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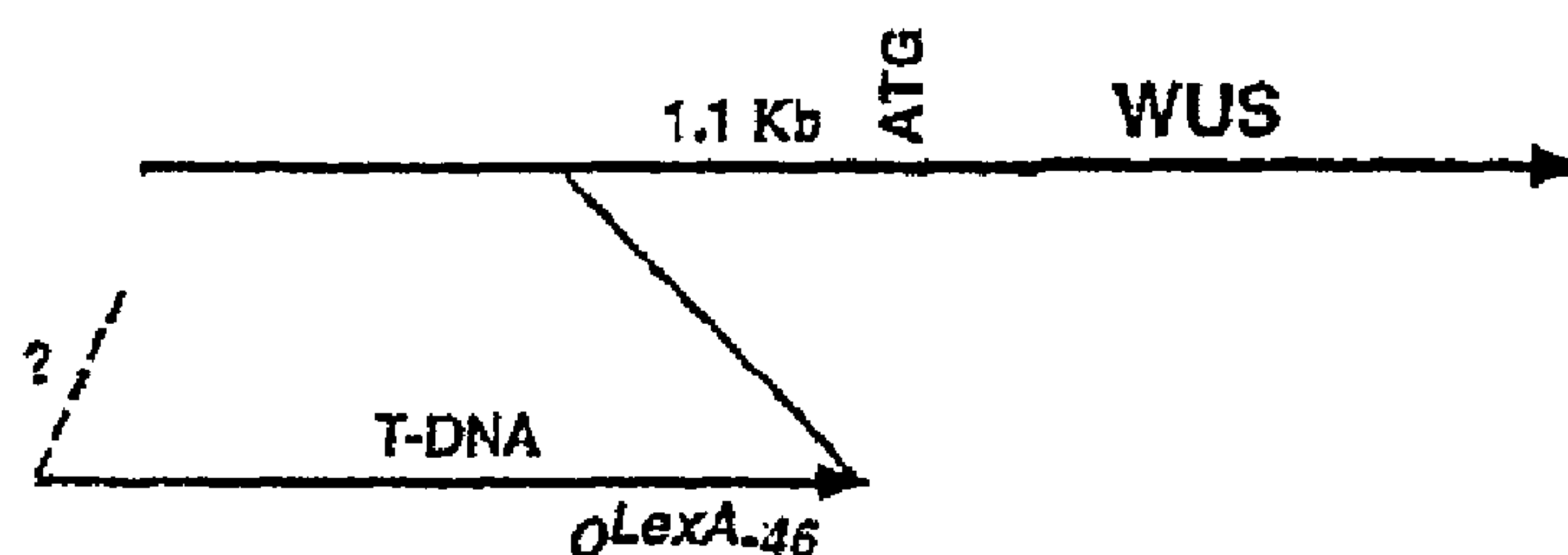
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(54) Titre : ACTIVATION DE L'EMBRYOGENESE SOMATIQUE CHEZ LES PLANTES PAR EXPRESSION D'UN GENE WUSCHEL

(54) Title: PROMOTION OF SOMATIC EMBRYOGENESIS IN PLANTS BY WUSCHEL GENE EXPRESSION



(57) Abrégé/Abstract:

The present invention relates to methods for promoting somatic embryogenesis from a tissue or organ of a plant, by overexpressing a Wuschel gene in said tissue or organ. In one embodiment, such overexpression can be used as a silent selectable marker for transgenic plants. In another embodiment, such expression can be used to confer apomixis to a plant. In another embodiment, such overexpression can be used to create haploid plants, which can be used to produce dihaploid plants.

Abstract

The present invention relates to methods for promoting somatic embryogenesis from a tissue or organ of a plant, by overexpressing a Wuschel gene in said tissue or organ. In one embodiment, such overexpression can be used as a silent selectable marker for transgenic plants. In another embodiment, such expression can be used to confer apomixis to a plant. In another embodiment, such overexpression can be used to create haploid plants, which can be used to produce dihaploid plants.

TITLE OF THE INVENTION**PROMOTION OF SOMATIC EMBRYOGENESIS IN PLANTS BY WUSCHEL
GENE EXPRESSION**BACKGROUND OF THE INVENTION

5 Somatic embryogenesis is a unique pathway for asexual propagation or somatic
cloning in plants. The developmental process of somatic embryogenesis shares
considerable similarity with that of zygotic embryogenesis (Zimmerman, 1993;
Mordhorst et al., 1997) and this is likely due to the conservation in the underpinning
cellular and molecular mechanisms between the two processes. Therefore, somatic
10 embryogenesis provides an attractive model system for studying zygotic embryogenesis,
particularly because zygotic embryos are encased by maternal tissues and difficult to
access by biochemical and molecular tools. Moreover, in biotechnological applications,
most economically important crop as well as non-crop plants are regenerated via somatic
embryogenesis.

