and *Smed\_netR* are required for the final targeting of the visual axons to the visual center of the brain (Fig. 5; Cebrià and Newmark 2005). Netrins are expressed in the visual center and would act as attractants for the axons of the photosensitive cells that express a netrin receptor (Cebrià and Newmark 2005). Moreover, *netrin2/netR* also seem to regulate the projections that form the chiasm, as RNAi knockdown of those genes leads to the generation of axons that project ectopically in an anterior direction along the midline (Fig. 5; Cebrià and Newmark 2005). Interestingly, the length of the projections of the photosensitive axons toward the visual center seems to be regulated not only by netrins but also by other cues such as a homologue of a semaphorin cytoplasmic domain-associated protein (*semcap-1*). After RNAi silencing of this gene, visual axons project abnormally to a more posterior region of the brain (Fig. 5; Cebrià and Newmark 2005). A *robo* homologue also seems to be required for the regeneration of proper visual pattern. After silencing of *Smed\_roboA*, ectopic projections forming loops were observed (Fig. 5; Cebrià and Newmark 2007). The shape and localization of those loops showed some variability, making it more difficult to determine the exact function of *Smed\_roboA*. One possibility is that *Smed\_roboA* could have a role in preventing or correcting pathfinding errors, as has been described for a zebrafish *robo* homologue (Hutson and Chien 2002). In the absence of *Smed\_roboA* function, ectopic projections that, under





**Fig. 5** Cues involved in visual axon guidance during regeneration. Double whole-mount immunostaining with an anti-phosphotyrosine antibody (light green) to label the cephalic ganglia and the monoclonal antibody VC-1 (bright green; Sakai et al. 2000) to reveal the stereotypical pattern of visual axon projections. Control planarians regenerate a normal pattern, and the visual axons project correctly to the visual center of the brain (white arrowheads). After *Smed\_netrin2* or *Smed\_netR* RNAi, the visual axons do not grow from the optic chiasm (oc) to the visual center (white arrowheads). In some cases, ectopic visual axons project anteriorly along the midline (red arrow;

Cebrià and Newmark 2005). After *Smed\_semcap1* RNAi, the visual axons project to more posterior regions of the brain compared to the controls (white arrowheads; Cebrià and Newmark 2005). After *Smed\_roboA* RNAi, ectopic visual projections form loops (red arrowheads). In the absence of the anterior brain commissures, the visual axons project anteriorly without crossing the midline (white arrow). The diagram shows a proposed model in which different molecules act as positive (attractant) or negative (repulsive) cues for the growth and guidance of visual axons. Question marks refer to putative cues that remain to be identified

normal conditions, would be corrected could give rise to the observed ectopic loops.

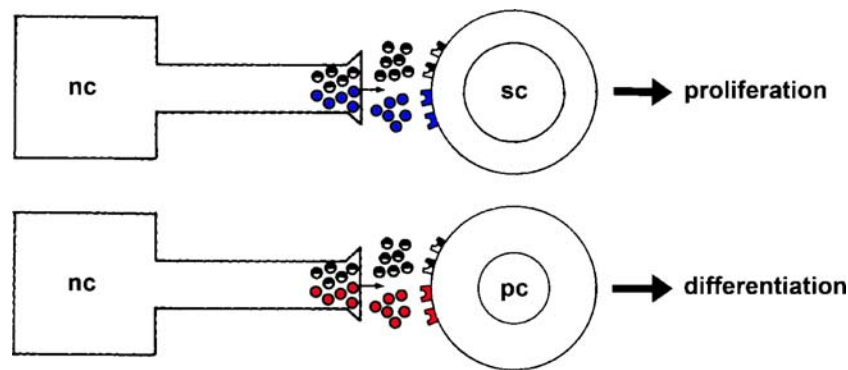
Therefore, at least four different genes (*netrin2*, *netrin receptor*, *semcap1*, and *roboA*) have been shown to play a role in the regeneration of planarian visual axons (Cebrià and Newmark 2005; Cebrià and Newmark 2007). However, additional unknown cues may also be involved in visual axon patterning, as suggested in the model shown in Fig. 5. For example, what are the cues that guide visual axons from the eye-cup toward the point at which some of them project ipsilaterally to the visual center of the brain and others cross the midline? Also, when the visual axons project contralaterally to form the chiasm, they always do it along the posterior end of the anterior brain commissure, which connects the two cephalic ganglia (Fig. 5). After *Smed\_roboA* RNAi, the anterior brain commissure is absent in some animals; in all those cases, the visual axons do not cross the midline and instead keep projecting anteriorly (Fig. 5; Cebrià and Newmark 2007). This observation suggests that some factor(s) that guide the visual axons across the midline may be present in the anterior commissure. Interestingly, a similar abnormal anterior projection of visual axons is observed after RNAi for a BMP-1 homologue (Reddien et al. 2005), although,

