Cellular and Molecular Dissection of Pluripotent Adult Somatic Stem Cells in Planarians

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Freshwater planarians, Plathelminthes, have been an intriguing model animal of regeneration studies for more than 100 years. Their robust regenerative ability is one of asexual reproductive capacity, in which complete animals develop from tiny body fragments within a week. Pluripotent adult somatic stem cells, called neoblasts, assure this regenerative ability. Neoblasts give rise to not only all types of somatic cells, but also germline cells. During the last decade, several experimental techniques for the analysis of planarian neoblasts at the molecular level, such as in situ hybridization, RNAi and fluorescence activated cell sorting, have been established. Moreover, information about genes involved in maintenance and differentiation of neoblasts has been accumulated. One of the molecular features of neoblasts is the expression of many RNA regulators, which are involved in germline development in other animals, such as vasa and piwi family genes. In this review, we introduce physiological and molecular features of the neoblast, and discuss how germline genes regulate planarian neoblasts and what differences exist between neoblasts and germline cells.

Key words: adult somatic stem cell, germline-specific genes, neoblast, planarian, pluripotency.

Introduction

Adult somatic stem cells (ASCs) are maintained by self-renewal and differentiate into function-specific cells in order to replace dead and injured cells in various tissues. Due to their scientific appeal and potential medical application, stem cells in mammalian tissues are the best documented ASCs. However, ASCs exist in many species belonging to various phyla (Sánchez Alvarado & Kang 2005; Agata et al. 2006; Bosch 2008). Whereas the fundamental cellular and molecular bases of these ASCs are still poorly understood, the accumulation of knowledge about ASCs from diverse species may give us a good opportunity not only to understand the common principles of stem cells, but also guide their use in regenerative medicine.

Freshwater planarians, turbellarians belonging to phylum Plathelminthes, are known to possess ASCs called neoblasts (Baguña 1981). Dugesia japonica is a common planarian species in Japan. It measures up to 2 cm in size and has clearly defined organs such as a well-organized brain with different types of neurons, a pharynx for feeding and excretion in the central portion of its body, and an intestine composed of three main branches (Fig. 1; Umesono et al. 1997; Agata et al. 1998; Kobayashi et al. 1998; Umesono et al. 1999; Cebria et al. 2002b c; Nishimura et al. 2007a, b; Umesono & Agata 2009). Despite their complex body structure, planarians have robust regenerative ability, in other words, asexual reproduction ability. Almost any small fragment from anywhere behind the eyes of the planarian body can regenerate and develop into a complete animal, with a functional brain, within a week after amputation (Agata et al. 2003; Rossi et al. 2008; Umesono & Agata 2009). Planarians’ remarkable ability to regenerate is strictly dependent on their neoblasts (Baguña et al. 1989; Agata & Watanabe 1999; Newmark & Sánchez Alvarado 2002; Salò & Baguña 2002; Agata et al. 2003, 2006; Reddien & Sánchez Alvarado 2004; Sánchez Alvarado 2006, 2007; Rossi et al. 2008). During regeneration, the neoblasts give rise to all types of cells, not only somatic but also germline cells (Sato et al. 2006; Handberg-Thorsager & Salò 2008).
Neoblasts are the only cell population possessing continual proliferative ability in planarians. Newmark & Sánchez Alvarado (2000) were able to visualize mitotic cells using BrdU in a related species, *Schmidtea mediterranea*. Only neoblasts incorporate BrdU immediately after treatment, and almost all neoblasts incorporate BrdU within 2 days of injection (Kang & Sánchez Alvarado 2009). Some BrdU-incorporating cells are also visualized with anti-phosphorylated histone H3 antibody (pH3), an indicator of mitotic (M-phase) cells (Newmark & Sánchez Alvarado 2000). *D. japonica* neoblasts also incorporate BrdU specifically, and can be labeled with anti-pH3 antibodies (Fig. 2A–D; Inoue et al. 2007; Yoshida-Kashikawa et al. 2007; Higuchi et al. 2008). Genes related to the process of DNA replication such as *minichromosome maintenance 2* homologue, *DjMCM2*, or *proliferating cell nuclear antigen*, *Djpcna*, are also specifically expressed in the neoblasts (Salvetti et al. 2000; Orii et al. 2005). The cell cycle of neoblasts is accelerated by feeding or amputation of the animals (Bagunha 1974, 1975; Kang & Sánchez Alvarado 2009), which probably indicates the expeditious supplying of cells that accompanies regeneration and growth of an individual.