15 In contrast to organogenesis, which requires a high cytokinin to auxin ratio (Skoog
and Miller, 1957; Sugiyama, 1999; Sugiyama, 2000), somatic embryogenesis does not
require any external cytokinins, but rather is dependent on high concentrations of 2,4-D
(Zimmerman, 1993; Mordhorst et al., 1997; Sugiyama, 2000), a synthetic chemical that
has long been used as a functional analog of auxin. It is generally believed that somatic
20 embryogenesis is mediated by a signaling cascade triggered by external auxin or 2,4-D
(Zimmerman, 1993; Mordhorst et al., 1997; Schmidt et al., 1997). However, very little is
known about the signal transduction pathway, particularly the molecular mechanism
involved in the transition of a vegetative cell to an embryogenic competent cell.

 During the last two decades, considerable efforts have been made to identify genes
25 with altered expression patterns during somatic embryogenesis (Schmidt et al., 1997; Lin
et al., 1996; Thomas, 1993). Most of these genes, however, are up-regulated only in late
developmental stages, suggesting that they do not play a direct role in the vegetative-to-
embryogenic transition. Thus far, the only exception is the carrot *Somatic Embryogenesis*
Receptor-like Kinase (SERK) gene the expression of which appears to mark the
30 vegetative-to-embryogenic transition; however, its function remains unclear (Schmidt et
al., 1997). An additional molecular approach was attempted by manipulating certain

embryo-specific genes. The *Arabidopsis Leafy cotyledon 1 (LEC1)* gene, encoding a subunit of the HAP heterotrimeric transcription factor complex (HAP3) has been proposed as a key regulator for embryonic identity (Lotan et al., 1998). Mutations in the *LEC1* locus result in defective embryo maturation as well as the conversion of cotyledons into true-leaf-like structures (Lotan et al., 1998; Meinke, 1992; Meinke et al., 1994). Constitutive overexpression of *LEC1* leads to severely abnormal plant growth and development with occasional formation of somatic embryo-like structures (Lotan et al., 1998). The developmental fate of these embryo-like structures, however, remained unknown due to the lethality of *LEC1* overexpression.

The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, and for convenience, are referenced by author and date in the text and respectively grouped in the appended List of References.

SUMMARY OF THE INVENTION

One aspect of the present invention is a method to promote somatic embryogenesis from a tissue or organ of a plant, said method comprising overexpressing a *Wuschel* gene in said tissue or organ.

A second aspect of the invention is a method to generate somatic plant embryos wherein said method comprises overexpressing a *Wuschel* gene in a tissue or organ of a plant.

Another aspect of the invention is a method for generating shoots from a tissue or organ of a plant, said method comprising overexpressing a *Wuschel* gene in said tissue or organ.

Yet another aspect of the invention is a method of selecting plants transformed with a vector comprising a silent selectable marker wherein the marker is a *Wuschel* gene.

Another object of the invention is a method of producing an apomictic plant line.

Another object of the invention is a method of producing haploid plants.

Another aspect of the invention is a method for conferring apomixis to a plant comprising:

- (a) stably transforming a plant cell with a DNA molecule comprising at least one *Wuschel* coding sequence under the control of a promoter to produce a transgenic plant cell, wherein the promoter is selected from the group

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consisting of a nucellus-specific promoter and a promoter that is both
nucellus-specific and inducible, and

- (b) regenerating a transgenic plant from said transgenic plant cell,
whereby overexpression of a *Wuschel* polypeptide from the *Wuschel* coding sequence
5 in the transgenic plant results in the formation of an apomictic embryo.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a schematic diagram of the XVE activation tagging vector pER16.

Figures 2A-F illustrate the *pga6* gain-of-function mutant phenotype. Root explants derived from *pga6* seedlings were cultured on the non-inductive SCM (SCM minus 17- β -estradiol) for 20 days (Figure 2A); or on the inductive SCM for 10 days (Figure 2B), 20 days (Figure 2C), or 30 days (Figure 2D). Figure 2E shows an enlarged view of a germinating somatic embryo isolated from the explant shown in (Figure 2D). Figure 2F shows a germinating seedling derived from a somatic embryo grown on MS medium (45 days). Scale bar, 100 μ m for Figures 2A and 2E; 1 mm, for Figures 2B, 2C, 2D and 2F.

Figures 3A-D are electron microscopic analyses showing somatic embryogenesis in *pga6* mutant explants (culturing conditions were identical to those shown in Figures 2A-F). Figure 3A shows a pre-embryo stage before the first embryonic cell division (arrows) and a two-cell stage after the first asymmetric division with a smaller apical cell (A) and a larger basal (B) cell. Figure 3B shows embryos at the globular (G) and the early heart (H) stages. Figure 3C shows a germinating embryo. C: cotyledon; H: hypocotyl. Figure 3D shows an abnormal somatic embryo with three cotyledons (C) anchored on the hypocotyl (H). Scale bar, 10 μ m for Figure 3A; 100 μ m for Figures 3B-D.

