Micromere lineages in the glossiphoniid leech *Helobdella*

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SUMMARY

In leech embryos, segmental mesoderm and ectoderm arise from teloblasts by lineages that are already relatively well characterized. Here, we present data concerning the early divisions and the definitive fate maps of the micromeres, a group of 25 small cells that arise during the modified spiral cleavage in leech (*Helobdella robusta*) and contribute to most of the nonsegmental tissues of the adult. Three noteworthy results of this work are as follows. (1) The c″ and dm′ clones (3d and 3c in traditional nomenclature) give rise to a hitherto undescribed network of fibers that run from one end of the embryo to the other. (2) The clones of micromeres b′ and b‴ (2b and 3b in traditional nomenclature) die in normal development; the b″ clone can be rescued to assume the normal c′′ fate if micromere c″ or its clone are ablated in early development. (3) Two qualitative differences in micromere fates are seen between *H. robusta* (Sacramento) and another *Helobdella* sp. (Galt). First, in *Helobdella* sp. (Galt), the clone of micromere b′ does not normally die, and contributes a subset of the cells arising exclusively from c″ in *H. robusta* (Sacramento). Second, in *Helobdella* sp. (Galt), micromere c‴ makes no definitive contribution, whereas micromere dm′ gives rise to cells equivalent to those arising from c‴ and dm′ in *H. robusta* (Sacramento).

Key words: Cell cycle, Cell lineage, Equivalence group, *Helobdella*, Leech, Lophotrochozoa, Spiralia

INTRODUCTION

Spiral cleavage is characterized by cell divisions that are oriented obliquely with respect to the animal-vegetal (A-V) axis of the embryo. This results in an offset of approximately 45° between animal and vegetal tiers of sister cells. The offset of successive tiers of cells alternates between clockwise and counterclockwise due to corresponding alternations in the spindle orientations with each round of divisions. The divisions are typically unequal, beginning with third cleavage and generating quartets of animal micromeres and vegetal macromeres.

Roughly ten protostome phyla are classified as exhibiting spiral cleavage (Brusca and Brusca, 1990). Of these, all but the arthropods fall within the Lophotrochozoan clade, as defined by recent molecular phylogenies (Aguinaldo et al., 1997), and the question of whether the division patterns seen in basal arthropods represent true spiral cleavage or convergence was debated even prior to this time (Anderson, 1973). By contrast, it seems beyond question that the spiral cleavage patterns (and trochophore larvae) seen in mollusks and annelids are homologous. Thus, comparisons of cell fates and cell fate specification processes between annelids and mollusks may yield insights about the nature of the ancestral Lophotrochozoan, and into how modern animals with such different body plans could have evolved from that ancestor.

The modified pattern of spiral cleavage in glossiphoniid leech embryos generates three size classes of blastomeres, called teloblasts, macromeres, and micromeres (Fig. 1) (Bissen and Weisblat, 1989; Sandig and Dohle, 1988). In the traditional nomenclature for spiralian embryos, micromeres and macromeres were defined according to the relative positions of sister cells along the A-V axis. This system has led to ambiguities as to the names of clearly homologous cells in different species (e.g. Fischer, 1999; Sandig and Dohle, 1988). For simplicity, we therefore define micromeres as the 25 small cells arising during cleavage (Bissen and Weisblat, 1989; Smith and Weisblat, 1994), independent of the orientation of the division by which they arise.

The micromeres give rise to a mixture of definitive and provisional progeny, in nonsegmental neural and non-neural tissues (Nardelli-Haefliger and Shankland, 1992; Smith and Weisblat, 1994; Weisblat et al., 1984). Micromere derivatives are also important in determining cell fates of certain segmental founder cells (Ho and Weisblat, 1987; Huang and Weisblat, 1996). Moreover, certain micromeres in leech embryos are homologous with blastomeres that have different fates in the embryos of other annelids and mollusks (Damen and Dictus, 1994; Dohle, 1999). Another question of interest
is how cell fates are assigned so that micromeres derived from spiral cleavages contribute to the bilaterally symmetric body plan of the leech. To understand how cell fates are assigned in the micromere lineages in leech and how cell fate decisions might have evolved within the spiralia, we have analyzed the micromeres in embryos of the leech Helobdella robusta with respect to cell cycle composition, timing and orientation of their initial divisions, and the distribution of their clones in the juvenile. For these purposes, we have fate mapped micromeres using fluorescent lineage tracers injected at the time of their initial divisions, and the distribution of their clones in the late embryo using video time-lapse microscopy and the fates and clonal distribution patterns for the individual micromeres. The results allow us to identify a new equivalence group, lay a groundwork for understanding the morphogenesis of the proboscis and other nonsegmented tissues, including some hitherto undescribed neurons, and to compare leeches and gastropod mollusks (another derived spiralian group) in terms of the undescribed neurons, and to compare leeches and gastropod mollusks (another derived spiralian group) in terms of the

**MATERIALS AND METHODS**

**Embryos**

Unless specified, the experiments reported here employed embryos of *H. robusta* (Shankland et al., 1992). They were obtained from animals collected from a minor tributary of the American River in Sacramento, California or, more commonly, from a laboratory breeding colony founded with such animals. Embryos for some experiments were obtained from leeches collected near Galt, California. Where necessary, to distinguish between the two, they are designated as *H. robusta* (Sacramento), and *Helobdella sp.* (Galt), respectively. Helobdella eggs are fertilized internally and arrest at metaphase I until zygote deposition (Fernández and Olea, 1982; Wedeen et al., 1990). Individual clutches of embryos, typically deposited over the course of an hour or more, were divided into subpopulations of more closely synchronized siblings by pooling embryos that underwent a selected cell division within a time window of 5-10 minutes. For example, to analyze the cell cycle and mitotic patterns of micromere d', large clutches of embryos were divided into smaller, more synchronous groups as blastomere CD cleaved to yield blastomeres C and D, which is the parent cell of micromere d'. Micromeres are designated according to Bissen and Weisblat (Bissen and Weisblat, 1989) (Fig. 1). For the purpose of comparing one micromere lineage to another, it is useful to indicate the timing of cell divisions in terms of clonal age at which they occur, i.e. hours since the birth of the given micromere. To place events within the context of overall development, we also designate timings in terms of hours after zygote deposition (AZD).

