Plant Cell Identity. The Role of Position and Lineage

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Cells in multicellular organisms acquire different identities in an ordered spatial arrangement. How do cells learn about their identity? The first three-quarters of the past century provided essentially two different explanations. On the one hand, descriptions of reproducible cell lineage and surgical experiments indicated that some cells only give rise to one particular progeny. These findings suggested that cell fate was restricted early in development and that cells passed on this decision to their progeny: a lineage-based mechanism (Fig. 1A). On the other hand, cell fate was not always correlated with lineage and many cells in developing organisms changed their fate in a new spatial context even at late stages of development: a position-based mechanism (Fig. 1B). Hence, two concepts of pattern formation emerged in which ancestral or neighboring cells determine the fate of a given cell. This review attempts to examine how these two concepts became substantiated over the past 25 years. A short account like this can only be incomplete and personally biased, but may still serve as a primer for the interested reader to make her/his own historical reconstruction.

PLANT PATTERNING IN THE 1970s

An important role for cell lineage in the acquisition of cell identity was derived more than a century ago from the regular layering of cells in shoot and root apices (8). Later studies stressed variability in cell division patterns (4) and flexibility of plant cell fate in meristems and tissue culture (1, 21, 17). Textbooks on plant development that appeared in the early 1970s used this information to reject lineage-based scenarios for shoot development, but a more pronounced role for lineage in root meristems was still considered possible (5, 19). The textbooks of the 1970s provided essentially two different explanations for position-dependent cell differentiation. On the one hand, nutrients and growth factors were supposed to form a network of stimuli for cell differentiation, and from tissue culture experiments it was extrapolated that pattern formation was under the control of balances between phytohormones (5). On the other hand, Jacob and Monod's *lac* operon model inspired the notion that shifting patterns of gene expression could accomplish cell differentiation (19).

Physiological control and gene regulation were mentioned in the 1977 and 1978 editions of widely read plant anatomy books of Esau and Cutter. Thus the plant community of the 1970s widely appreciated the idea that pattern formation resulted from position-dependent interactions with little emphasis on cell lineage.

MOSAIC ANALYSIS CONFIRMED THE IMPORTANCE OF POSITIONAL INFORMATION

Periclinal chimeras—genetically different ("mosaic") cell clones with an easily scorable phenotypic trait (e.g. albinism or ploidy level)—were already known for decades and were shown to span one of the parallel layers of a shoot apical meristem (11). For a considerable period of time, chimeras were studied mainly to determine how many stem cells ("initials") existed in each layer of the shoot apical meristem. A new and very important realization occurred in the early 1970s, but was not yet emphasized in prominent textbooks: rare cell layer invasion events, observed in chimeras, provided strong evidence that stem and leaf cell fate was determined by position rather than by lineage even at late stages of development (20). The realization that mosaic sectors could provide detailed information on cell fate restriction was subsequently taken up, and refined versions of mosaic analysis in the 1970s and 1980s provided us with a detailed view on the flexible ontogeny of cellular patterns in many plants (10).

GENES FOR PATTERN FORMATION, TRANSCRIPTION FACTORS FOR IDENTITY

Landmark papers on mutational analysis of pattern formation in the fruit fly changed the entire field of developmental biology around 1980. Systematic analysis of developmental mutants and isolation of the corresponding genes allowed investigators to describe development in terms of the ordered activity of gene products in space and in time. In the mid-1980s, the identification of many of these genes led to the isolation of instructive molecules that directed the expression of transcription factors (TFs) to groups of cells in the fruit fly (15, 18). These TFs, often of the homeodomain class, then instructed cell identity. Whereas positional signaling was important to dictate the expression of specific TFs in cells at early stages, their stable transcription was later ensured by