Figures 4A-H illustrate phytohormone-independent somatic embryo formation caused by the *pga6* gain-of-function mutation. Figure 4A is an overview of *pga6* mutant seedlings germinated and grown on MS medium (first seedling from the left) or the inductive MS medium (MST: 5 μ M 17- β -estradiol) for 7 days. Figures 4B-D show *pga6* seedlings that were cultured on the inductive MS medium for 10 days (Figure 4B), 14 days (Figure 4C) or 30 days (Figure 4D). Figures 4E-F show seven-day-old *pga6* seedlings germinated and grown on MS medium which were transferred onto an inductive MS medium and cultured for 5 (Figure 4E) or 10 (Figure 4F) days. Figure 4G shows *pga6* root explants which were cultured on the inductive MS medium for 20 days. Figure 4H is an enlarged view of Figure 4G. Scale bar, 1 mm.

Figures 5A-D show that the *pga6* phenotype is due to the inducer-dependent overexpression of *WUS*. Figure 5A is a schematic diagram illustrating the insertion site of the T-DNA upstream of the *WUS* gene (not shown to scale). Arrows indicate the directions of transcription. Figure 5B shows *pga6* seeds (T2, homozygous) which were germinated and grown on MS medium supplemented with various concentrations of the inducer as indicated. Ten-day old seedlings are shown. The scale bar represents 1 mm. Figure 5C shows the expression of *PGA6/WUS* induced by different concentrations of the inducer. Ten-day-old *pga6* seedlings were germinated and grown on MS medium and transferred to an MS medium containing various concentrations of 17- β -estradiol as indicated and were cultured for an additional 16 hours before total RNA extraction. Five μ g total RNA were used for Northern blot analysis using a *WUS* cDNA fragment as a probe. Positions of two RNA molecular weight markers are indicated at the right (GIBCO BRL, catalog number, 15620-016). Figure 5D shows ethidium bromide staining of the gel as a control for RNA loading and transfer.

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Figures 6A-H are photographs showing that 35S- or XVE-controlled overexpression of *WUS* cDNA phenocopies the *pga6* phenotype. Figure 6A shows embryogenic callus and Figure 6B shows somatic embryo formation from root tips of XVE-*WUS* cDNA T2 seedlings grown for 15 days in A medium supplemented with 17- β -estradiol (10 μ M). Figures 6C-H show 15 day-old T1 35S::*WUS* seedling phenotypes. Figure 6C shows the tips of the roots are enlarged and show an embryo-like structure. Figure 6D shows the adventitious root tip. Figure 6E shows that *WUS* overexpression induces both organogenesis and embryogenesis from the root. Figure 6F shows detail of early embryo structure formation. Figure 6G shows the shoot apical meristem is dramatically altered and, besides forming lateral organs with altered shaped, gives rise to adventitious shoots and somatic embryos. Figure 6H shows the entire shoot apical meristem expands and lateral organs transform into meristematic tissues. Scale bar is 1 mm.

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Figures 7A-C are Northern blots of RNA from root explants prepared from *pga6* seedlings cultured on the screening medium (SCM) for different times as indicated. On

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day 28, when somatic embryos were apparent, cultures were transferred onto a freshly-prepared SCM or control medium (SCM without the inducer) and incubated for an additional day (28 + 1) or two days (28 + 2). Five micrograms of total RNA, prepared from the frozen materials, were analyzed by Northern blotting using *WUS* (Figure 7A) and *LEC1* (Figure 7B) cDNA as probes. The blot was rehybridized with an actin cDNA probe (Figure 7C) to ensure that equal amounts of RNA were loaded.

Figures 8A-B illustrate formation of somatic embryos from isolated zygotic embryos of *PGA6* transgenic plants grown in the presence (Figure 8A) or absence (Figure 8B) of an inducer of *PGA6*.

DETAILED DESCRIPTION OF THE INVENTION

To dissect the signaling pathway during somatic embryogenesis, we have employed a genetic approach to identify gain-of-function mutations that can promote embryogenic callus formation from *Arabidopsis* root explants. *Arabidopsis thaliana* is known to be a species difficult for somatic embryogenesis. Thus far, embryogenic calli could only be induced from immature embryos of wild-type (WT) plants or from the *primordia timing (pt)* mutant plant (Wu et al., 1992; Mordhorst et al., 1998; and references therein). Therefore, *Arabidopsis* vegetative explants appear to be reliable materials for screening for genetic mutations involved in the vegetative-to-embryonic transition. Herein we disclose the identification of the *Plant Growth Activator 6 (PGA6)* gene by a novel genetic screen. Overexpression of *PGA6* promotes the formation of somatic embryos from various vegetative tissues as well as from zygotic embryos independently of any external plant hormones. These somatic embryos, following a developmental process remarkably similar to that of zygotic embryogenesis, are able to germinate and grow into healthy, fertile plants, suggesting that *PGA6* is involved in the maintenance of embryonic cell identity. *PGA6* was found to be identical to the *Wuschel* gene (*WUS*), a homeodomain protein that was previously characterized as a key regulator for specification of meristem cell fate (Laux et al., 1996; see, also, WO 01/23575 regarding *WUS* homologs). The nucleic acid and protein sequences of *Wuschel* are those as shown by GenBank Accession No. AJ012310. Our results reveal an additional

function of WUS/PGA6 during embryogenesis, and also open a new avenue in biotechnological applications.