**Lineage tracing**

Micromeres were pressure-injected (Smith and Weisblat, 1994) about 20 minutes after their birth with either 1,1'-dioctadecyl-3,3,3',3'-tetramethylindocarbocyanine perchlorate (diI; Molecular Probes, Eugene, Oregon, USA; 50 mg/ml in ethanol, then diluted 1/50 in walnut oil) or with a mixture of lysinated, rhodamine-, or fluorescein-conjugated dextran (RDA or FDA, Molecular Probes; 75 mg/ml final concentration) and fast green (1% final concentration) in 0.2 M KCl. Injected embryos were cultured in Helobdella embryo (HL) medium (4.8 mM NaCl, 1.2 mM KCl, 2 mM MgCl2, 8.0 mM CaCl2 and 1 mM maleic acid, pH 6.6) at 23°C. For regular fluorescence microscopy, embryos were counterstained with Hoechst 33258 (1 µg/ml final concentration) after fixation. For confocal microscopy, embryos were fixed in 4% formaldehyde, 0.75× PBS, overnight at 4°C, then rinsed in 1× PBS, incubated for 1 hour in a solution of 50 µg/ml of RNAse in 1× PBS at 37°C, rinsed in sodium chloride, sodium citrate buffer (1× SSC) (Sambrook et al., 1989), incubated in 16.7 µM Sytox Green (Molecular Probes, Eugene, OR) in 1× SSC for 45 minutes, rinsed in 1× SSC and transferred to 100% glycerol for viewing.

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Fig. 1. Time line showing relevant stages of Helobdella development. The numbers on the time line are given in hours after zygote deposition (hours AZD). Micromeres arise by stereotyped cleavages; shaded cells at 7:40, 15:55, 19:45 and at 36 hours AZD represent the micromeres born since the previous time point (for details, see Fig. 2). According to the numerical staging system of Fernández (Fernández, 1980), the micromeres are born during stages 4a to 6b, but the strictly temporal staging system is required for most of the experiments described here. For some fate-mapping experiments, embryos in later stages are designated less precisely using the numerical staging system.
Cell ablations

In some experiments, specific micromeres were killed prior to their first division by ‘over-injection’, i.e. injecting the cell with RDA or FDA until the cell was seen to lyse, as judged by the abrupt leakage of the fast green tracking dye. In other experiments, clones of specific micromeres were killed by photoablation. For this purpose, the parent micromere was injected with FDA as described above, allowed to develop normally for various lengths of time and then exposed to UV light for 2-4 minutes 4× planapo objective on a fluorescence microscope (Nikon E800 equipped with a 100 W Hg bulb) through the fluorescein filter set. This treatment did not bleach the FDA completely from the labeled clone, but did kill the cells; 24 hours later, cells in the FDA-labeled clone had failed to divide and either remained rounded up or had lysed, as judged by the appearance of widely distributed fluorescent debris. This treatment did not affect the development of RDA-labeled clones.

Nomenclature for micromere progeny

To designate progeny within the micromere lineages, we named the cells arising at each division according to the parent cell and their relative positions along the main axis of the division by which they arise, as is used for the nematode Caenorhabditis elegans. Trying to map the definitive axes (anterior/posterior, dorsal/ventral and left/right) onto the early embryo is difficult because of the cell movements involved in later development. To avoid this problem, we designated the relative positions of sister cells with respect to the polar coordinates as follows: for cell divisions that occur mainly parallel to the radius of the embryos, sister cells were designated either a or b quadrant micromeres arise with opposite handedness to those divided subequally. To map the definitive axes (anterior/posterior, dorsal/ventral and left/right) onto the early embryo is difficult because of the cell movements involved in later development. To avoid this problem, we designated the relative positions of sister cells with respect to the polar coordinates as follows: for cell divisions that occur mainly parallel to the radius of the embryos, sister cells were designated either a or b quadrant micromeres arise with opposite handedness to those divided subequally.

RESULTS

Micromere lineages

To study micromere lineages, we used two complementary techniques. Video time-lapse microscopy of micromeres labeled with fluorescent lineage tracers allows us to determine cell cycle duration, defined as the interval between two cytokinases. However, this technique is limited by the need to expose the embryos to UV light. To be sure that the embryos were developing normally, we took fluorescence images no more than once per hour. This resulted in ambiguities in tracking cell divisions, especially once the clone of interest had increased to more than three cells. To overcome this problem, we identified progeny of recent divisions as they entered S phase of the next cell cycle, using immunohistochemical detection of BrdUTP incorporation in carefully staged embryos in which one or more micromere clones were marked by previously injected lineage tracer (see Materials and Methods). The deduced micromeres lineages are shown in Fig. 2. Although BrdUTP incorporation was analyzed mainly to identify mitotic sister cells, these experiments also allowed us to determine the duration of S phase and thus the composition of cell cycle in some micromeres and their progeny (Table 1).

Primary quartet micromeres (a-d')

The primary quartet of micromeres arise sequentially in three steps during third cleavage: first d', then c', then a' and b' together (Bissen and Weisblat, 1989; Sandig and Dohle, 1988). We confirm that glossiphoniid leeches deviate from the standard spiralian pattern in that at each round of division the B quadrant micromeres arise with opposite handedness to those...
in the other quadrants. That is, b' and b'' arise by levorotatory spiral cleavages, whereas b'' arises by a dextrorotatory one (Sandig and Dohle, 1988). The first divisions of the primary quartet micromere are unequal and the larger, animal daughter cells (a',a, b',a, c',a and d',a) divide before the vegetal daughter (a',v, etc.) in each lineage (Fig. 2; Table 1). This stem-cell-like pattern of divisions is maintained for at least three rounds of division, and the smaller, vegetal progeny form columns of cells reminiscent of the blast cells emanating from the teloblasts (Fig. 3). As summarized in Table 1, micromeres d' and c' each divide at 8.75 hours clonal age (15.75 and 16.1 hours AZD, respectively), whereas a' and b' divide at 9 hours clonal age (17.25 hours AZD). Subsequent 'stem cell' cycles are approximately 3 hours each (Fig. 2; Table 1). S phase is estimated at 15 minutes for the stem cells but is significantly longer and ranges from 60 to 95 minutes for the progeny. No appreciable G1 phase is seen in any of the early divisions analyzed.

The similarities of cell division patterns within the a' and d' clones and the b' and c' clones, respectively, are mirrored by their fate maps in the stage 10 embryo (160 hours AZD). As previously described, the primary quartet micromeres contribute neurons to the supraesophageal ganglion, to prostomial epidermis and to epithelial cells of the provisional integument (Fig. 4A,B; moreover, the clones of a' and d' are situated across the embryonic midline from those of b' and c', respectively; not shown) (Nardelli-Haefliger and Shankland, 1993; Weisblat et al., 1984). We also find that all four primary quartet clones contribute progeny to the proboscis, including what we believe are longitudinal muscle fibers, plus cells that constitute the epithelial covering of the proboscis and the proboscis sheath. By stage 10, the remaining epidermal cells of the provisional integument lie along the dorsal midline (Fig. 4B).

**Secondary and tertiary trio micromeres (a''-c'' and a''-c''*)

Beginning with fourth cleavage, the pattern of cell divisions within the D quadrant lineage diverges dramatically from those of the A, B and C quadrants, and will therefore be treated separately in following sections. Within the A, B and C quadrants, two further rounds of highly unequal, spiral cleavages produce secondary and tertiary trios of micromeres (Fig. 2). For the most part, the initial divisions within this group of cells follow a common pattern of equal divisions and slow cell cycles of about 24 hours each, and exhibit similar cell cycle compositions (Fig. 2; Table 1).

