discovery of a novel structural conformation that can be assumed by mammalian telomeres. Electron micrographs of psoralen cross-linked telomeric DNA preparations has revealed that telomeres can fold back such that the single-strand terminus of the G-rich strand of the telomere invades duplex DNA to form a duplex "lariat" structure, called the t-loop (*8*). The biochemical properties of TRF1 and TRF2 suggest a role for both proteins in t-loop formation (see the figure). TRF1 most likely promotes t-loop formation through its ability to bend and otherwise alter DNA conformation. TRF2 is localized to the junction where the 3′ end invades the duplex tract, suggesting that TRF2 and associated proteins aid in strand invasion. Formation of a t-loop thereby provides a means by which telomere replication could be regulated by a higher order structure—in this "closed" conformation, the tucked away 3′ terminus should be inaccessible to telomerase.

Does budding yeast Rap1 promote telomere length homeostasis through a similar t-loop mechanism? The functional similarities between budding yeast and human telomere length regulation certainly argue in favor of this possibility. Furthermore, the presence of large duplex loops at the chromosome termini of a ciliated protozoan (*9*) suggest that this type of end structure is a feature that is not necessarily restricted solely to mammalian chromosomes. If negative regulation of telomerase is indeed conserved, this raises the expectation that human orthologs of positive regulators of yeast telomere replication, such as Cdc13 and Est1 (*10*), are waiting to be discovered. Although the identification of the human Rap1 protein ties up one loose end, the story is far from over.

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PERSPECTIVES: DEVELOPMENT

A Degrading Way to Make an Organ

Jeff Hardin

Building an organ is a precise business. Organ rudiments must often navigate through a complex, three-dimensional terrain as their shape is transformed, and they must do so in a way that is carefully orchestrated with other concurrent developmental events. Many organ rudiments develop as tubular structures that are elaborated as the rudiment grows. In such cases, cells at the tip of the growing tube can be key regulators of organogenesis. Examples include gut formation in echinoderms, the tracheal system of *Drosophila*, and branching morphogenesis in vertebrates (*1*). As such growing organ rudiments extend, they must contend with a variety of extracellular matrices (ECMs), some of which may serve as barriers to migration. It has long been presumed that matrix metalloproteases, the major family of proteolytic enzymes responsible for degrading ECM components, play a key role in remodeling the ECM during cell migration (*2*). On page 2205 of this issue, Nishiwaki *et al.* (*3*) provide evidence that just such a protease, encoded by the *mig-17* gene, is required for directional migration of another well-studied tubular organ rudiment, the gonad of the nematode *Caenorhabditis elegans*. Together with other recent experiments in *C. elegans*, these results provide clear evidence that metalloproteases are important regulators of organogenesis.

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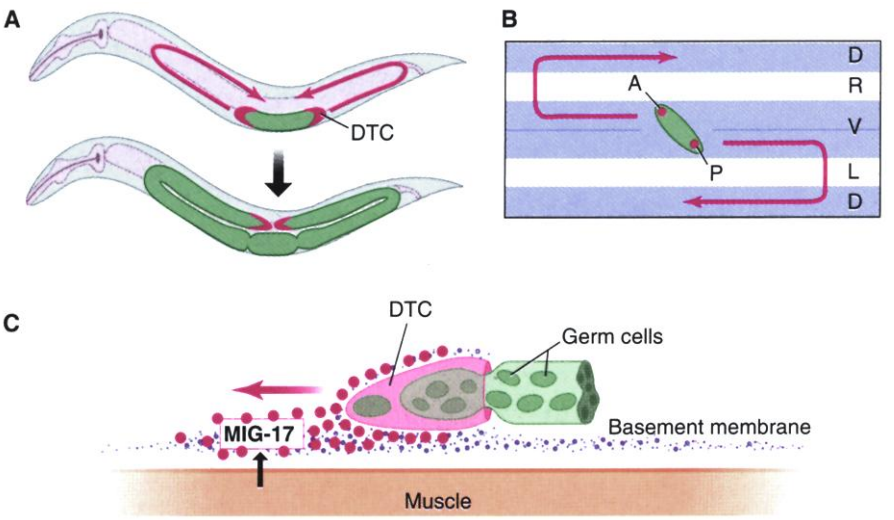
The hermaphrodite gonad of *C. elegans* has two U-shaped arms (see the figure). Both laser ablation (*4*) and genetic analyses (*5, 6*) indicate that the shape of the developing gonad is largely determined by the migration of somatic cells at the tips of the growing arms known as distal tip cells (DTCs). DTCs are born during the first larval stage, and they begin to migrate during the second larval stage. Normally, they migrate in opposite directions: the anterior DTC migrates anteriorly and the posterior DTC migrates posteriorly. During the third larval stage, the anterior DTC turns toward the right and the posterior DTC turns toward the left side of the animal, as each migrates across lateral epidermal cells toward muscle cells that lie in two dorsal quadrants. Upon reaching the dorsal muscle cells, the two DTCs turn again, this time leading their respective gonad arms back toward the center of the animal. This labyrinthine migration comes to an end in the fourth larval stage, after the tip of each arm has migrated hundreds of micrometers.