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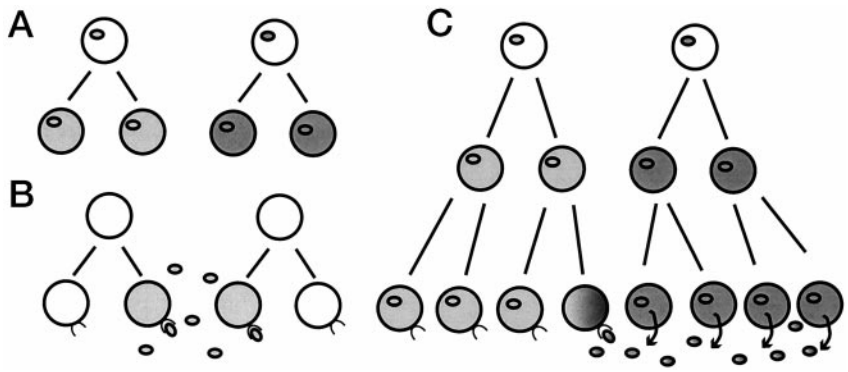

Figure 1. Cell fate: instructed by parents or neighbors? A schematic representation of possible mechanisms to specify cell identity. White, Unspecified cell. Gray, Specified cell. Ellipse, Information for specification. A, Lineage-based mechanism for specification. B, Position-based mechanism for cell specification. C, Successive utilization of lineage- and position-based mechanisms.

cell-autonomous mechanisms (encoded among others by "Polycomb Group" genes). The responsible gene products allowed the stable inheritance of a TF expression profile by progeny cells and hence provided nuts and bolts for a lineage-based mechanism of fate propagation. A description of the reproducible cell lineage of the soil nematode *Caenorhabditis elegans* gave new support to the idea that lineage strategies might dominate in some multicellular organisms. However, subsequent molecular genetic analyses clarified that much of this lineage invariance reflected the reproducible outcome of positional signaling mechanisms (3). Thus it was convincingly shown that reproducible lineage in the worm did not automatically imply lineage-based mechanisms. On the other hand, early position-dependent activation of TFs was fixed in some worm cell lineages, and these changes modified the response of cells to later-acting positional cues (hence, making late positional signaling responses "lineage-dependent").

In summary, molecular-genetic dissection of fly and worm development revealed an alternation of lineage- and position-dependent mechanisms for the specification of cell fate (Fig. 1C).

MOLECULAR GENETICS IN PLANT DEVELOPMENT

Undoubtedly inspired by the new successes in animal development, molecular genetic analysis of plant development took off in the mid-1980s. The maize *KNOTTED* gene was shown to encode a homeodomain protein with similarity to animal TF-encoding lineage selector genes, and genes encoding TFs of the MADS-box class formed a combinatorial code to specify cell fates in floral primordia of Arabidopsis (2, 7). These findings marked a change in perception that pervaded the plant sciences, as they emphasized the establishment of distinct cell lineages by TFs. In a similar vein, genetic dissection of embryogenesis in Arabidopsis resulted in mutants that were at first interpreted to signify the early establishment of distinct embryonic lineages. Soon thereafter, detailed analysis of these embryo-defective mutants and clonal analysis of embryogenesis led to the abandonment of this lineage-centered view on embryogenesis and renewed emphasis was put on positional information in combination with lineage-propagated differences in responsiveness to these cues (9). Manipulation of cell position by laser ablation and other experiments demonstrated that even in the Arabidopsis root, with the type of cell lineage regularity that led to the proposition of lineage-based mechanisms more then a century ago, cell-to-cell signaling was of crucial importance for the acquisition of cell identity (12). So, halfway into the 1990s, an important role for positional information in cellular patterning of plants surfaced again.

IDENTIFYING MECHANISMS OF PLANT CELL PATTERNING

A tremendous accumulation of genetic and molecular data over the last 5 years has begun to provide the first glimpses of pattern formation mechanisms. Three examples relevant for this discussion will be given below.

First, it was discovered that a Polycomb group-like gene controlled late repression of AGAMOUS (AG), one of the MADS-box TFs involved in floral organ identity (6). This finding, together with earlier observations on temperature-sensitive *apetala2* (*ap2*) alleles, suggested that restriction of AG by spatial regulation through other TFs (like AP2) was only required early in flower development, and that MADS-box protein expression might be controlled by a lineage-mechanism of cell fate at later stages of development. The recent successful generation of Cre-*loxP* based ag^{-} clones (16) should now allow us to distinguish between spatial or lineage-based regulation at late stages of flower development.