At stages 10-11, micromeres a'' and c'' contribute bilaterally symmetric sets of cells to a localized domain within the proboscis, roughly midway along its length (Fig. 4C,D,E); by stage 11, these cells project narrow processes, suggesting that they are differentiating as neurons or connective tissue, or both (Fig. 4D). By contrast, the clones arising from micromeres a'' and c'' within the tertiary trio are not complementary along either the left/right or the dorsal/ventral axes. Some progeny of a'' run along the dorsal surface of the proboscis, whereas others envelop the supraesophageal ganglion (Fig. 4G). Progeny of c'' give rise to a prominent pattern of circular muscle fibers in the proboscis and to a novel set of neuron-like cells that seem to project within the proboscis and posteriorly

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**Fig. 2.** Partial cell lineage diagram for *Helobdella*, emphasizing micromere lineages. The scale on the left indicates the time since zygote deposition (hours AZD). Micromeres, proteloblasts and teloblasts are indicated by capital letters; blast cells (segmental founder cells derived from teloblasts) are indicated by lower case letters. Micromeres and their progeny are indicated by ' '; circled lowercase letters denote the original 25 micromeres. Progeny of the micromeres are designated by a system modified from that used in *C. elegans* (see Materials and Methods for details). Within the lineages leading to the micromeres and their progeny, unequal divisions are indicated by a thickened horizontal line leading to the larger daughter cell. Cell divisions for which the timing is indeterminate are indicated by diagonal lines. NOPQs divisions mirror those of NOPQ, and are omitted from this diagram. a, animal; d, deep; L and R, left and right; pb, polar body; s, superficial; v, vegetal.
## Table 1. Summary of micromere cell cycle and cell fate data for *H. robusta*

<table>
<thead>
<tr>
<th>Cell</th>
<th>Total*</th>
<th>M+G1</th>
<th>S</th>
<th>G2</th>
<th>N*</th>
<th>Size†</th>
<th>Contribution at n=10 (16/16 A/ZD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>d</td>
<td>6.75</td>
<td>5.25</td>
<td>2.5</td>
<td>&gt;7</td>
<td>362</td>
<td>(d' and d) scored together</td>
<td># Neurons to splayophaegalian ganglion, putative longitudinal muscles and other cells to proboscis, epithelial cells to proboscis, proboscis sheath,othorax and posteroventral segment (Figure 4F). Clones d’ and d are scored among those of b’ and c*, respectively (Weisblat et al., 1984; Nardelli-Haefinger and Shankland, 1993).</td>
</tr>
<tr>
<td>d a</td>
<td>2.75</td>
<td>0.25</td>
<td>2.5</td>
<td>&gt;7</td>
<td>112</td>
<td>(a’ and c’ scored together)</td>
<td></td>
</tr>
<tr>
<td>d v</td>
<td>3.675</td>
<td>0.25</td>
<td>1</td>
<td>&gt;5</td>
<td>5</td>
<td>1.5</td>
<td># Cell cycle progression for micromeres c’ and a’ is the same as for d’ and b’, respectively, and is omitted.</td>
</tr>
<tr>
<td>d’ av</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td># Bilaterally symmetric sets of cells to proboscis, roughly midway along its length (Figure 4, C, E); by stage 11, these cells project narrow processes, suggesting that they are differentiating as neurons and/or connective tissue (Figure 4D).</td>
</tr>
<tr>
<td>a at</td>
<td>244</td>
<td>1.75</td>
<td>1.75</td>
<td>&gt;1</td>
<td>175</td>
<td>0.75</td>
<td>0.25</td>
</tr>
<tr>
<td>b b’ t s’</td>
<td>244</td>
<td>1.75</td>
<td>0.25</td>
<td>0.5</td>
<td>224</td>
<td>0.75</td>
<td>0.25</td>
</tr>
<tr>
<td>c c’ d’ s’</td>
<td>244</td>
<td>0.25</td>
<td>0.25</td>
<td>&gt;1</td>
<td>0.25</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td>d m’ d’ s’</td>
<td>18.5</td>
<td>1.25</td>
<td>0.25</td>
<td>&gt;1</td>
<td>17.5</td>
<td>0.75</td>
<td>0.25</td>
</tr>
<tr>
<td>doppq</td>
<td>153</td>
<td>-</td>
<td>0.25</td>
<td>-</td>
<td>0.25</td>
<td>-</td>
<td>111.5</td>
</tr>
<tr>
<td>doppq’ y doppq a</td>
<td>-</td>
<td>0.25</td>
<td>0.25</td>
<td>-</td>
<td>0.25</td>
<td>111.5</td>
<td># Epithelial cells to proboscis sheath (Figure 4H), connective tissue or sheath to subesophagalian ganglion.</td>
</tr>
<tr>
<td>doppq’ va doppq’ vv</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td># Epithelial cells of the subesophagalian ganglion at ventral side of the embryo (Figure 4L).</td>
</tr>
<tr>
<td>doppq v doppq a</td>
<td>-</td>
<td>0.25</td>
<td>0.25</td>
<td>-</td>
<td>0.25</td>
<td>12.5</td>
<td>25.25</td>
</tr>
<tr>
<td>doppq’ va/ds</td>
<td>-</td>
<td>0.25</td>
<td>0.25</td>
<td>-</td>
<td>0.25</td>
<td>12.5</td>
<td>25.25</td>
</tr>
<tr>
<td>w v’ a’</td>
<td>12.25</td>
<td>0.25</td>
<td>0.25</td>
<td>-</td>
<td>0.25</td>
<td>11.75</td>
<td>0.25</td>
</tr>
<tr>
<td>w” v” a”</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

Cells are designated as described in the text (and see Fig. 2). Estimations of cell cycle composition were made using data from video time-lapse microscopy of labeled clones in living embryos, or from BrdU incorporation by groups of synchronized embryos fixed at selected time points, or both (see Materials and Methods for details). *The total duration of the cell cycle was defined as the interval between the times at which cells rounded up in the course of successive divisions. Mitosis was not scored in these embryos, but lasts ~30 minutes in all early blastomeres examined in *H. triseriatus* (Bissen and Weisblat, 1989). Time intervals are given in hours. ^1We assume that cytokinesis initiates during mitosis and completes soon after mitosis. Thus, when a given cell at one time point was unlabeled and at the next time point (30 minutes later) it had divided and entered S phase, it meant that mitosis and G1 phase (if any) had ended within the previous 30 minutes, and that G1 phase was brief or nonexistent, denoted in this table by ~. Time points in which some portion of the newly divided cells had not yet entered S phase were interpreted as evidence of a definitive G1, but less than 0.25 hours. ^2The duration of S phase was estimated by the number of intervals at which BrdU was incorporated (15 pulses at 30 minute intervals). ^3G2 phase is estimated as the time interval between the end of S phase and the point at which the cell rounds up to divide. This probably overestimates G2 duration, because mitosis usually begins before cell rounding, but the error introduced is small relative to the long G2 phases observed. ^4Total number of embryos used in BrdU/TP pulse experiments to analyze cell cycle composition. **Relative sizes of sister cells (see Materials and Methods for definition of unequal division).
from the subesophageal ganglion, lateral to the ventral midline within the germinal plate, reaching at least as far as midbody segment M17 (Fig. 5A-C,E). A third set of cells arising from c” appears as mesenchyme or neurons, or both, within the presumptive anterior sucker (Fig. 5C,D).