In this study, we identified a genetic locus *PGA6* by a novel functional screen aimed at elucidating the molecular mechanism of somatic embryogenesis. A gain-of-function mutation at this locus causes a rapid transition from vegetative or somatic to embryonic cells, leading to somatic embryo development from various tissues and organs. The *pga6* mutation-dependent cell fate reprogramming can occur either in the presence or absence of external plant hormones, although the local concentration of endogenous growth regulators might play an important role in the vegetative-to-embryonic transition. In addition, the hormone-independent somatic embryogenesis in *pga6* strikingly resembles zygotic embryo development. These observations suggest that PGA6 plays a critical regulatory role during embryogenesis, likely involved in maintaining embryonic cell identity. Molecular and genetic analyses indicate that *pga6* is a gain-of-function allele of the previously characterized *wus* loss-of-function mutation (Mayer et al., 1998).

In addition to causing vegetative tissues or organs to become embryogenic, inducing overexpression of *PGA6* in zygotic embryos also results in the generation of somatic embryos at very high frequency, whereas no somatic embryos or embryogenic calli were observed in the absence of the inducer. Wu et al. (1992) previously reported the generation of somatic embryos from isolated *Arabidopsis* zygotic embryos at very low efficiency, which involved tedious multiple subculturing and hormone treatments. Our finding that the simple manipulation of a single gene (*WUS*) was able to generate somatic embryos at very high frequency is a major advance in plant biotechnology.

Loss-of-function mutations in *WUS* have been shown to cause impaired development of shoot and floral meristems in *Arabidopsis*, resulting in the absence of the shoot and floral meristems in all developmental stages of *wus* embryos and adult plants (Laux et al., 1996; Mayer et al., 1998). Genetic studies revealed that *WUS* interacts with *CLAVATA* (*CLV*), and the *WUS/CLV* self-regulatory loop, in which *CLV* presumably acts upstream of *WUS* (Clark, 2001) appears to be critical for the maintenance of stem cell identity (Schoof et al., 2000; Brand et al., 2000; Waites and Simon, 2000). On the other hand, ectopic expression of *WUS* results in enlarged meristems (Schoof et al., 2000). Collectively, these observations suggested an instructive role of *WUS* for the

specification of meristematic stem cell fate. Interestingly, the *WUS* gene is not expressed in the stem or meristem cells; rather its expression is restricted to a small group of cells underneath the stem cells during the entire embryogenesis and post-embryogenesis stages (Mayer et al., 1998; Schoof et al., 2000). The cluster of *WUS* expressing cells was
 5 termed as the organizing center (Mayer et al., 1998). The unexpected expression pattern led to postulations that *WUS* promotes and/or maintains the stem cell fate by a diffusion mechanism or acted in a non-cell-autonomous manner (Mayer et al., 1998; Waites and Simon, 2000).

Our observation that *WUS* is capable of promoting vegetative-to-embryonic
 10 transition and eventually somatic embryo formation uncovers an additional critical function of this homeodomain protein during embryogenesis. Presumably, the highly restrictive expression of *WUS* hallmarks the putative embryonic organizing center which, in turn, may give rise to stem cells during embryogenesis and later development. Therefore, *WUS* is involved in promoting and maintaining the identity of embryonic cells
 15 from which stem cells are derived. Because *WUS*-expressing cells have not been morphologically and functionally characterized, it remains of interest to determine whether this cluster of cells indeed represents a functional organizing center similar to Spemann's organizer discovered nearly 80 years ago in *Xenopus* embryos (Spemann and Mangold, 1924).

20 Interestingly, the *LEC1* transcript was barely detectable in the organizing center or the *WUS* expressing domain, albeit *LEC1* was found to express throughout embryogenesis as well as in seeds (Lotan et al., 1998). Consistent with these observations, somatic embryo expression of *LEC1*, presumably resembling that in zygotic embryos, was found to be promptly repressed by the *WUS* activity. In addition, the *LEC1*
 25 function appeared to require unidentified embryo- and or seed-specific cofactors, since inducible overexpression of *LEC1* by the XVE system (Zuo, et al., 2000b) during post-germination stages did not result in any detectable phenotype. By contrast, *WUS* appears to be a key player in promoting embryonic potential as its activity does not appear to require any developmentally specific factors under our tested conditions. Taken together,
 30 these observations further suggest that *WUS* plays a predominant role in inducing the embryonic potential, whereas *LEC1* is likely involved in promoting differentiation of

embryonic cells at later developmental stages. A reasonable assumption would be that the *LEC1* activity, a driving force for embryo cell differentiation, must be excluded in order to fully maintain the embryonic potential in the putative organizing center.

