elements of similar structure are known in *Drosophila*, but are untested. For some years it has seemed inconceivable that *Drosophila* is unique among insects in its ability to be transformed. One obvious rule is to choose an element absent from the target species; if the element is present, its transposition may be repressed. Savakis and colleagues chose the *Minos* element (*10*), which they had isolated from *D. hydei* and which had been shown to work in *D. melanogaster* (*11*). A similar strategy is being used by others; for example the *Hermes* element from the housefly will transform *Drosophila* (*12*) and is now being tested for the transformation of the Queensland fruit fly, *Bactrocera tryoni* (*13*). Many elements of similar structure, some known to be mobile, are being identified in a wide range of other insect species. Several, like *Minos*, are members of the Tc1 family of elements; others, such as *hobo* and *Hermes*, belong to the hAT family. Their characterization should now be seen as a top priority for research. The importance of using *Drosophila* as a test-bed, both for testing possible vectors and for testing possible marker genes, should not escape attention.

Will the successful transformation of the medfly result in better methods to control this pest? Readers should be wary of my predictive powers, but yes, in the long run. Certainly, it will allow us to learn much more about the basic biology of this beast. But the result has greater import; it should relieve the frustration of those trying to transform other insects; it should, in Voltaire's immortal words (writing, I admit, about the English habit of killing off the odd Admiral), be an example "pour encourager les autres."

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Ages of the Oldest Clusters and the Age of the Universe

Sidney van den Bergh

One of the most heated debates in the history of astronomy focuses on the numerical value of the Hubble parameter H_o. This parameter is of fundamental importance because it gives the scale-size of the universe and provides constraints on world models and the age of the universe. The most direct path to the determination of the extragalactic distance scale is through the Cepheids in the Virgo cluster. The relative merits of other techniques for determining H_o have recently been reviewed in great detail by Jacoby *et al.* (*1*), van den Bergh (*2*, *3*), and Kennicutt *et al.* (*4*).

Distance moduli of spirals in Virgo region

Galaxy	m_0	D (Mpc)	Telescope	Reference
NGC 4321 (M100)	31.00 ± 0.20	15.8	HST	Farrarese *et al.* (*9*)
NGC 4496	31.10 ± 0.15	16.6	HST	Saha *et al.* (*10*)
NGC 4536	31.05 ± 0.15	16.2	HST	Saha *et al.* (*10*)
NGC 4571	30.91 ± 0.15	15.2	CFHT	Pierce *et al.* (*11*)

HST, Hubble Space Telescope
CFHT, Canada-France-Hawaii Telescope

The table lists the true distance moduli μ_o, which is the apparent magnitude corrected for absorption that a star of absolute magnitude M = 0.0 would have, in four spiral galaxies in the Virgo region in which Cepheid variables have been observed so far. The distances of all four of these spirals are in excellent agreement. The data in this table yield a formal weighted mean distance modulus $\langle\mu_o\rangle$ = 31.02 ± 0.08 (mean error) for the Virgo cluster. To this quoted mean error should be added a 0.1-magnitude (mag) systematic uncertainty resulting from possible errors in the calibration of the zero-point of the Hubble Space Telescope (HST) photometry and an uncertainty of ~0.1 mag in the distance modulus of the Large Magellanic Cloud relative to which the Virgo distances were determined. In the subsequent discussion, it will be assumed that the true distance modulus of the Virgo cluster is μ_o(Virgo) = 31.02 ± 0.2 (D = 16.0 ± 1.5 Mpc). This distance modulus for four Virgo spiral galaxies is consistent with the value μ_o(Virgo) = 31.12 ± 0.26 that Whitmore *et al.* (*5*) have recently determined with HST by comparing the luminosity function of globular clusters in the Virgo elliptical galaxy M87 with that for globular clusters in the Milky Way system and in the nearby Andromeda galaxy. Because M87 lies at the center of the Virgo cluster, this observation appears to rule out the possibility that the spirals listed in the table lie a significant distance in front of the core of the Virgo cluster.

Tanvir *et al.* (*6*) have used HST observations of Cepheids in NGC 3368 to derive a distance modulus μ_o = 30.32 ± 0.16 for the Leo I cluster. In conjunction with a difference $\Delta\mu_o$ = 0.99 ± 0.15 between the distance moduli of the Virgo and Leo I clusters this yields μ_o(Virgo) = 31.31 ± 0.22. This indirect distance determination is also consistent with, but slightly larger than, the value μ_o(Virgo) = 31.02 ± 0.20 derived above from Cepheids observed in four Virgo spirals. It is concluded that the distance of the Virgo cluster is now well determined.

Because both the peculiar motion of the Virgo cluster and the magnitude of the retardation of the Local Group by the Virgo supercluster remain controversial, it is safest to determine the Hubble parameter from the Coma/Virgo distance ratio and the Coma velocity relative to the microwave background. The difference in the distance moduli of the Virgo and Coma clusters is well determined. From 12 concordant determinations, van den Bergh (*2*) finds $\Delta\mu_o$ = 3.71 ± 0.05. Adopting $\Delta\mu_o$ = 3.71 ± 0.05, in conjunction with a distance modulus μ_o(Virgo) = 31.02 ± 0.20, yields μ_o(Coma) = 34.75 ± 0.21, corresponding to a distance D(Coma) = 89 ± 9 Mpc. Durret *et al.* (*7*) found a mean redshift $\langle V\rangle$ = 6901 ± 72 km s^{-1} for the Coma cluster. With a correction of +258 ± 10 km s^{-1} to place Coma in the cosmic microwave background frame, this yields a true velocity V(Coma) = 7159 ± 73 km s^{-1}. From these values, one obtains H_o =