Classically, electron microscopic observations revealed the typical morphological features of neoblasts. Neoblasts are approximately 10 μm in size, of round or ovoid shape, and show a high nucleus/cytoplasm ratio (Fig. 2E). No obvious organelles other than free ribosomes and mitochondria are observed in their scanty cytoplasm (Pedersen 1959). An unambiguous structural feature of neoblasts is cytoplasmic chromatoid bodies. Chromatoid bodies are observed as are round, electron-dense structures that are not surrounded by a membrane (Fig. 2E; Morita 1967; Coward 1974; Hori 1982). These structures show sensitivity to Ribonuclease A and actinomycin-D treatment (Hori 1982; Auladell et al. 1993), indicating that these structures are ribonucleoprotein (RNP) complexes. The size and number of chromatoid bodies decreases during the neoblast cell differentiation process (Hori 1982).
suggesting that these structures may be involved in neoblast maintenance.

**Pluripotency of the neoblasts**

Although there is no definitive experimental evidence for the pluripotency of neoblasts, which could be proved by clonal cell culture or single cell transplantation, multiple experiments support the notion of the pluripotency of the neoblasts. Planarians irradiated with the appropriate dose of X- or gamma-rays lose their regenerative ability due to the specific elimination of neoblasts (Wolff & Dubois 1948). Planarians with an irradiated anterior half of the body can regenerate a head due to migration of neoblasts from a non-irradiated posterior part (Wolff & Dubois 1948). A population of stem cells, isolated via size fractionation, can restore the regenerative ability of irradiated planarians (Baguñà et al.; Kobayashi et al. 2008). Furthermore, planarian regeneration proceeds in an intercalative, position-dependent manner (Agata et al. 2003), and superfluous body structures, such as a brain or pharynx, are induced when a head fragment is transplanted into the tail region of planarians (Kobayashi et al. 1999). Finally, when a small piece of the middle region of the body is grafted at the original position but in the dorsoventral-reversed orientation, ectopic structures such as a head or tail are frequently formed at the grafted position (Kato et al. 1999, 2001). These observations and the fact that almost any tiny fragment of the planarian body can regenerate an entire organism (Morgan 1898) show not only that the neoblasts can respond to changes of their environment, but also that neoblasts can give rise to all types of cells.

**Heterogeneity of the neoblasts**

We developed a fluorescence activated cell sorting (FACS) method for cells of *D. japonica*, based on Hoechst staining for DNA content and Calcein-AM staining for cell size (Hayashi et al. 2006). Comparison of cell sorting profiles of intact and X-ray irradiated planarians revealed two different X-ray sensitive cell fractions: X1 and X2 (Fig. 3A,B). The X1 fraction is composed of S to M-phase neoblasts, as confirmed by higher DNA
content and gene expression profiles (Fig. 3A; Hayashi et al. 2006). About half of the cells sorted into the X2 fraction are G1 neoblasts, and the remaining half of the X2 fraction and most of the X-insensitive fraction (XIS) are differentiated cells showing tolerance to irradiation (Fig. 3A,B).