in that case, it was not shown whether the anterior commissure was present or not. Future experiments should try to isolate additional cues involved in those different aspects of visual axon development. It would be interesting to characterize the role of planarian homologues of ephrins in this process, as these factors have been shown to be important for guidance of vertebrate retinal axons (reviewed in Inatani 2005).

### The influence of the nervous system on planarian regeneration

The extent to which planarian regeneration is under the influence of the nervous system is an important issue that still needs to be clarified. When considering this question, it should be kept in mind that such an influence could be found in multiple processes, such as cell proliferation, differentiation, and/or migration, and regulation of more general morphogenetic events. Over the years various experimental observations have suggested a role for the nervous system in planarian regeneration. However, the exact nature of that neural influence is currently unknown.





**Fig. 6** Possible actions of neurotransmitters on regeneration. Different molecules from nerve cells (*nc*) could signal through receptors in planarian stem cells (*sc*) to control their proliferation either activating or inhibiting it. On the other hand, the same (black and white circles)

or different neural factors (red circles) could act on already committed precursor cells (*pc*) regulating their differentiation (adapted from Baguña et al. 1989)

### Classical evidences of a neural influence on regeneration

Several experiments indicated that overall regeneration was inhibited by removal of the nervous system in some species (Child 1904a,b; Morgan 1905). However, in other species, lateral pieces without any VNC could regenerate a head (Morgan 1898; Morgan 1900). Bondi (Bondi 1959) described that, during head regeneration, a planarian with a very shortened lateral nerve cord on one side formed symmetrical blastemas, but the eyes corresponding to the longer nerve cord appeared 3 days before those corresponding to the shorter nerve cord. Later, Lender and Gripon (1962) found that the retardation of eye formation because of the shorter nerve cord was only 24 h, but they nevertheless observed a delay. Sperry et al. (1973) showed that lateral pieces with no VNC give rise to “head-hump” regenerates, which have an abnormally large head with no differentiation of post-cephalic structures. They suggested a head-inhibiting influence of the nerve cords during regeneration. Kishida and Kurabuchi (1978) analyzed regenerating fragments deprived of nerve cords and observed that regeneration was delayed by about 2 days compared to normal regenerating pieces. Wolff and Lender (1950a, b) suggested an inductive role of the brain for eye differentiation, with the eye-inducing factor being of a neuro-humoral nature (Lender 1955). Using a different kind of approach, Stéphan-Dubois and Lender (1956) concluded that wound neurohormones would trigger the migration of neoblasts at the beginning of regeneration and suggested that the nervous system was involved in this early event in the regenerative process. Lender and Klein (1961) and Lender (1964) observed secretory cells in the brain and found that their number increased during subsequent regeneration. Similarly, Sauzin-Monnot (1972) described neurosecretory cells all along the nerve cords and observed an accumulation of neurosecretory granules 6 h after amputation.

The application of modern techniques and the availability of numerous molecular markers allow us to revisit these classical observations and try to characterize the nature of the neural factors involved in regeneration. Remarkably, although a neural influence has also been postulated in other regenerating systems such as the amphibian limb and tail (Dinsmore and Mescher 1998; Singer 1952), no definitive molecule has been reported in those cases. Thus, the benefits of understanding the role of the nervous system during planarian regeneration are clear.