Second, insight into the specification of cell types has come from molecular-genetic analysis of trichome formation. Evidence is accumulating that transcription factors like GLABRA1, required for the determination of trichome cell fate, may initiate (by influencing the production of inhibitors of their own activity that act in neighboring cells) and be the target of cell-to-cell communication involved in pattern formation, creating self-regulatory loops (13). In

this case of pattern formation, cells decide on their fate only after the last cell division, and hence do not transmit this decision to their progeny through lineage-based mechanisms.

Third, a network of interacting gene products consisting of homeodomain transcription factors (such as WUSCHEL) and transmembrane signaling components (such as the CLAVATA1–3 proteins) appears to regulate the size of the stem cell population of the shoot apical meristem and of subjacent organizing cells. The current view is that cell-to-cell signaling from CLV3-expressing stem cells regulates the pool size of WUSCHEL-expressing cells and vice versa (14). Thus a homeodomain transcription factor that is required for the identity of a group of cells remains subject to continuous regulatory input from neighboring cells, and hence is not maintained by cell-autonomous mechanisms. Similar cell-to-cell signaling events might operate over long periods of time to maintain cell fate differences in other plant regions.

CONCLUSIONS

Twenty-five years ago, a major role for positional information in plant cell fate specification was generally accepted. Clonal analyses in the 1970s and 1980s reinforced concepts of position-dependent differentiation that were hitherto mostly derived from intrusive surgical approaches. However, it took molecular genetic approaches to begin the dissection of mechanisms of cell specification. As in animals, lineage- and position-based mechanisms operating in succession are tentatively identified in plants, although many components are still missing. At this stage it is premature to assess how frequently either of these mechanisms is used and how they interact. Nevertheless, it seems plausible that position-dependent mechanisms operate all the time in embryos and indeterminate meristems and that lineage mechanisms to pass cell fate decisions on to progeny may act in more limited time windows. Such a ratio of relative importance would account for much of the prolonged flexibility that is seen in plant development.

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LITERATURE CITED

1. **Ball E** (1952) Growth **16:** 91–110
2. **Coen ES, Meyerowitz EM** (1991) Nature **353:** 31–37
3. **Emmons SW** (1987) Cell **51:** 881–883
4. **Foster AS** (1939) Bot Rev **5:** 454–470
5. **Galston AW, Davies PJ** (1970) Control Mechanisms in Plant Development. Prentice-Hall, New Jersey
6. **Goodrich J, Puangsomlee P, Martin M, Long D, Meyerowitz EM, Coupland G** (1997) Nature **386:** 44–51
7. **Hake S** (1992) Trends Genet **8:** 109–114
8. **Hanstein J** (1868) Festschr Niederrhein Ges Natur u Heilk 109–143
9. **Jürgens G** (1995) Cell **81:** 467–470
10. **Poethig RS** (1987) Am J Bot **74:** 581–594
11. **Satina S, Blakesly AF, Avery AG** (1940) Am J Bot **27:** 895–905
12. **Scheres B** (1997) Curr Opin Genet Dev **7:** 501–506
13. **Schnittger A, Folkers U, Schwab B, Jürgens G, Hülskamp M** (1999) Plant Cell **11:** 1105–1116
14. **Schoof H, Lenhard M, Haecker A, Mayer KF, Jürgens G, Laux T** (2000) Cell **100:** 635–644
15. **Scott MP, Carrol SB** (1987) Cell **51:** 689–698
16. **Sieburth LE, Drews GN, Meyerowitz EM** (1998) Development **125:** 4303–4312
17. **Skoog F, Miller CO** (1957) Symp Soc Exp Biol **11:** 118–131
18. **St. Johnston D, Nüsslein-Volhard C** (1992) Cell **68:** 201–219
19. **Steeves TA, Sussex IM** (1972) Patterns in Plant Development. Prentice-Hall, New Jersey
20. **Stewart RN, Burk LG** (1970) Am J Bot **57:** 1010–1016
21. **Sussex IM** (1952) Nature **170:** 224–225