Detailed analysis of cells collected by FACS revealed heterogeneity in the neoblast population (Higuchi et al. 2007). Cells were categorized into one of three types according to their morphological features: stem cell, differentiating cell, or differentiated cell. Surprisingly, a considerable number of differentiating cells were observed in the X1 fraction (17% of X1 cells; Higuchi et al. 2007). Neoblasts are thought to stop proliferation after commitment, but this finding indicates that some differentiating cells possess the ability to divide. Heterogeneity among morphologically classified stem cells was also reported, and stem cells classified as “Type B”, which here we rename “Type 2” cells, exist in the X2 fraction (Fig. 3D; Higuchi et al. 2007), and stem cells smaller in size than typical neoblasts (originally “Type A” stem cells, which we rename “Type 1” stem cells, here). Type 2 cells also have a smaller number of chromatoid bodies, and contain more tightly condensed heterochromatin (Fig. 3C,D). It is possible to consider Type 2 stem cells as typical neoblasts in a different phase of the cell cycle from Type 1 neoblasts (Gurley & Sánchez Alvarado 2008). However, the majority of stem cells in the X2 fraction are definitely Type 1 stem cells, which suggests that Type 2 cells may belong to a distinctly new class of planarian stem cells.

Recently, the existence of a highly dormant state of hematopoietic stem cells has been reported (Wilson et al. 2008). In many cases, true stem cells have shown a state of slow cell cycle progression (Fuchs 2009), suggesting that Type 2 stem cells may be slow-cycling stem cells. Type 2 cells may also be descendents of Type 1 stem cells on their way to commitment, which is comparable to reported observations in S. mediterranea (Eisenhoffer et al. 2008). Gene expression analysis in D. japonica has also revealed heterogeneity of the neoblasts (Rossi et al. 2006, 2007; Sato et al. 2006; Salvetti et al. 2009). It seems that, after all, the planarian stem cell system is a more complex system than the homogenous cell population of the neoblasts they were previously thought likely to be.
Molecular features of the neoblasts

Components of the chromatoid bodies

As mentioned above, a distinguishable characteristic of the neoblasts is the presence of chromatoid bodies. The morphological features of chromatoid bodies in planarian ASCs resemble those of well-documented RNP granules in the cytoplasm of germ cells of several animals (Seydoux & Braun 2006), implying commonality of the protein and RNA components between such cytoplasmic structures. Thus far, only two chromatoid body protein components have been identified in planarian neoblasts: DjCBC-1 and SpolTud-1 (Yoshida-Kashikawa et al. 2007; Solana et al. 2009). Both of these proteins are homologues of components of germline granules in other organisms. We identified chromatoid body component-1 (Djcbc-1), which is a gene in *D. japonica* that codes for a protein about 70% identical to members of the RCK/p54/Me31b/Dhh1p family of DEAD box RNA helicases (Yoshida-Kashikawa et al. 2007). DjCBC-1 protein is observed in the chromatoid bodies (Fig. 4A). Expression of tudor homologues in planarian neoblasts has been reported by us and others (Fig. 5A; Yoshida-Kashikawa et al. 2007; Solana et al. 2009). A Tudor-domain-containing protein from *Schmidtea polychroa* was also shown to localize to chromatoid bodies, and to be required for long-term stem cell self-renewal (Solana et al. 2009). Another component is nanos mRNA, which is detected in chromatoid bodies of germline precursor cells described below (Sato et al. 2006).

Piwi and interacting small RNAs in the neoblasts

The Piwi sub-family of Argonaute proteins, and small non-coding Piwi-interacting RNAs (piRNA) are essential for germline development, germline stem cell renewal, epigenetic regulation, and repression of transposable elements (Cox et al. 1998; Aravin et al. 2007; Girard & Hannon 2007; Yin & Lin 2007; Siomi et al. 2008; Malone & Hannon 2009). Piwi-deficient animals show severe defects in germline stem cell maintenance and germ cell differentiation (Lin & Spradling 1997; Cox et al. 1998; Kuramochi-Miyagawa et al. 2004; Carmell et al. 2007). Piwi homologues in planarians, Smedwi-1, -2 and -3 (or DjpiwiA, B, and C, respectively), are exclusively or preferentially expressed in neoblasts (Fig. 2A; Reddien et al. 2005b; Rossi et al. 2007; Yoshida-Kashikawa et al. 2007; Palakodeti et al. 2008; Hayashi et al. in this issue), and are essential for precise cell differentiation and/or stem cell maintenance (Reddien et al. 2005b; Palakodeti et al. 2008). Comprehensive sequence analysis revealed enrichment of piRNAs in neoblasts of *S. mediterranea*, of which 32% mapped to transposons (Friedländer et al. 2009), suggesting that Piwis prevent transposable element activity in the neoblasts of planarians. Piwi family proteins localize to germline granules in fly and mouse (Seydoux & Braun 2006; Kotaja & Sassone-Corsi 2007). Although both DjCBC-1 and DjPiwiA protein are present in the neoblasts (Fig. 4A), DjPiwiA does not seem to co-localize with DjCBC-1 in chromatoid bodies in *D. japonica* (Fig. 4B–D).
Expression of germline-specific genes in the planarian ASCs