### *Nou-darake* restricts brain differentiation to the head

In 2002, a new gene related to the FGF receptor family was reported called *nou-darake* (“brains everywhere” in Japanese; Cebrià et al. 2002a). This gene is expressed in the entire cephalic region (brain and surrounding tissues), and RNAi led to an unexpected posterior expansion of brain tissues along the length of the body of treated animals. Those results seemed to suggest that *nou-darake* could be involved in an inhibitory pathway that would restrict the differentiation of brain tissues to the anterior region. That the planarian brain could have a role in inhibiting a new brain in more posterior regions was also postulated on the basis of classical observations (reviewed in Brondsted 1969); however, our observations with *nou-darake* provided the first molecular support for that possibility. Unfortunately, the function of other FGF receptors or FGF ligands has not been characterized in these animals. One feature of the *nou-darake* knockdown phenotype is that the ectopic brain tissue does not differentiate throughout the body but rather on top of the preexisting VNCs. This situation is somewhat reminiscent of what happens in some species of Platyhelminthes that reproduce asexually by paratomy, that is, where the differentiation of the new organs starts before fissioning of the animal. In *Microstomum lineare*, it has

been observed that the first cells of the new brain appear in close contact with the existing nerve cords, suggesting an important role of those cords in the differentiation of the new cephalic ganglia (Reuter and Gustafsson 1996; Reuter and Palmberg 1989). In both cases, it could be supposed that some neural factor derived from the VNCs would affect neoblasts (or neural precursors) around them to regulate their proliferation and/or differentiation.

Morphogenesis defects are associated to abnormal nervous system regeneration

More recently, abnormal regeneration of the CNS has been correlated with morphogenesis defects. After *Smed\_roboA* RNAi, the newly differentiated cephalic ganglia appear disconnected from the truncated VNCs, which themselves do not appear to regenerate normally; in those cases, differentiation of ectopic pharynges and dorsal outgrowths are observed (Cebrià and Newmark 2007). Based on those observations, it has been proposed that, in the absence of a properly connected CNS (cephalic ganglia and VNC), putative neurally derived signals could be present in the surrounding tissues, altering the behavior of the neoblasts and inducing the morphogenesis defects observed (Cebrià and Newmark 2007). The use of the functional genomics techniques that are now available may help to identify those putative neural signals.

Neurotransmitters and planarian regeneration

Finally, an alternative approach that can be used to unravel the influence of the nervous system on planarian regeneration is to systematically characterize the role of neurotransmitters and growth factors in this process. In other systems, such molecules have been also implicated in regulating the fate of stem cells or neural precursors. In planarians, neurons positive for serotonin, FMRFamide, EGF receptor, met-enkephalin (opioid neuropeptide), and neuropeptide F have been detected by immunohistochemistry (Reuter et al. 1995a, b; Venturini et al. 1983). A peptide named GYRFamide was the first neuropeptide isolated in planarians (Johnston et al. 1995), and a neuropeptide receptor from *Girardia tigrina* has been reported (Omar et al. 2007). Recently, dopaminergic and serotonergic neurons have been described after in situ hybridization for tyrosine hydroxylase and tryptophan hydroxylase, respectively (Nishimura et al. 2007a, b). Also, by using agonists or antagonists of some of these neurotransmitters, it has been proposed that serotonin and dopamine increase the rates of planarian regeneration (Franquinet 1979; Franquinet and Le Moigne 1979), that substance P and substance K could have a stimulatory effect on neoblast proliferation (Baguña et al. 1989; Bayascas et al. 1997), that somatostatin might inhibit proliferation (Bautz

and Schilt 1986), and that exposure of regenerating pieces to neuropeptide F or FMRFamide may stimulate pharyngeal regeneration (Sheiman et al. 2004). However, most of these observations are based on indirect pharmacological approaches. By combining current tools such as ESTs and genomic information, RNAi-based functional analyses, and cell culturing of neural cells (Asami et al. 2002), it should be possible to first characterize these factors in the planarian genome and then analyze their role during regeneration (Fig. 6).

## Conclusions and future prospects

There is no doubt that, in the last 10 years, planarians have regained their popularity as a model in which to study regeneration. As modern techniques have been applied to them, we have begun to characterize, for example, some of the molecular factors that control stem cell proliferation, differentiation, and/or maintenance. Numerous genes expressed in the planarian CNS have now been reported, and analysis of their expression patterns has revealed a high degree of compartmentalization. Also, RNAi experiments have begun to provide data on the role of several genes in brain patterning and in the proper wiring of the regenerating CNS. In summary, we now have the tools to unravel how neural regeneration is accomplished in these animals. Some of the important questions that should be answered in the near future include how many different neuronal populations are found in the planarian CNS, how neoblasts become committed to the neural lineage, and what is the role of the nervous system during regeneration.

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