Micromeres b” and b’” were unique in that we were unable to detect any definitive progeny from these two cells in stage 10 embryos. In these experiments, b” or b’” was injected in more than 70 embryos. Of these, -40 b”-injected and -40 b’”-injected embryos survived to stage 10, but no labeled cells were observed in any of these specimens. Further experiments revealed that the clones arising from cells b’ and b” die in normal development, which explains this result.

**Cell fate plasticity in the b” lineage**

Previous fate mapping experiments revealed that all six ‘trio micromeres’ form similarly compact and well-labeled clones at clonal ages 49.7-52.2 hours (Smith and Weisblat, 1994). Using video microscopy to follow b” and b’” clones during later development (Fig. 6), we found that small fluorescent particles appeared around the clones at some time between 50-75 hours clonal age (Fig. 6B; 60-85 hours AZD). We interpret these particles as cellular debris resulting from the death of the labeled cells. Over time, this debris either remained confined within a fluorescent ‘bag’ (Fig. 6C-E) or scattered over the embryo beneath the provisional integument.

These observations confirm that the clones derived from micromeres b” and b’” normally die prior to stage 10. Is the death of the b micromere clones induced by cell interactions? To address this question, we attempted to rescue b” or b’” micromeres by ablating one or more nearby cells, as shown in Table 2.

Rescue of b” was obtained in all 21 embryos in which micromere c” was ablated. In these embryos, the distribution of the surviving b” progeny at stage 10 resembled the normal pattern of c” progeny (compare Fig. 4D,E; Fig. 7A,B). No rescue of b” was obtained by ablating any other cell of those tested, including cell a”, which makes a clone that is bilaterally symmetric to the normal c” clone (Table 2).

As a further step towards understanding the nature of the interactions signaling the fate of the b” clone, we performed a series of experiments in which c” was labeled with FDA and b” was labeled with RDA; the c” clone was photolesioned at progressively later times and the fate of the b” clone was determined. These experiments revealed that the b” clone could be rescued to the normal c” fate with 100% efficiency when it was less than 50 hours clonal age (59 hours AZD) and not at all by the time it had reached 58 hours clonal age (67 hours AZD; Fig. 8). This result suggests that the b” is committed to die at ~50 hours clonal age, which is also the time we see the first evidence of dying cells in the b” clone in normal development. These results do not conclusively identify the source of the fate-determining signals, and we cannot exclude the possibility of direct or indirect signaling by the debris of the lesioned c” clone. But the simplest interpretation of our results is that the b” clone dies in response to a signal from the c” clone and that b” commits to die soon after receiving the signal from the c” clone. At this time, the b” and c” clones each comprise six to ten cells.

In the rescue experiments described above, the entire set of cells in the normal c” clone arose from either c’” (in eight normal embryos; Fig. 7A) or from b” (in 21 embryos where c” was killed before the b” clone committed to die; Fig. 7B) or were missing (in five embryos where the c” clone was killed after the b” clone was committed to die; not shown). However, in one embryo in which the c” clone was photolesioned at 48 hours clonal age, the resultant stage 10 embryo contained an intermingled mosaic of RDA- and FDA-labeled cells (Fig. 7C); the total number of labeled cells seemed normal. We interpret this result as reflecting a partial kill of the c” clone, with a correlated partial rescue of the b” clone.

In contrast to the results with the b” lineage, attempts to rescue the b’” clone were seemingly successful in only 1 of 54 experimental embryos (Table 2). In this embryo, the a’” micromere was supposed to have been ablated just prior to injecting b’” with lineage tracer, and the labeled clone closely resembled the normal a’” pattern (not shown). Given this low success rate and the technical difficulty of the experiment, it seems likely that this apparent rescue of the b’” cell resulted from accidentally killing b” and labeling a’” with lineage tracer.

**DM-derived micromeres (dm’ and dm”)**

Cells dm’ and dm” are similar in the duration (~19 hours) and composition of their cell cycles (Fig. 2; Table 1). Further
divisions have been observed only for dm’. The secondary cells divide equally and, as in other micromere lineages, with a much shorter cell cycle than the parent micromere (~5 hours).

The definitive fates of these two cells differ greatly. At stage 10, dm’ gives rise to a prominent pattern of circular muscle fibers in the proboscis that is complementary to those generated by micromere c” (Fig. 5A-C, D). In addition, as with micromere c””, well-labeled dm’ clones include one or more cells exhibiting a previously uncharacterized neuronal morphology within the proboscis and germinal plate; thin processes of these cells seem to have grown throughout the surface of the germinal plate (Fig. 5A,B). A more prominent process runs near the lateral edge of the germinal plate for the entire length of the embryo and then ramifies just dorsal to the fused ganglia in the posterior sucker (Fig. 5E,F). A third set of cells arising from dm’ appears as mesenchyme or neurons, or both, within the presumptive anterior sucker (Fig. 5C,D).