As mentioned in the Introduction, the first gene shown to be expressed in planarian neoblasts was vasa-like gene A. DjvlgA codes for proteins with sequence similarity to Vasa, a DEAD box RNA helicase component of germ granules in other animals (Lasko & Ashburner 1988; Fujiwara et al. 1994; Yoon et al. 1997; Shibata et al. 1999). DjvlgA and DjvlgB are expressed in mature testes and ovaries of sexual planarians. DjvlgA, however, is also expressed in neoblasts and differentiating blastema cells, suggesting that DjvlgA may be involved in commitment and differentiation of neoblasts (Shibata et al. 1999; Newmark & Sánchez Alvarado 2002). In fact, DjvlgA and DjvlgB belong to the PL10/DDX3 subfamily of helicases, which is a subfamily of DEAD box proteins, closely related to vasa (Mochizuki et al. 2001). An actual member of the vasa subfamily of DEAD box proteins has been identified in the planarian Dugesia dorotocephala (Mochizuki et al. 2001), and its orthologue is also present in our D. japonica expressed sequence tag (EST) database.

Homologues of several proteins involved in post-transcriptional regulation in the germline of different organisms have since been shown to be relevant to planarian neoblasts. Djpum, a member of the PUF (Pum and FBF)-domain family of proteins required for the maintenance and function of germline cells in flies and nematodes (Lin & Spradling 1997; Parisi & Lin 1999; Crittenden et al. 2002; Wickens et al. 2002), is expressed in planarian neoblasts and brain neurons (Salvetti et al. 2005). RNAi-mediated knock-down of Djpum leads to loss of regeneration and a reduction of neoblast number in D. japonica (Salvetti et al. 2005). Notably, DjCBC-1 homologue Dhh1p interacts physically with Pumilio homologue Mpt5p in yeast extracts (Goldstrohm et al. 2006), which implies that DjPum may also be associated with chromatoid bodies. Similar results with regard to phenotype and expression pattern were observed for bruli in S. mediterranea (Guo et al. 2006). Smed-bruli is a member of the Bruno-like family of proteins, which includes bruno, an RNA-binding protein that represses translation of osk mRNA in Drosophila germline cells (Webster et al. 1997; Nakamura et al. 2004).

Other RNP component homologue genes in the neoblasts

Genes shown to be components of dense ribonucleoprotein structures such as mammalian chromatoid bodies, stress granules and processing bodies (P bodies) are expressed in the neoblasts. These ribonucleoprotein
Table 1. Classification of RNA-binding proteins in planarians according to their expression patterns