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$V(\text{Coma})/D(\text{Coma}) = 81 \pm 8$ km s^{-1} Mpc^{-1}. For a matter-dominated $\Omega = 1$ Einstein–de Sitter universe (Ω is the ratio of the actual density of the universe to the critical density), the corresponding age $t_o = (2/3)H_o^{-1} = (2/3) \times 9.78 \times [100/(81 \pm 8)] = 8.0 \pm 0.8$ billion years. Such a short age conflicts with the age of 15.8 ± 2.1 billion years that Bolte and Hogan (*8*) obtained from main sequence fitting of the metal-poor globular cluster M92 to the subdwarf main sequence derived from trigonometric parallaxes. If the oldest galactic globular clusters have ages of ~16 billion years, and if the time interval between the "Big Bang" and the formation of the first globular clusters was ~1 billion years, then the age of the universe is ~17 billion years. This value is twice as large as the value 8.0 ± 0.8 billion years previously found from H_o in an Einstein–de Sitter universe.

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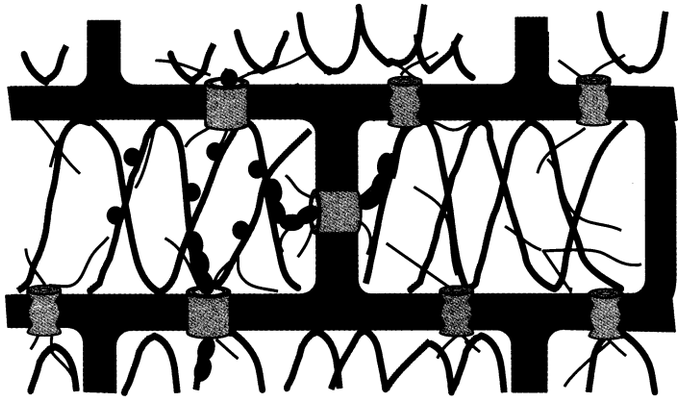
Plasmodesmata: Plant Channels for Molecules on the Move

Patricia Zambryski

Intercellular communication in plants occurs through cytoplasmic bridges called plasmodesmata (PD) (*1*). In contrast to their animal counterparts—gap junctions between closely appressed cells—PD are elongated structures that traverse the thick cell walls that surround plant cells. PD have an outer sheath that is contiguous with the plasma membrane, a central core of endoplasmic reticulum, and a collar or neck region. Historically, PD have been assigned a passive role: creating cytoplasmic continuity between plant cells to allow free transport of small metabolites and growth hormones less than 1 kilodalton (kD). When it was discovered that plant viruses pirate PD for movement of their genomes during infection, it was proposed that viruses altered the PD to allow transport of very large molecules. Now, several recent reports, one of which is in this issue of *Science*, provide compelling evidence that PD are inherently dynamic, rapidly altering their dimensions to increase their transport capabilities on contact with both viral (*2*, *3*) and endogenous plant proteins (*4*). Two other new studies, one in this issue (*5*), describe the cytoskeleton as a major tracking system to PD (*5*, *6*).

The movement protein (MP) of plant viruses has been extensively used to probe the function of PD (*7*). Recently, purified MPs have been microinjected into single plant cells to follow the movement of MP itself, complexes consisting of MP and single-strand nucleic acid, or co-injected fluorescent dextrans (*2*). These studies demonstrate that MPs increase the permeability of (that is, gates) PD within minutes of microinjection, implying that MPs operate an endogenous PD transport pathway.



Model for macromolecular transport between plant cells. Macromolecules track through the plant cytoplasm on microtubules, then interact with actin filaments to move to and through PD. Cell walls between individual plant cells, green; PD in either closed (constricted at either end) or open (smooth cylinder) configurations, yellow; microtubules, thick blue lines; actin filaments, red; elongated complexes between viral MP and single-strand nucleic acid, purple; and generic proteins capable of PD trafficking, orange.

Comparing MP-mediated transport in different plant cell types reveals that PDs are functionally diverse (*3*). In tobacco leaves, trichome hair cells have a greater basal size exclusion limit, 7 kD, than mesophyll cells (1 kD). Furthermore, although MP-induced gating in mesophyll cells permits movement of dextrans larger than 20 kD, MP does not gate trichome cells for these big dextrans. However, 30-kD MP itself moves in both cell types, and in trichome cells 30-kD MP mediates movement of a 68-kD reporter protein in cis but not in trans. Thus, an essential PD transport signal residing in MP dictates transportability in trichome cells, not size per se. Molecules to be transported are likely selected on the basis of at least four criteria: size, shape, signal (targeting) sequence, and gating function. From the perspective of PD, cell and tissue type, as well as developmental stage, regulate intercellular transport.

During maize development, RNA encoding the KNOTTED1 (KN1) homeodomain protein is found in all cell layers of the meristem except the outermost L1, whereas KN1 protein is found in both the inner and outer L1 layers. Likewise, in leaves of plants with the dominant *Kn1* mutation, RNA is located in the inner vascular cells, and protein is found in a broader domain including the L1. These findings (*8*) prompted speculation that KN1 protein might be transported through PD to the outer layer. Support for this idea comes from clonal analysis demonstrating that *Kn1* action in the inner layer nonautonomously influences adjacent cells (*9*). Now Lucas *et al.* have shown that, just as viral MPs gate and move, the KN1 protein itself both moves between mesophyll cells and facilitates the movement of dextrans and proteins larger than 20 kD (*4*). Furthermore, KN1 protein selectively transports *kn1* sense but not antisense RNA between cells. That an important regulator of plant development can move between cells has significant implications for how plants program differentiation. For example, the distribution, as well as the permeability, of PD between adjacent cells may regulate development by providing channels for exchange of regulatory signals. However, these intriguing studies provoke many questions. How common is macromolecular transport

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