The dm’ clone contributes bilaterally to the ventral covering progeny to the epithelium of the provisional integument, which by stage 10 lie compressed along the dorsal midline (arrows). (C,D) Anterior end of an embryo in which micromere d’ was injected with RDA shows labeled progeny in supraesophageal ganglion (black arrow), prostomial epidermis (white arrow), and epithelial cells of the provisional integument (arrowhead). (B) An entire embryo in which micromere a’ had been injected with RDA. This view illustrates that, in addition to the anterior cells (as in A), the primary quartet micromeres contribute progeny to the epithelium of the provisional integument, which by stage 10 lie compressed along the dorsal midline (arrows). (C,D) Anterior ends of embryos at early and late stage 10, respectively, in which micromere a” had been injected with RDA. At early stage 10, the a”’ clone comprises an undifferentiated set of cells within the left half of the proboscis (C); by late stage 10 (D), these cells project narrow processes, suggesting that they are neurons (arrow) or connective tissue (arrowhead), or both. (E) Right side of the anterior end of an embryo in which micromere c” had been injected with RDA (compare with C). (F) Right side of the anterior end of an embryo in which micromere b”’ had been injected with RDA and micromere c” was ablated by over-injection (compare with E). (G) Anterior end of an embryo in which micromere a”’ had been injected with RDA. Progeny include putative neural or connective tissue cells (arrowheads), or both, associated with the supraesophageal ganglion and a parallel array of elongated cells (arrow), perhaps retractor muscles, within the dorsal proboscis sheath. (H) Right side of the anterior end of an embryo in which micromere dnpq’ had been injected with RDA. Progeny include epidermal cells of the proboscis sheath, what appear to be glial cells in the subesophageal (slanted arrow) and supraesophageal (arrowhead) ganglia, and some neurons or connective tissue in the proboscis (horizontal arrow). Micromere dnpq’’ generates a mirror image clone on the left side of the embryo (not shown). (I) Side view, focusing on the posterior sucker, of an embryo in which micromere opq’ had been injected with RDA. Progeny include epidermal cells in the provisional integument (horizontal arrow), which are in the process of being sloughed off in this late stage 10 embryo and in the skin of the posterior sucker (vertical arrow). Inset shows a ventral view of the posterior sucker, where the opq’-derived epidermal cells seem to persist. (J) Right side of the anterior end of an embryo in which micromere dm” had been injected with RDA. Progeny include what appear to be epidermal cells on the outer surface of the proboscis sheath (arrow); from this clone, cell debris (arrowheads) is usually seen between the yolk cell and the germinal plate. (K) Side view of an embryo in which nopq’ had been injected with RDA and nopq’’, had been injected with FDA. Both clones gives rise to epidermal cells of the provisional integument (arrowheads) plus a few neurons in the anterior portion of the subesophageal ganglion (vertical arrow) and, more anteriorly, epidermal cells in the anterior sucker or mouth, or both (horizontal arrow). Within this latter group, the nopq”-derived cells invariably lie anterior to the nopq”-derived cells. The right nopq’ and nopq” clones (not shown) are bilaterally symmetric to those of the left nopq’ and nopq” clones, respectively. (L) Side view of an embryo in which the opq’ clone was uniquely labeled with RDA by injecting blastomere OPQ with RDA and OPQ’ with FDA (see Materials and Methods). Progeny (arrow) comprise cells in the putative anterioventral adhesive organ. Inset shows boxed area at higher magnification.

Scale bar: 50 μm in A,C,D-H; 100 μm in B,I-L; 50 μm in inset to I; 30 μm in inset to L.
of the proboscis sheath (Fig. 4J). Other dm" progeny appear to be connective tissue or sheath associated with the anterior portion of the nerve cord, including the subesophageal ganglion. In addition, when micromere dm' had been labeled, we observed a random pattern of irregular fluorescent spots throughout the embryo (Fig. 4J). We interpret this material as cell debris, suggesting that a significant amount of cell death occurs among the dm" progeny.

Fig. 5. Definitive progeny of micromeres dm' and c" at stage 10 (~160 hours AZD). (A) Digital montage, combining the in focus portions of 59 optical sections (10×, 0.45 NA objective; 0.8 μm steps; 2D ‘no neighbors’ deconvolution (Metamorph, UIC) of each section prior to montaging) comprising a side view through an embryo in which micromere dm' had been injected with RDA and micromere c" with FDA (dorsal is up; anterior to the left; see Materials and Methods for details). (B) The same embryo and imaging procedures as in A, but viewed through a 20×, 0.75 NA objective for higher resolution (74 optical sections; 0.7 μm steps), and without the Hoechst fluorescence images, to bring out the details of the labeled cells. The dm' and c" clones contribute prominent, interdigitated sets of circumferential fibers, presumably muscles, to the proboscis. Additional labeled cells lie within the proboscis (arrows in C), some of which appear to be part of a most curious and hitherto undescribed network of nonsegmental, interconnected fibers that reaches throughout the body wall of the embryo. (The following abbreviated description of this network was drawn from observations of more than 15 embryos in which both c" and dm' were labeled, three in which c" alone was labeled and six in which dm' alone was labeled.) The network consists of five main fibers on each side of the animal. Two roughly parallel fibers on each side (vertical arrows) run the length of the animal near the surface of the body wall; a dorsolateral fiber runs near the edge of the germinal plate and a ventromedial fiber lies ~1/4 of the distance from the ventral midline to the dorsal midline. These two fibers extend to the posterior end, where one or both ramify just dorsal to the seven fused ganglia that innervate the tail sucker. Within the anterior midbody, three more main fibers on each side loop between the dorsolateral and ventromedial fibers, at the approximate levels of midbody segments 2, 5 and 8 (horizontal arrows). Additional fibers are present in the anterior midbody segments, but could not be reconstructed in their entirety. This accounts for apparent discontinuities in some fibers; note that many breaks in the fibers in the low resolution image (A) are shown to be continuous in the higher resolution image (B). Note in particular that individual, apparently continuous fibers comprise juxtaposed segments of distinct red (dm'-derived) and green (c"-derived) cells. (C) Lateral view of the proboscis of the same preparation (anterior towards the left, dorsal is upwards) using the same imaging procedures as in A, but viewed through a 40×, NA 0.75 objective (29 optical sections; 0.5 μm steps). Arrows indicate additional cells within the proboscis and proboscis sheath. (D) Combined fluorescence and brightfield (DIC optics) images of a transverse plastic section (~10 μm) through the proboscis at about the level of the vertical arrow in C. Circumferential fibers are visible within the proboscis (p). Segments of the fiber network (arrows) are visible in the sheath (s). (E) Digital montage of fluorescence micrographs made from three obliquely horizontal plastic sections (~10 μm each) through the dorsal region of the posterior sucker in a roughly horizontal plane (anterior is upwards). The dm'-derived region of the fiber network ramifies in a bilaterally symmetric fashion (better visible on the left, owing to the oblique plane of section). The branches tend to lie between the seven segmental ganglia that have fused to form the caudal ganglion (see also A). Some cell bodies are visible (arrows). (F) Digital montage of the developing posterior sucker of the embryo shown in A,B (20×, 0.75 NA objective; 58 sections, 0.7 μm steps) showing a side view of the ramifying fibers in the tail sucker, just dorsal to the seven fused ganglia (C1-C7). To maintain the same orientation as in A,B, prospective dorsal is downwards in this panel, owing to the curvature of the embryo. Scale bar: 100 μm in A,B; 50 μm in C-F.
Fig. 6. Rise and fall of the micromere b‘’ clone in normal development. Combined brightfield and fluorescence live images of one typical embryo (22 total) in which micromere b‘’ had been injected with RDA (0 hours clonal age, 12 hours AZD, not shown). (A) Animal view at 24 hours clonal age (36 hours AZD; see Fig. 1); the labeled clone comprises two cells (arrowheads) within the micromere cap (dotted contour). (B) Dorsal view at 63 hours clonal age (75 hours AZD, see Fig. 1). By this point, the clone (arrowhead) comprises six to ten cells within the anterior portion of the germinal plate (dotted contour shows germinal plate and part of right germ band), but cell death is probably already under way, as evidenced by isolated cellular debris (arrow). (C) Lateral view at 111 hours clonal age (123 hours AZD); by this stage the remnants of the b‘’ clone (arrow) are confined to a fluorescent ‘bag’ trapped between the germinal plate and the yolk. (D,E) Each panel shows the b‘’ clone follows a very similar time course (not shown). Scale bar: 100 μm.