Recently, Stone et al. (2001) showed that *LEC2* encodes a transcription factor
 5 containing a B3 domain unique to several other plant transcription factors including
ABI3/VP1 and *FUS3*. Overexpression of *LEC2* leads to formation of somatic embryos as
 well as the formation of callus, cotyledon-like and leaf-like structures, a phenotype
 similar to that of *pga6* mutant, suggesting that *LEC2* might be functionally close to *WUS*.
 It will be interesting to determine if the *LEC2* activity is also dependent on embryo-
 10 and/or seed-specific cofactors as in the case for *LEC1*.

Systems for hormone-dependent somatic embryo formation have been well
 established in several model species, and rapidly extended to other species (Zimmerman,
 1993; Mordhorst et al., 1997). In all these *in vitro* systems, phytohormones, particularly
 auxin or 2,4-D, are essential for induction of somatic embryo formation. *Arabidopsis* has
 15 been known to be a species difficult for somatic embryogenesis, even though with limited
 success by using wild-type immature zygotic embryos (e.g., Wu et al., 1992) or certain
 vegetative tissues of the *pt* mutant plants (Mordhorst et al., 1998). Overexpression of
Leafy cotyledon 1 (Lec1) causes severe developmental abnormality and growth arrest, a
 phenotype similar to that of the *pga6* mutant (Lotan et al., 1998). Formation of somatic
 20 embryos is occasionally observed in the *Lec1* overexpression plants (Lotan et al., 1998),
 but these embryos never germinate or develop into normal adult plants. The finding that
 the *pga6* gain-of-function mutation or overexpression of *WUS* results in hormone-
 independent somatic embryo formation at a high frequency will have significant impact
 on plant biotechnology, and provides a convenient and attractive model system for many
 25 aspects of plant biological research.

In another embodiment of the invention, embryogenesis is induced in haploid
 cells, such as pollen cells, to produce haploid plants. This can be achieved by stably
 transforming a plant cell or tissue with a *WUS* gene under the control of a tissue specific
 promoter that is active in a haploid cell or tissue, and expressing the *WUS* gene therein, or
 30 by introducing the *WUS* gene into a plant tissue or cell under the control of an inducible
 promoter and applying the inducer to cause expression of the *WUS* gene therein. In a

preferred embodiment, the *WUS* gene is under the control of a promoter that is both haploid-tissue specific and inducible. In a preferred embodiment, a promoter is used that is both inducible and tissue-specific, giving greater control over the process. In a most preferred embodiment, a *WUS* gene linked to an inducible pollen-specific promoter is used to induce somatic embryogenesis in pollen cells.

Expression of the gene in the haploid tissue or cell (for example, by application of the inducer specific for the inducible promoter) results in the formation of haploid somatic embryos, which can be grown into haploid plants using standard techniques. When an inducible promoter is used (whether tissue specific or not), a preferred method comprises exposing excised transgenic tissue containing the haploid cells (e.g., pollen or ovules) to the inducer specific for the inducible promoter for a time sufficient to induce the formation of a somatic embryo, withdrawing the inducer, and growing the somatic embryo into a transgenic haploid plant in the absence of the inducer.

Diploidization of the haploid plants to form dihaploids, either spontaneously or by treatment with the appropriate chemical (e.g. colchicine) will significantly expedite the process of obtaining homozygous plants as compared to a method of conventional genetic segregation. This technology will not only be beneficial for breeding purposes but also for basic research such as studies of mutagenesis and other genetic studies, because dihaploids are truly homozygous down to the DNA level, containing two identical copies of each gene.

Additionally, *WUS* genes will be useful for inducing apomixis into plants. Apomixis and methods of conferring apomixis into plants are discussed in several patents (see, e.g., U.S. Patent Nos. 5,710,367; 5,811,636; 6,028,185; 6,229,064; and 6,239,327 as well as WO 00/24914). Reproduction in plants is ordinarily classified as sexual or asexual. The term *apomixis* is generally accepted as the replacement of sexual reproduction by various forms of asexual reproduction (Rieger et al., IN Glossary of Genetics and Cytogenetics, Springer-Verlag, New York, N.Y., 1976). In general the initiation of cell proliferation in the embryo and endosperm are uncoupled from fertilization. Apomixis is a genetically controlled method of reproduction in plants where the embryo is formed without union of an egg and a sperm. There are three basic types of apomictic reproduction: 1) apospory-embryo

develops from a chromosomally unreduced egg in an embryo sac derived from a somatic cell in the nucellus, 2) diplospory-embryo develops from an unreduced egg in an embryo sac derived from the megaspore mother cell, and 3) adventitious embryony-embryo develops directly from a somatic cell. In most forms of apomixis, pseudogamy or fertilization of the polar nuclei to produce endosperm is necessary for seed viability. These types of apomixis have economic potential because they can cause any genotype, regardless of how heterozygous, to breed true. It is a reproductive process that bypasses female meiosis and syngamy to produce embryos genetically identical to the maternal parent. With apomictic reproduction, progeny of specially adaptive or hybrid genotypes would maintain their genetic fidelity throughout repeated life cycles. In addition to fixing hybrid vigor, apomixis can make possible commercial hybrid production in crops where efficient male sterility or fertility restoration systems for producing hybrids are not known or developed. Apomixis can make hybrid development more efficient. It also simplifies hybrid production and increases genetic diversity in plant species with good male sterility.