What role does the ECM play in the



Gonads on the go. (**A**) Mid-sagittal views of a *C. elegans* hermaphrodite larva showing the growth of the two gonad arms (dark gray). The two distal tip cells (DTCs) are shown in red. (**B**) A "filet" of a hermaphrodite at the first larval stage, opened up along the dorsal midline. Dorsal (D) and ventral (V) muscle quadrants are shown in purple; right (R) and left (L) lateral epidermal cells are shown in beige. The migratory routes of anterior (A) and posterior (P) DTCs in subsequent stages are shown (black arrows). (**C**) Hypothetical mechanism of MIG-17 release and activity. MIG-17 is produced by muscle cells, but can move to cover the surface of the migrating gonad primordium. It then acts on the extracellular matrix to support DTC migration. [(A) adapted from (*9*); (B) and (C) adapted from (*5*)]

guided extension of these simple tubular structures? The arms themselves are surrounded by basement membrane, and the DTCs must migrate over other basement membranes along their migratory routes. Remodeling of those membranes appears to regulate DTC migration and gonadal expansion. Support for this comes from the demonstration that the metalloprotease GON-1 is crucial for the earliest stages of DTC migration; in the absence of GON-1 activity, the gonad arms do not migrate at all (*7*). The *gon-1* gene encodes a secreted member of a small subfamily of metalloproteases, which includes the mouse protease ADAMTS-1 and bovine procollagen I N-protease. These proteins are characterized by both a metalloprotease domain and one or more thrombospondin type 1 repeats, which may allow them to become anchored within the ECM. They would then be positioned such that they could cleave their targets with maximum efficiency. As DTCs migrate they express *gon-1*; driving expression of *gon-1* using DTC-specific promoters rescues the DTC migration defects in *gon-1* mutant gonads, thus, GON-1 activity is required for DTC migration. However, *gon-1* is also normally expressed in muscle; other experiments suggest that GON-1 is required not merely for DTC migration, but for general expansion of the gonad rudiment (*7*).

Like *gon-1*, *mig-17* appears to be specifically required for the formation of gonads in *C. elegans* (*8*). In contrast to *gon-1*, *mig-17* is involved in regulating the direction of migration of the gonad arms, rather than their general ability to migrate. Although arm extension occurs in *mig-17* mutants, its direction is strongly perturbed once the DTCs attempt to make their dorsal turn (*3, 8*). The *mig-17* gene encodes a metalloprotease that, like *gon-1*, bears striking structural similarities to ADAM family proteases, although it lacks thrombospondin repeats. Surprisingly, using translational fusions of MIG-17 with green fluorescent protein, Nishiwaki *et al.* show that MIG-17 is initially synthesized by muscle cells rather than by DTCs. However, the protein is found on the surface of the gonad arms at the time migration defects are first observed in *mig-17* mutants. This suggests that although it is normally produced by muscle, MIG-17 diffuses to the gonad, where it is required for DTC migration. Consistent with this view, unlike GON-1, expression of MIG-17 by either muscle or DTCs is sufficient to rescue gonad arm migration defects.