DNOPQ-derived micromeres (dnopq’, dnopq’’ and dnopq’’’)

As outlined by Dohle (Dohle, 1999), the particular pattern of divisions by which the ectodermal precursor cell DNOPQ (micromere 2d in classic nomenclature) makes three micromeres before dividing equally to form left and right homologs is a characteristic and highly conserved feature of annelid development. Our results extend previous observations (Smith and Weisblat, 1994) that cells dnopq’ and dnopq’ act as left/right homologs, whereas dnopq’’ follows a different fate.

Table 2. Ablation of neighboring micromeres can rescue the b’’ clone, but not b’’’

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In each of 103 embryos, either b’’ or b’’’ was injected with RDA; one or more neighboring micromeres was ablated by over-injection and the fate of the RDA-labeled clone was determined. The diagram on the right depicts the relative positions of the various micromeres after a’’’ and b’’ are born, but experiments involving b’’ were initiated before those cells arise.

Similarities between dnopq’ and dnopq’’’, and the differences between these cells and dnopq’’’, are apparent as soon the cells are born, in that dnopq’ and dnopq’’’ exhibit a 15 minute G1 phase that is absent in dnopq’’’. The brief G1 phase in these cells was not observed by previous workers (Bissen and Weisblat, 1989), presumably because the 30 minute pulses of BrdUTP incorporation they employed did not permit them to discriminate shorter events. By contrast, we find no G1 phase for dnopq’’’ even using 15 minute pulses of BrdUTP. We described two to three further cell cycles in each of the three dnopq micromere lineages (Table 1, Fig. 2). Divisions in the dnopq’ lineage preceded those in the dnopq’’’ lineage by the amount expected from the 1 hour difference in the times of their births. As for the other lineages, the secondary cells generally divided more rapidly than did the parent micromeres. Cell dnopq’’’ divides unequally after ~15 hours, giving a smaller cell (dnopq’’’a) closer to the primary quartet micromeres and a larger cell (dnopq’’’v) closer to the OPQ blastomeres. The daughters of micromere dnopq’’’ exhibit much greater variability in cell cycle duration than for any lineage, except opq’’ and n’, ranging from 4 to 8 hours for dnopq’’’p and from 9 to 13 hours for dnopq’’’a.

As previously described for stage 7 (Smith and Weisblat, 1994), dnopq’ and dnopq’’ clones appeared as a left/right pair at stage 10. Each clone contributes cells to the epithelium of the provisional integument (not shown), to the epithelium of the proboscis and its sheath, plus what appear to be glial cells in the subesophageal and supraesophageal ganglia and some neurons associated with the proboscis (Fig. 4H). Later still, cell
Fig. 7. Micromere fate differences between *H. robusta* (Sacramento) and *Helobdella* sp. (Galt). Fluorescence micrographs of stage 10 embryos in which micromeres b" and c" had been injected with RDA and FDA, respectively. (A-C) *H. robusta* (Sacramento). (A) In normal development, c" contributes a group of cells to the proboscis (see also Fig. 4), and the b" clone has died. (B) When c" is ablated (by photolesioning at clonal age 36 hours; see Fig. 8), the b" clone survives and generates a set of cells resembling the normal c" progeny. (C) In a single embryo in which the c" clone was photolesioned at clonal age 48 hours, some progeny of both b" and c" survived and intermingled both anteroposteriorly and dorsoventrally. (D) In contrast to the foregoing, the normal development of *Helobdella* sp. (Galt) entails the contribution of definitive progeny by both micromeres b" and c". Note that in this species, the b" and c" progeny are largely confined to the ventral and dorsal portions of the proboscis, respectively. Scale bar: 50 μm.

debri is observed just within the anterior ventral body wall when either dnopq" or dnopq" are labeled (not shown), suggesting that significant numbers of cells die in both these clones.

Micromere dnopq" gives rise exclusively to epithelial cells of the provisional integument (Smith and Weisblat, 1994). By stage 10, all the remaining cells in this clone lay along the dorsal midline (not shown).

**NOPQ-derived micromeres (nopq"LR and nopq"LR')**

Although the left and right nopq' and nopq" micromeres arise as true bilateral homologs, we have observed slight but reproducible differences in the cell cycles of the parent NOPQ blastomeres. Thus, the right nopq' and nopq" micromeres are each born ~5 minutes before their contralateral homologs. In contrast to most other serially produced micromeres but similar to dnopq' and dnopq", micromeres nopq' and nopq" seem to follow quite similar fates, as judged both by their division patterns and by the fates of their clones at stage 10.

Immediately upon their birth, cells nopq' and nopq" go into a 20 minute S phase followed by a 12.5 hour G2 phase. Each of these micromeres divides unequally, giving rise to a smaller animal cell (nopq'.a; nopq".a) and a larger vegetal cell (nopq'.p; nopq".p) having roughly twice the diameter. Both sister cells exhibit an S phase of ~3 hours duration, but although the larger cell in each pair has a 2.5 hour G2 phase, the small cell in each pair has a G2 phase longer than 8 hours. The larger cells (nopq'.v and nopq".v) divide after 5.5 hours and give rise to equal-size daughter cells with no detectable G1 phase and an S phase of ~1 hour duration.

By stage 10, each nopq' and nopq" clone has contributed some epithelial cells to the provisional integument; epidermal cells to the anterior sucker or oral opening, or both; plus a few neurons to the anterior portion of the subesophageal ganglion. As expected, the left nopq' and nopq" clones are bilaterally symmetric to those of the right nopq' and nopq" clones, respectively. On each side, the contributions of nopq' and nopq" are similar, but not identical (Fig. 4K). Moreover, ablating the nopq' cells does not affect the fates of the nopq" cells, and vice versa (data not shown).

**OPQ-derived micromeres (opq"LR and opq"LR')**

Of all the 25 micromeres, the pair of opq' cells are the most difficult to observe or label by direct microinjection (Smith and Weisblat, 1994). The cells are born beneath the micromere cap between cells N and OPQ'; attempts to inject them with lineage tracer often result in labeling other micromeres. For this reason, we used a subtractive method (Smith and Weisblat, 1994; Zackson, 1982) for labeling opq' clones, injecting OPQ with RDA and OPQ' with FDA, so that the opq' clone was uniquely labeled with RDA only. By contrast, the opq" micromeres arise in a prominent location between the OPQ" blastomeres and are easily identified and injected.

The opq' cells have a cell cycle of ~17.5 hours, most of which is spent in G2 phase. There is no detectable G1 phase and S phase lasts only ~25 minutes. The division is somewhat unequal, yielding a larger cell called opq'.v (proximal to the teloblasts) and a smaller cell called opq'.a (distal to the teloblasts). Cell opq'.v divides ~4 hours later (Table 1); we did not observe the division of opq'.a in the time periods we sampled, up to 22 hours clonal age of the parent opq' micromere.

At stage 10, the opq' clone is confined to a structure located
anterior to the subesophageal ganglion at or near the surface on the ventral side of the embryo (Fig. 4L). We believe that this structure is the adhesive organ by which the embryos normally attach to the ventral surface of their parent in the time interval between hatching from the cocoon and developing a functional rear sucker.