<table>
<thead>
<tr>
<th>Homology</th>
<th>Predicted localization</th>
<th>Published gene name or clone ID in planarians</th>
<th>Subcellular localization in planarians</th>
<th>References</th>
<th>E-value (closest Dm or Hs)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neoblasts (Type A)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TIA1 cytotoxic granule associated protein (Homo sapiens)</td>
<td>SG PB</td>
<td>00412_HN (Dj)</td>
<td></td>
<td>Kedersha et al. 1999, 2005</td>
<td>4e-26 HsTIA1</td>
</tr>
<tr>
<td>Y-Box factor protein (Aplysia californica)</td>
<td>SB</td>
<td>03689_HH (Dj)</td>
<td></td>
<td>Nakamura et al. 2001</td>
<td>1e-22 DmYps</td>
</tr>
<tr>
<td>Translation eIF4E protein (A. californica)</td>
<td>SG PB PG</td>
<td>03978_HH (Dj)</td>
<td></td>
<td>rev Eulalio et al. 2007</td>
<td>2e-39 HsEIF4E</td>
</tr>
<tr>
<td>Tudor protein (Xenopus laevis)</td>
<td>CB PG</td>
<td>05895_HH Spoltud-1 (Sp)</td>
<td>CB</td>
<td>Solana et al. 1999; Hosckawa et al. 2007; Boswell &amp; Mahowald 1985</td>
<td>3e-05 Dmtud</td>
</tr>
<tr>
<td>Seawi (Strongloocentrotus purpuratus)</td>
<td>CB PG</td>
<td>DjPiwiA (Dj) Smedwi1 (Sm)</td>
<td>Cytosol</td>
<td>This review; Yoshida-Kashikawa et al. 2007; Reddien et al. 2005a,b; Harris &amp; Macdonald 2001; Kotaja et al. 2006; Houwing et al. 2007; rev Eulalio et al. 2007; rev Kotaja &amp; Sassone-Corsi 2007</td>
<td>2e-68 HsPIWIL1</td>
</tr>
<tr>
<td>Piwi (Botryllus primigenus)</td>
<td>CB PG</td>
<td>Smedwi2 (Sm)</td>
<td>?</td>
<td>Reddien et al. 2005a,b; Palakodeti et al. 2008; Harris &amp; Macdonald 2001; Kotaja et al. 2006; Houwing et al. 2007; rev Eulalio et al. 2007; rev Kotaja &amp; Sassone-Corsi 2007</td>
<td>3e-69 HsPIWIL1</td>
</tr>
<tr>
<td>Neoblasts + other cells (Type B)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Translation initiation factor 3 90 kDa subunit (eIF3 p90) (Schizosaccharomyces pombe)</td>
<td>SG</td>
<td>00218_HN (Dj)</td>
<td></td>
<td>Kedersha et al. 2002</td>
<td>3e-17 HseIF3B</td>
</tr>
<tr>
<td>me31B protein (Drosophila melanogaster)</td>
<td>PB SG PG SB</td>
<td>Dj(CBC-1/Dj)</td>
<td>CB</td>
<td>Yoshida-Kashikawa et al. 2007; rev Eulalio et al. 2007</td>
<td>1e-157 Dmme31b</td>
</tr>
<tr>
<td>PL10 (Danio rerio)</td>
<td>SG PG CB</td>
<td>DjvioAg (Dj) SpolvMgA (Sp)</td>
<td>?</td>
<td>Shibata et al. 1999; Solana et al. 2009; Ming-Chih Lai et al. 2008</td>
<td>1e-161 HsDDX3X</td>
</tr>
<tr>
<td>Putative RNA helicase (DEAD box protein) (D. rerio)</td>
<td>SG PG CB</td>
<td>02217_HH (Dj)</td>
<td></td>
<td>Ming-Chih Lai et al. 2008</td>
<td>5e-70 HsDDX3X</td>
</tr>
<tr>
<td>DEAD (Asp-Glu-Ala-Asp) box poly peptide 48 protein (D. rerio)</td>
<td>NG, nucleus</td>
<td>05792_HH (Dj)</td>
<td></td>
<td>Giorgi et al. 2007</td>
<td>0.0 HsEIF4A3</td>
</tr>
<tr>
<td>Fragile X mental retardation protein 1 (X. laevis)</td>
<td>SG PB NG</td>
<td>06718_HH (Dj)</td>
<td></td>
<td>Antar et al. 2005; Barbee et al. 2006; Kwak et al. 2008</td>
<td>9e-49 HsFXR1</td>
</tr>
<tr>
<td>Putative pumilio (Schistosoma mansoni)</td>
<td>SG PG</td>
<td>DjPum (Dj)</td>
<td>?</td>
<td>Salvetti et al. 2005; Vessey et al. 2006; Noble et al. 2008</td>
<td>2e-130 Dmpum</td>
</tr>
<tr>
<td>Bruno-3 (Tribolium castaneum)</td>
<td>CB Brui (Sm)</td>
<td></td>
<td>Cytosol</td>
<td>Guo et al. 2006; Snee &amp; Macdonald 2004</td>
<td>9e-48 Dmaret</td>
</tr>
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</table>
complexes are implicated in different modes of post-transcriptional regulation of gene expression, such as mRNA decay, mRNA storage and translational repression (Eulalio et al. 2007; Besse & Ephrussi 2008; Balagopal & Parker 2009). In order to consider the composition and function of chromatoid bodies in planarians, we have categorized genes encoding planarian RNA-binding proteins into Type A, Type B, or subpopulation of neoblasts (Table I). Type A means neoblast-specific genes (Fig. 5A). Among proteins encoded by Type A genes, TIA is a stress granule and P body component involved in translational repression and stress granule formation (Forch et al. 2000; Kedersha et al. 2000; Dixon et al. 2003). This gene is also known to regulate alternative splicing of apoptosis-promoting factor Fas mRNA (Izquierdo et al. 2005). Interestingly, neoblast death seems to occur in an apoptotic manner not only under stress conditions, such as irradiation or depletion of vital factors, but also in intact planarians (Hwang et al. 2004; Salvetti et al. 2005). The TIA expression in the neoblasts suggests that stress granules could exist in neoblasts under stress conditions. Type B genes, some of which are required for neoblast maintenance, are expressed in both the stem cells and brain neurons (Fig. 5B; Salvetti et al. 2005; Guo et al. 2006; Yoshida-Kashikawa et al. 2007), indicating that those two types of cells have similar post-transcriptional regulation mechanisms. Interestingly, not all chromatoid bodies contain DjCBC-1 (categorized as Type B) (Fig. 5B and Table 1 Yoshida-Kashikawa et al. 2007), which suggests heterogeneity of chromatoid bodies. One possible reason for this heterogeneity may be an association of the chromatoid bodies with other kinds of RNP granules.