It would be ideal to find genes controlling obligate or a high level of apomixis in the cultivated species and be able to readily hybridize cross-compatible sexual x apomictic genotypes to produce true-breeding F_1 hybrids. In reality, most desirable genes controlling apomixis are found in the wild species which are distantly related to the cultivated species. Although interspecific crosses may be possible between the cultivated and wild species, chromosome pairing between genomes is usually low or nonexistent.

Although apomixis is effectively used in Citrus to produce uniform and disease- and virus-free rootstock (Parlevliet et al, 1959) and in buffelgrass (Bashaw, 1980) and Poa (Pepin et al, 1971) to produce improved cultivars, it has not been successfully transferred to a cultivated crop plant. The transfer of apomixis to important crops would make possible development of true-breeding hybrids and commercial production of hybrids without a need for cytoplasmic-nuclear male sterility and high cost, labor-intensive production processes. An obligately apomictic F_1 hybrid would breed true through the seed indefinitely and could be considered a vegetative or clonal method of reproduction through the seed. The development of apomictically reproducing cultivated crops would also provide a major contribution toward the food security in developing nations (Wilson et al, 1992).

The present invention is further detailed in the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below are utilized.

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Example 1

Plant materials, growth conditions and plant transformation

The Wassilewskija, Columbia and Landsberg ecotypes of *A. thaliana* were used. Plants were grown under continuous white light at 22°C on solid A medium (1 X MS salts
10 (Murashige and Skoog, 1962), 3% sucrose, 0.8% agar) supplemented with appropriate antibiotics and/or the inducer 17- β -estradiol. Unless indicated otherwise, 5 μ M 17- β -estradiol was used for induction. *In planta* transformation of *Arabidopsis* plants (the Columbia ecotype) was performed as described by Bechtold et al. (1993). Transformation of root explants was carried out according to Koncz et al. (1989).

15 Light and electron microscope analyses were carried out as previously described (Zuo et al., 2000b).

Example 2

Screening of *pga* mutants

20 *Agrobacteria ABI* cells carrying pER16 were used to transform *Arabidopsis* (the Wassilewskija ecotype) root explants. Infected root explants were cultured on the screening medium (SCM; 1 X MS salts, 1% sucrose, 0.5 g/L MES (2-[N-morpholino]ethanesulfonic acid), 0.15 mg/L IAA (indole acetic acid), 5 μ M 17- β -estradiol, 50 mg/L kanamycin, 100 mg/L carbenicillin and 0.2% phytigel, pH 5.7) at 22°C
25 under a 16-hour white light/8-hour dark cycle. Putative *pga* mutants, which appeared as rapidly growing green-yellowish or green cell clumps or calli upon culturing on the SCM for 10-15 days, were transferred onto a non-inductive shoot induction medium (SIM; for green calli; 1 X MS salts, 1% sucrose, 0.5 g/L MES, 1 mg/L 2-IP (N⁶, δ^2 -isopentenyladenine), 0.15 mg/L IAA, 50 mg/L kanamycin, 100 mg/L carbenicillin and
30 0.2% phytigel, pH 5.7) to recover mutant shoots. The green-yellowish calli were transferred onto the callus induction medium (CIM; 1 X B5 salts (Sigma), 2% glucose,

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0.5 g/L MES, 0.5 mg/L 2,4-D, 0.05 mg/L kinetin, 50 mg/L kanamycin, 100 mg/L carbenicillin and 0.2% phytigel, pH 5.7). After culturing on the CIM for 7-10 days, the amplified calli were then transferred onto a SIM to regenerate shoots. Regenerated shoots, usually formed after culturing on the SIM for 2-3 weeks, were then transferred to
 5 a root induction medium (RIM; identical to SIM but without 2-IP) to promote root formation. Whereas most putative *pga* mutant plantlets, including *pga6*, were able to set seeds after transferring to soil, a portion of roots were excised and placed on the CIM to reinduce callus formation, followed by repeating the above-described screening procedure to confirm the inducer-dependent *pga* phenotype. The *pga6* mutant was backcrossed with
 10 wild-type (*Wassilewskija*) plants twice for further genetic and phenotypic analyses.

Example 3

Molecular manipulations

Molecular manipulations were performed as specifically stated or by the methods
 15 as taught by Sambrook et al. (1989). The XVE inducible expression vector pER10 is identical to pER8 (Zuo et al., 2000a) except that the hygromycin selectable marker of pER8 was replaced with a kanamycin selectable marker. To construct the mutagenesis vector pER16, pER10 was digested with *SpeI* and *Asp718I* followed by Klenow enzyme fill-in reaction and religation. The resulting pER16 vector lacked the *rbcsS3A* polyA
 20 addition sequence of the *OLexA-46::T3A* expression cassette (see Figure 1 of Zuo et al. (2000a)).