The first division of opq” is equal and occurs 9 hours after its birth, yielding cells opq”d and opq”s. For these daughter cells, S phase is as rapid as in a teloblast, lasting less than 15 minutes, but the overall cell cycle is much longer, ranging from 11 to 14 hours for both cells. There is no fixed order to the divisions of opq”d and opq”s and the subsequent divisions of cells in the opq” clone are rapid but variable in terms of orientation and timing. The average size of the opq” clone increases from 4.5±0.8 (n=6) cells at 21.75 hours clonal age to 6.8±1.1 (n=6) cells at 24.25 hours clonal age. The indeterminacy of the divisions in the opq” clones (along with the n’ and dnpq” clones) correlates with the fact that they give rise to a pure and apparently homogeneous population of epithelial cells for the provisional integument. By stage 10, the opq” clones occupy the posterior end of the dorsal midline and on the ventral and lateral surfaces of the posterior sucker (Fig. 4I).

N-derived micromeres (n’L/R)
The first division of n’ is unequal and occurs ~12 hours after birth. S phase in the progeny lasts less than 15 minutes and the larger, more vegetal, cell n’v divides first, after ~9 hours. As in the dnpq” and opq” clones, subsequent divisions in the n’ clones are equal and variable in terms of timing and orientation. G1 phase is lacking and S phase seems constant and usually short (15 minutes or less) in these cells; thus, the variability is due to variable length of G2 phase.

Micromere n’ gives rise exclusively to epithelial cells of the provisional integument (Smith and Weisblat, 1994). By stage 10 (155 hours AZD), no remnant of the n’ clone could be detected.

Micromere fate differences between H. robusta (Sacramento) and Helobdella sp. (Galt)

In the course of our experiments, we had occasion to use embryos from leeches collected from a site near Galt, California, roughly ten miles from where the paratype and holotype H. robusta were obtained (Shankland et al., 1992). We initially assumed that these leeches were simply another population of H. robusta, and as expected, their embryonic development was indistinguishable from that of the Sacramento population in most respects (data not shown). Two sets of observations put this assumption of identity in doubt, however, and comparisons of mitochondrial DNA sequences strongly suggest that they are in fact two different species (F. Z. Huang and A. E. Bely, personal communication).

First, in embryos of Helobdella sp. (Galt), the clone of micromere b” did not die. Instead (Fig. 7D), b” and c” each contributed to a set of neurons similar to those arising exclusively from c” in H. robusta (Sacramento). The contributions from b” and c” did not intermingle, in contrast to the one H. robusta (Sacramento) in which both b” and c” clones survived (Fig. 7C). Second, in Helobdella sp. (Galt), micromere c” does die, and circumferential fibers in the proboscis arise entirely from micromere dm’ (not shown). These differences between Helobdella sp. (Galt) and H. robusta (Sacramento) were observed with complete reproducibility (25 embryos from two different individuals for Helobdella sp. (Galt) and more than 70 embryos from more than seven individuals for H. robusta (Sacramento).

DISCUSSION

Micromere lineages in leech

In glossiphoniid leeches, 25 small cells arise during cleavage (7−22 hours AZD in H. robusta). This set of cells is not identical to cells defined as micromeres according to the classical notions of spiral cleavage, but we group them together as micromeres in Helobdella because they all contribute to nonsegmental tissues, and exclude others (2d=DNOPQ and 4d=DM”) because they are proteloblasts. It had been shown previously that, by the onset of epiboly (~60 hours AZD), these micromeres in Helobdella embryos make stereotyped contributions of cells either to the superficial epithelium of the provisional integument, or to sets of deep cells that presumably contributed to definitive nonsegmental tissues of the adult leech, or both (Smith and Weisblat, 1994). These contributions are stereotyped in terms of the approximate size and location of the clones and the distribution of their cells between deep and superficial layers.

We have further characterized the micromere lineages in two ways. First, we have detailed the initial division in each micromere lineage in terms of cell cycle duration and composition, and the symmetry and orientation of the divisions. Second, we have mapped their descendant clones to the clone of Helobdella sp. (Galt), the clone of H. robusta (Sacramento). The variability is first evident in the duration of G2 phase, and not S phase. Variability in cell cycle duration occurs from cell to cell within these clones, rather than on a clone to clone basis, so that the order of cell divisions within these five clones also varies.
As described previously (Smith and Weisblat, 1994), we found that opq clones proliferate at about twice the rate of the dnpq clones. Our present results indicate that this difference in proliferation rate results simply from differences in the average cell cycle duration between the clones and not from a difference in the pattern of cell division (i.e. not a case of geometric versus arithmetic proliferation).

For most of the cells studied, there is no obvious pattern to the cell divisions, but the primary quartet micromeres (a’, b’, c’ and d’) are an exception. For at least the first three cell divisions, all four of these cells exhibit teloblastic, stem-cell-like divisions. These divisions are unequal in terms of cell size; the larger sister cell lies posterior to the smaller one in each case and also has a shorter cell cycle time (Fig. 2; Fig. 3). The divisions are also unequal in cell fate, in that the smaller cells contribute exclusively to the superficial epithelium, whereas the larger, posterior cell is the one that ultimately contributes ‘deep’, definitive progeny to the supraesophageal ganglion and other nonsegmental tissues, as well as additional superficial epithelial cells. The point at which the deep and superficial cell fates are finally segregated remains to be determined.

As reported previously (Smith and Weisblat, 1994), micromeres b’ and b” contribute exclusively deep progeny at the onset of epiboly. And like the other cells that contribute exclusively to ‘deep cells’ (a”, a””, c”, c””, dm, dm”, opq18R), b” and b”” undergo a long G2 phase (~22 hours) prior to an equal first division. Thus, the discovery that neither micromere b” nor b”” make any definitive contribution to the embryo was unexpected. Moreover, the observation that these cells can be killed at birth without observable effects on development suggests that their clones are vestigial in H. robusta.

The finding that micromere b” can be rescued and induced to follow the c” fate when micromere c” is killed suggests that micromeres b” and c” constitute an equivalence group, in which giving rise to the normal c” clone is the primary fate, and in which the secondary fate is cell death. By contrast, we found no combination of ablations that was able to rescue the b”” clone.

Comparison with other leeches and oligochaetes

The patterns of micromere-forming divisions in H. robusta (Smith and Weisblat, 1994) are essentially identical to those in two other glossiphoniid leech species that have been examined, namely Theromyzon tessulatum (Sandig and Dohle, 1988) and Helobdella triserialis (Bissen and Weisblat, 1989). This is not surprising given the extensive conservation of micromere-forming cleavage patterns throughout the Annelida (Dohle, 1999).