miRNA in the neoblasts

Another class of small non-coding RNA that is robustly expressed in planarians is microRNAs (miRNAs), which are message-specific regulators of gene expression (Palakodeti et al. 2006; Friedländer et al. 2009; González-Estévez et al. 2009; Lu et al. 2009). Large-scale profiling by two different laboratories identified 10 S. mediterranea miRNAs whose expression was enriched in neoblasts, five of which were classified as enriched by both groups (Friedländer et al. 2009; Lu et al. 2009). Interestingly, the function of chromatoid body components during mouse spermiogenesis can be divided into repression of retrotransposons or miRNA processing, by the fact that Miwi and Mili are necessary for retrotransposon silencing, whereas Tudor domain protein Tdrd6 is required for proper expression of miRNAs (Vasileva et al. 2009; Wang et al. 2009). Something similar could be occurring in
the chromatoid bodies of planarian neoblasts, although DjPiwiA is not localized in the chromatoid bodies.

**Germline cell specification from neoblasts by nanos**

Chromatoid bodies are also detected in planarian germline cells (Teshirogi & Ishida 1987). Sexual-state planarians develop mature testes located dorsolaterally, and a pair of ovaries in the ventral side of the neck region, both of which are completely absent in asexual planarians (Newmark et al. 2008). The expression of some neoblast components has been confirmed in germline cells of sexual planarians (Shibata et al. 1999; Newmark et al. 2008; Solana et al. 2009), suggesting a parallel program for regulation of gene expression among neoblast and germline cells in planarians as well.