pER16 is shown in Figure 1. Only the region between the Right Border (RB) and Left Border (LB) is shown (not to scale). Two transcription units and the *OLexA-46* promoter are located between the RB and LB. In the first transcription unit, the *G10-90* promoter (Ishige et al., 1999) drives the *XVE* fusion gene terminated by the *rbcs* E9
 25 promoter (Ishige et al., 1999) drives the *XVE* fusion gene terminated by the *rbcs* E9 polyA addition sequence. The second transcription unit consists of the *Nopaline Synthase* (*NOS*) gene promoter, the coding sequence of the *Neomycin Phosphotransferase II* (*NPT II*) gene and the *NOS* polyadenylation sequence. The *OLexA-46* promoter consists of 8 copies of the *LexA* operator sequence fused to the -46 CaMV35S promoter. Upon
 30 integration into the plant genome, the *OLexA-46* promoter can activate the transcription of sequences fused downstream from the promoter in a 17- β -estradiol-dependent fashion.

The pER16-tagged genomic sequences were recovered by Tail-PCR (Liu et al., 1995), and the purified PCR fragments were directly subjected to DNA sequencing analysis.

The *WUS* cDNA was amplified from flower cDNA by polymerase chain reaction (PCR), using the primers WusUp (5' CTTATTTACCGTTAACTTGTGAACA 3') (SEQ ID NO:1) and WusLow (5' CACATAACGAGAGATAACTAGTTAAC 3') (SEQ ID NO:2). The 1062-bp long PCR fragment, harboring the entire protein coding region plus part of the 3' UTR, was first cloned into the pPCR-Script Amp SK(+) vector (Stratagene) and then cut with *Xho*I (vector polylinker site) and *Spe*I (site in the 3' UTR of the *WUS* cDNA) for the subsequent cloning into the corresponding sites of both the pER10 vector (17- β -estradiol inducible) and the pBA002 vector (constitutive 35S promoter) for the 35S::*WUS* expression. The correct sequence of the *WUS* cDNA was confirmed by DNA sequencing analysis.

Genomic DNA Southern and RNA Northern blotting analyses were carried out as previously described (Zuo et al., 2000a; Zuo et al., 2001).

Example 4

Screening of the *plant growth activator* mutants

Explants derived from *Arabidopsis* vegetative tissues are known to be incapable of forming somatic embryos or embryogenic calli promoted by external plant hormones. We presumed that external hormones alone were incapable of activating key regulators of *Arabidopsis* necessary for vegetative-to-embryogenic transition. With appropriate hormone treatments, gain-of-function mutations in these regulatory genes may activate the vegetative-to-embryonic transition. Such gain-of-function mutations, on the other hand, may also cause severe defects during subsequent plant growth and development. Therefore, if the expression of the mutated gene and/or the biological activity of related gene products is not appropriately controlled, it will be difficult to maintain the identified mutations. An example is the constitutive overexpression of the *LEC1* gene (Lotan et al., 1998). As a consequence, we carried out the screen by using a previously developed chemical-inducible XVE system, which has been demonstrated to be stringently controlled and to be highly responsive to the inducer 17- β -estradiol, a mammalian

hormone with no apparent physiological effects on plant growth and development (Zuo et al., 2000a). The use of an inducible promoter thus allows us to recover normal mutant plants by withdrawal of the inducer, even in the case that the gain-of-function mutation is lethal.

5 *Arabidopsis* root explants were transformed with *Agrobacteria* (Koncz et al., 1989) carrying an XVE vector pER16 (Figure 1). Transformed explants were cultured on a screening medium (SCM containing auxin, 17- β -estradiol and kanamycin but without cytokinin). Note that mutations functionally analogous to *cytokinin independent 1* (*ckil*; Kakimoto, 1996) should also be recovered under the screening conditions. In the primary
10 screen, we isolated 35 putative mutants by interrogating approximately 38,000 independent transformation events. As expected, most of these mutants (33 out of 35) showed a *ckil*-like phenotype, i.e., shoot regeneration independent of cytokinin. The remaining two mutants gave rise to green-yellowish embryogenic calli. We collectively named these two classes of mutations as *pga* for *plant growth activator*. Here, we
15 disclose a detailed characterization of one of these mutants which is named *pga6*.

Example 5

The *pga6* gain-of-function mutation promotes the vegetative-to-embryonic transition

The *pga6* mutant was initially identified by its ability to form embryogenic calli
20 on SCM. The embryogenic calli were transferred onto a shoot induction medium containing both auxin and cytokinin but without the chemical inducer 17- β -estradiol. After 2-3 weeks, shoots were regenerated from the isolated calli. Explants derived from different organs of the regenerated shoots were cultured on SCM as described before; a portion of the excised explants was cultured in SCM without the inducer to serve as
25 controls. After culturing for 7-10 days, only slowly growing calli were occasionally observed in the absence of inducer (Figure 2A). In the presence of the inducer, however, the explants produced numerous, rapidly growing, yellowish embryogenic calli (Figure 2B), which subsequently developed into distinctive somatic embryos (Figure 2C). After being transferred onto a non-inductive medium, all these somatic embryos were able to
30 germinate (Figures 2D and 2E) and develop into fertile adult plants, most of which were morphologically indistinguishable from wild-type plants (Figure 2F).