The only other annelid for which a comparable analysis of embryonic cell cycle compositions has been carried out is the closely related species H. triserialis, by Bissen and Weisblat (Bissen and Weisblat, 1989), who did not treat all the micromeres or any of their progeny. The cell cycles for which data is available from both species exhibit similar compositions, except that S phase in the secondary and tertiary micromere trios ranges from 55 to 90 minutes in H. robusta (Table 1), significantly longer than the 15 minute S phases of the their homologs in H. triserialis (Bissen and Weisblat, 1989).

Given this extensive conservation of cleavage patterns and micromere cell cycle compositions, we were particularly surprised to find clear, qualitative differences in the fates of certain micromeres between two leeches that we initially assumed were the same species. In each population (H. robusta (Sacramento) and Helobdella sp. (Galt)), one micromere dies that makes definitive progeny in the other population. One can imagine that such cells are now ‘evolutionarily available’ for the production of novel structures.

Comparison with mollusks: cellular origins of bilateral symmetry

The Spiralia comprise about ten phyla, among which Annelida and Mollusca are the most speciose. Current molecular phylogenies suggest that all spiralian fall within the clade Lophotrochozoa, and that the spiral cleavage pattern reflects a well-conserved ancestral condition, in contrast to the wide variety of adult body plans. It has been proposed that equal cleavage (i.e. specification of the D quadrant by inductive interactions) and indirect development via a trochophore larva were basal traits in both annelids and mollusks (Freeman and Lundelius, 1992), but the former conclusion has been questioned for annelids (Dohle, 1999). In any event, comparisons of micromere fates and fate specification mechanisms between annelids and mollusks should provide insights into the ancestral condition of these taxa and the processes by which they diverged.

Molluscan cell cycle compositions have been most carefully described for Lymnaea stagnalis, an equal cleaver (van den Biggelaar, 1971a; van den Biggelaar, 1971b). In Lymnaea, the first three cell cycles are of equal length and composition; at the 24-cell stage, there is a pause in cell division that correlates with the shift of macromere 3D towards the center of the embryo. This pause entails a more than twofold prolongation of the cell cycles for the 24 blastomeres present (macromeres 3A-3D, micromeres 3a-3d and the eight daughters of the first two micromere quartets). The main conclusion of this work was that the changes in cell cycle duration in Lymnaea were achieved mainly by lengthening G2 phase; no G1 phase was detected in any of these cells.

Comparing Helobdella and Lymnaea, there are dramatic differences in the absolute and relative lengths of analogous cell cycles. Overall, early cell cycles are much slower in Helobdella than in Lymnaea (3-24 hours at 23°C versus 1.3-6.7 hours at 25°C, respectively), and we detect no global pause in early cell divisions in Helobdella. Moreover, in Helobdella the cell cycles of the secondary trio micromeres are prolonged like those of the tertiary trio, whereas in Lymnaea, the analogous cells (quartet 2a-2d) divide with a relatively rapid time course like the primary quartet micromeres. In Helobdella, as in Lymnaea, changes in cell cycle duration in the early embryo are achieved mainly by changes in the length of G2 phase (Bissen and Weisblat, 1989), although we did detect significant cell-specific differences in the duration of S phase, and brief G1 phases in the secondary trio of micromeres.

Regarding micromere cell fates, two carefully characterized mollusks are the gastropods Patella vulgata, an equal cleaver (Damen and Dictus, 1994) and Ilyanassa obsoleta, an unequal cleaver (Render, 1991; Render, 1997). Both Patella and Ilyanassa are highly derived relative to the ancestral mollusk, which presumably resembled the bilaterally symmetric Monoplacophorans. Among annelids, there is no clear candidate for the most basally derived group, but the leeches,
as direct developing clitellates, are also highly derived. Although it is therefore impossible to make detailed comparisons between micromere fates in annelids and mollusks at present, our results reveal significant differences between leeches and mollusks, even in terms of how bilateral symmetry is generated from these spiral cleaving embryos.

Bilateral symmetry becomes evident at various points in the modified spiral cleavages of Helobdella, Ilyanassa and Patella. The formation of bilateral mesendoderm (in leech) from the equal division of micromere 4d (DM” in leech) is regarded as an ancestral spiralian trait (Brusca and Brusca, 1990). Similarly, micromere 2d in Patella makes a bilaterally symmetric contribution to post-trochal ectoderm and apparently establishes left and right precursors at its first division (Damen and Dictus, 1994); the homologous cell in leech, proteloblast DNOPQ, serves as a precursor of segmental ectoderm for both sides of the leech, but only after making three micromeres (dnopq′-dnopq″), which seem to be lacking in Patella. The dnpq′ and dnpq″ micromeres give rise to bilaterally symmetric clones, despite the fact that they arise by sequential divisions (of DNOPQ and DNOPQ′). As expected, the bilateral pairs of micromeres arising from the further cleavages in the NOPQ lineages (i.e. nopql′ and nopq′r, and nopq″l and nopq″r also form bilaterally symmetric clones; this paper) (Smith and Weisblat, 1994).

Another way in which leech differs from the typical pattern of spiral cleavage is that the micromeres arising from the B quadrant arise with opposite handedness to those in the other three quadrants (Sandig and Dohle, 1988; Bissen and Weisblat, 1989) and thus mirror symmetric orientation with respect to the A quadrant micromeres. This correlates with clear differences between leech and mollusk in terms of micromere fates, and is summarized below.

In Patella, micromeres 1a and 1c contribute progeny to the left and right sides, respectively, as do cells 2a and 2c contribute mirror symmetric clones to the left and right sides; the clones of cells 1b, 1d, 2b and 2d, however, each more or less straddle the midline (Dictus and Damen, 1997). The bilateral pairs of micromeres I and II also form bilaterally symmetric clones (this paper) (Smith and Weisblat, 1994).

In Helobdella, by contrast, primary quartet micromeres a′ and b′ appear as left/right homologs (as do c′ and d′) in terms of their early lineages (this paper), the morphogenetic movements of their clones (Nardelli-Haefliger and Shankland, 1993) and the definitive fates of their progeny (this paper). Within the secondary trio, we have shown that b″ normally makes no definitive contribution and that a″ and c″ normally give rise to bilaterally symmetric clones, as in the mollusks. But we also find that when c″ is ablated, b″ assumes the c″ fate and thus is capable of serving as a contralateral homolog to a″.

In the third quartet of micromeres, symmetry relationships differ. In Patella and Ilyanassa, cells 3a and 3b form clones that are mirror images of one another, as do cells 3c and 3d (Dictus and Damen, 1997; Render, 1997), whereas in H. robusta, the clones of the three micromeres that contribute definitive progeny all straddle the midline. Among these, c′″ and dm′ (homologs of 3c and 3d, respectively) give rise to seemingly identical clones. As in the second tier of micromeres, the third B quadrant micromere also fails to contribute definitive progeny, but within this group, b′″ is not capable of replacing a″ or c″. Whether this constellation of differences between the micromere cell fates in annelid and mollusk will hold true for more basally derived representatives of the two phyla remains to be determined. In any event, we propose that the situation in leech represents an evolutionary ‘transition’ in which the A and B lineages are becoming true contralateral homologs.

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