What regulates the emergence of the mature germ-line? Which genes are responsible for germline cell specification? These questions were partially answered with the identification of nanos, a CCHC zinc-finger protein, which plays a crucial role in germline cell establishment in early embryogenesis, and in germline stem cell maintenance and differentiation, by inhibiting translation of specific mRNAs (Forbes & Lehmann 1998; Asaoka-Taguchi et al. 1999; Kraemer et al. 1999; Wang & Lin 2004; Kobayashi 2005; Nakamura & Seydoux 2008). In planarians, nanos (or nos) is specifically expressed in sparmatogonia and oogonia of sexual planarians, as well as in germline precursor cells in asexual animals (Fig. 5C; Sato et al. 2006; Wang et al. 2007). Depletion of nanos by RNAi in *S. mediterranea* causes clear loss of testis, ovaries and germ cell precursors, but not neoblasts. The co-expression of several neoblast marker genes and nanos in asexual planarians indicates that nanos-expressing cells are a subpopulation of neoblasts (Table 1; Wang et al. 2007). These cells differentiate into mature gonads during epigenetic sexual specification in planarians, suggesting that nanos-positive cells in asexual individuals are germline precursor cells (Sato et al. 2006). Neoblasts show constant cell division, even in intact animals (Newmark & Sánchez Alvarado 2000; Kang & Sánchez Alvarado 2009), whereas germline precursors seem to be arrested at the G2 phase, analogous to Nos-regulated presumptive germline precursor cells (PGCs) in *Drosophila* (Asaoka-Taguchi et al. 1999; Sato et al. 2006).

**Conclusions regarding “molecular features of the neoblasts”**

A pattern is emerging, in which homologues of post-transcriptional regulators in the germline and early development of other organisms (Wickens et al. 2000; Seydoux & Braun 2006) are expressed in the neoblast and/or required to maintain the stemness and viability of neoblasts. Thus, neoblast chromatoid bodies are likely to be involved in post-transcriptional regulation of mRNA, although further studies will be needed to determine their function in detail (Fig. 6A). The mentioned reports indicate that molecular mechanisms common to planarian pluripotent somatic stem cells and germline cells are required for neoblast maintenance: strong post-transcriptional regulation by several RNA-binding proteins and miRNAs, and the assurance of genomic stability required for pluripotency or totipotency by inactivation of transposable elements by Piwi and piRNAs (Fig. 6A).

Generally, the most fundamental difference between somatic and germline stem cells is the inability of

![Fig. 6. Model of molecular mechanisms that regulate (A) neoblasts and (B) germline precursor cells.](image)
germline stem cells to differentiate into somatic cells, in order to assure progeny via sexual reproduction. In Drosophila, nanos-deficient PGCs adopt both somatic and germline fate (Hayashi et al. 2004), which indicates that nanos is crucial for preventing the adoption of somatic fate by germline precursors, and that PGCs have innate multipotency. Based on this, neoblasts maintain pluripotency and therefore can give rise to all types of cells for both asexual and sexual reproduction. Thus, neoblasts possess molecular mechanisms akin to those in germline cells, but germline precursors must maintain their germline-restricted fate until sexualization (Fig. 6B). It is likely that nanos is involved in inhibition of the cell cycle, apoptosis, and differentiation into the somatic state in asexual planarians as well as Drosophila PGCs (Hayashi et al. 2004; Sato et al. 2007). The molecular mechanisms for specification of germline precursors in planarians, apart from the involvement of nanos, are still unclear. Comprehensive gene analysis of germline-specific genes, however, will probably identify genes that play a role upstream, downstream, or with nanos (Zayas et al. 2005; Newman et al. 2008). Better understanding of the process of epigenetic germline specification in planarians should shed light on vertebrate gametogenesis and the evolution of germline cells (Extavour 2007). Thus, planarian stem cells will also provide a good opportunity to understand not only evolutionary aspects of pluripotent stem cells and germline cells, but also the RNA world in the stem cells.

**Signaling molecules involved in neoblast regulation**

Recently, it has been shown that differentiation of the neoblasts seems likely to be regulated by several signaling molecules. RNAi-silencing of β-catenin, which is known to be involved in Wnt signaling in other animals, in S. mediterranea leads to ectopic head formation in the tail region (Gurley et al. 2008; Petersen & Reddien 2008; Adell et al. 2009). Bone morphogenetic protein (BMP) is also required for proper regeneration and maintenance of the dorsoventral axis in planarians (Molina et al. 2007; Orii & Watanabe 2007; Reddien et al. 2007). _nou-darake_ (ndk) encodes a fibroblast growth factor receptor (FGFR) like protein, which lacks an intracellular domain (Cebria et al. 2002a). After knockdown of ndk, ectopic brains are formed beyond the head region (Cebria et al. 2002a). Triple knockdown of _ndk_ and two FGF receptors expressed in the neoblasts of D. japonica, _DjFGFR1_ and _DjFGFR2_ (Ogawa et al. 2002) inhibits ectopic brain formation, suggesting that FGF-like signaling is involved in brain cell differentiation (Cebria et al. 2002a; Umesono & Agata 2009). Also, hedgehog (Shh) signaling controls A-P patterning (Yazawa et al. in press). All of these facts suggest that several signaling molecules direct the proper differentiation of the neoblasts (Fig. 5A).