How might MIG-17 and GON-1 collaborate to regulate DTC migration? Although substrates have not been identified for either enzyme, there are several possibilities. One possibility is that both GON-1 and MIG-17 are required for structural remodeling of the ECM during DTC migration. In the absence of such remodeling, DTCs may be physically unable to make appropriate changes in direction. If this is the case, then GON-1 is clearly required earlier or more stringently than MIG-17, given the severity of defects in *gon-1* mutants. In this scenario, MIG-17 could be required for more subtle remodeling events, either subsequent to the action of GON-1 or concurrent with it.

Another intriguing possibility is that one or both proteases are involved in the modification of matrix-embedded guidance cues to which DTCs normally respond. Several extracellular cues appear to guide the DTCs during their journey, the best-characterized being those affecting dorsal-ventral migration (*9*). Ventrally, UNC-6/netrin, a secreted protein structurally related to laminin, serves as an extracellular cue whose effects are mediated by its receptors, UNC-5 and UNC-40/DCC (*6*). The transforming growth factor–β family member UNC-129 may play a similar role dorsally (*10*). Remodeling of the ECM could affect how migrating cells interact with both of these guidance systems. Although there is no evidence that GON-1 plays such a role, Nishiwaki and coworkers found a marked enhancement of DTC migration defects in *mig-17/unc-6* double mutants. This suggests that MIG-17 may be involved in processing or presentation of guidance cues mediated by the UNC-6/UNC-5 system. However GON-1 and MIG-17 act, the demonstration that these proteases play an important role during organogenesis in vivo will likely stimulate the search for other proteases that regulate cell migration during development.

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PERSPECTIVES: PALEOCLIMATE

A Causality Problem for Milankovitch

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According to a theory postulated by Milankovitch in the early 20th century, changes in Northern Hemisphere summer insolation (incident solar radiation) are responsible for driving Earth's ice ages. The detailed mechanism by which small changes in insolation become amplified to drive major climatic changes remains unclear. Nevertheless, the Milankovitch theory has become central to the work of paleoclimatologists interested in the timing of climatic cycles. But in 1992, measurements were reported (*1*, *2*) that created problems for the theory (*3*). Data from a cave in Nevada, called Devils Hole, appeared to show that the timing of the penultimate termination of the ice ages, called Termination II, was incompatible with the standard Milankovitch theory. The data indicated a shift in oxygen isotopic composition to interglacial values that was essentially complete by 135,000 years ago. But at this time, the calculated Northern Hemisphere summer insolation [based on orbital calculations by Quinn *et al.* (*4*)] had not yet increased to a point at which it would be expected to trigger anything extraordinary, let alone a glacial termination. The termination event appeared to precede its own cause (see the figure).

The Devils Hole data were not the first to indicate a problem. Already in 1974, Bloom *et al.* (*5*) suggested, on the basis of uranium-thorium (U-Th) radiometric ages of coral terraces from the Huon Peninsula in Papua New Guinea, that sea level had reached a high point—presumably from glacial melting, an indicator of warm conditions—as early as 142,000 years ago. But when Imbrie *et al.* (*6*) derived the SPECMAP time scale, the most widely used model for explaining how insolation could drive ice age cycles, they did not use these results. Instead, they set Termination II at 127,000 ± 6000 years ago, on the basis of radiometric dates from Barbados corals (*7*, *8*).

In 1991, Chen *et al.* (*9*) studied U-Th ages for different coral species from two Bahamian reefs. They concluded that "the high sea level stand began possibly by 132 ky [thousand years] and certainly by 129 ky ago, when sea level reached ~6 meters above present mean low sea level" (p. 82).

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