Interestingly, signaling molecules involved in these pathways are also involved in the regulation of ASCs or germline stem cells in other model organisms. Bone morphogenetic protein (BMP) and Shh are required for germline stem cell maintenance and differentiation in flies. Wnt signaling is required for hair follicle stem cell differentiation in mammals, and FGF for differentiation of embryonic stem (ES) cells (Wong et al. 2005; Kunath et al. 2007; Nishikawa & Osawa 2007; Ying et al. 2008). These connections indicate that the molecular basis for the regulation of pluripotency or multipotency is probably conserved in species among various phyla.

**Conclusions and future prospects**

The expression of genes that are exclusive to the germline in vertebrates is also observed in pluripotent or multipotent ASCs in basal metazoans and some bilaterians, archecocytes of Porifera, interstitial cells of Cnidaria, neoblasts of Annelida, and stem cells of parasitic Arthropoda (Mochizuki et al. 2000, 2001; Shukalyuk et al. 2007; Sugio et al. 2008; Funayama et al. unpubl. data, 2010). As is the case with planarians, these organisms perform asexual reproduction using pluripotent or multipotent ASCs, which suggests that the use of “germline-specific genes” by somatic stem cells may be a way to achieve asexual reproduction (Agata et al. 2006). Furthermore, these basal metazoans produce germline cells from ASCs, which implies that ASCs might have been the evolutionary origin of germline cells (Extavour 2007). Colonial ascidians belonging to Urochordata can also reproduce asexually; however, their multipotent ASCs don’t seem to express “germline-specific genes” (Sunanaga et al. 2006, 2007, 2008). One explanation for this could be the suggested separation of somatic and germline stem cells in colonial ascidians (Laird et al. 2005). Thus, basic research about ASCs in diverse species of various phyla provides a great opportunity to get insight into cell contributions to reproduction, as well as the origin and evolution of germline cells. Comparison of molecular signatures of ASCs in these animals and ASCs in relatively higher metazoans, such as vertebrates, will reveal the common molecular bases of stem cells.

In addition to the natural advantages of planarians, recent technical and bioinformatics advances in planarian stem cell research have made planarians the model organism of choice for studies of stem cell
biology in vivo (Sánchez Alvarado & Kang 2005; Rossi et al. 2008) and epigenetic specification of germ cells (Newmark et al. 2008). As reviewed here, planarians are also intriguing animals for research on RNA regulation and cytoplasmic ribonucleoprotein structures.

Many fundamental issues remain to be resolved. In 1990, Professor K. Watanabe established clonal strains, gifu iruma (GI) and sexualizing special planarian (SSP), from single D. japonica individuals. For approximately 20 years, both strains have been asexually maintained in the laboratory. However, we still don't know how neoblasts maintain pluripotency and genomic stability over time despite their continuous and rapid division (Kang & Sánchez Alvarado 2009). How planarians maintain a constant number of the neoblasts (~30%) in their body is also unclear. Whether there is a stem cell “niche”, which is known to be an important place or group of cells for the regulation of stem cells in other animals, is not known in planarians. We tried to identify neuronal stem cells in planarians by analysis of musashi homologues, but there was no clear evidence of their existence (Higuchi et al. 2008). In fact, whether there are any lineage-committed adult stem cells in planarians, apart from germline precursors, is still unclear. Understanding the complexity and biological-state flexibility of neoblasts in planarians will advance our knowledge of stem cells in general, and the application of ES or iPS cells in the medical field.

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