To further confirm the above observations, somatic embryo-derived plants, as shown in Figure 2F, were germinated on MS medium in the absence of the inducer. The inducer-dependent somatic embryo formation was reproducibly observed in *pga6* explants prepared from different organs/tissues of previously uninduced T1 plants. Similar to that observed in the T0 explants, the highest frequency of somatic embryo formation was observed from root explants, followed by leaf petioles, stems and leaves. Isolated zygotic embryos had a frequency similar to that of root explants. The above results suggested that the *pga6* gain-of-function mutation was able to promote vegetative-to-embryonic transition under our experimental conditions, and that the *PGA6* gene was most likely tagged by the inducer-responsive *O^{LexA}-46* promoter.

In addition to the formation of somatic embryos, which are characterized by the presence of cotyledons lacking trichomes on the surfaces, we also observed approximately 10% of the *pga6* calli developing into shoots, suggesting that *PGA6* is also involved in organogenesis.

Example 6

The development of *pga6* somatic embryos

morphologically and temporally resembles that of zygotic embryos

To more closely follow the somatic embryogenesis process of the *pga6* mutant, we performed a scanning electron microscopic analysis. Somatic embryogenesis in the inducer-treated *pga6* explants highly resembled zygotic embryogenesis. The process was initiated from an asymmetric division of a single cell, giving rise to a smaller apical cell and a larger basal cell (Figure 3A). Subsequently, embryo-like structures equivalent to that of zygotic embryos at the early globular stage were easily recognizable (Figure 3B). These somatic embryos underwent a typical embryogenesis process, including the heart stage, the torpedo stage, and the cotyledon stage (Figures 3B and 3C), and eventually germinated into healthy seedlings (Figure 2F). In addition to the relatively normal growth and development of the somatic embryo-derived mutant plants, we observed that a small fraction (approximately 10%) of somatic embryos generated seedlings with three cotyledons (Figure 3D). This abnormality is presumably caused by different expression

levels of the *PGA6* gene or by abiotic effects as occasionally observed in seedlings germinated from wild-type seeds. Nevertheless, these above results demonstrated that a conditional gain-of-function mutation in the *pga6* locus promoted vegetative-to-embryonic transition, leading to the initiation of somatic embryogenesis.

Example 7

Plant hormone-independent somatic embryo formation

The data described above were obtained under tissue culture conditions. To investigate the effects of the *pga6* mutation on normal plant growth and development, T1 seeds were germinated on MS media (Murashige and Skoog, 1962) with or without the inducer. No detectable abnormality in growth and development (phenotype) was observed in *pga6* plants germinated and grown in the absence of the inducer. On the inductive MS medium, progeny with the mutant and wild-type phenotype segregated in the ratio of 3:1, characteristic of a dominant mutation in a single locus. Compared to wild-type seeds, the *pga6* mutant seeds germinated substantially later, with a delay of 3-5 days, suggesting an inhibitory effect of the mutation on plant growth and development. Whereas approximately one third of the mutant seedlings stopped further growth after germination and eventually died, the remaining two thirds mutant seedlings rapidly turned into green calli upon germination. These two distinctive mutant phenotypes, with an approximately 2:1 ratio, were presumably due to segregations (heterozygous or homozygous) for the *pga6* gain-of-function mutation locus, leading to different *PGA6* expression levels in homozygous and heterozygous seedlings. This notion was supported by subsequent genetic analysis of the T2 generation derived from T1 plants grown under non-inductive conditions. Whereas all progenies of the putative homozygous T2 families (5 out of 16) showed only the "lethal" phenotype on the inductive medium, the remaining 11 heterozygous families gave rise to a typical 2:1:1 segregation for embryogenic calli, "lethal" and wild-type phenotypes. In addition, the strength of the mutant phenotype was dependent on the inducer concentrations and the induced *PGA6* expression levels *per se* (see Figures 5B-C).

In the absence of any external plant hormones, somatic embryos were formed from green embryogenic calli (Figures 4B and 4C), which were able to germinate and

grow normally into fertile adult plants (Figure 4D). Interestingly, a considerably higher frequency of embryogenic callus formation was observed from excised *pga6* roots cultured on the inductive MS medium (Figures 4G and 4H), suggesting the presence of an antagonistic activity to PGA6 in intact plants, which may promote post-embryogenesis growth and development.

Overexpression of *LEC1* leads to abnormal plant growth and development as well as the occasional formation of embryo-like structures (Lotan et al., 1998). The *LEC1* gain-of-function phenotype, however, appeared to be strictly restricted to developmental stages prior to germination. After seedling germination, overexpression of *LEC1*, controlled by the XVE inducible expression system (Zuo et al., 2000a), did not produce any apparent abnormality in plant growth and development, although the *LEC1* transgene was highly responsive to the inducer during post-germination stages. On the other hand, the same transgenic line showed a strong phenotype if germinated directly in the presence of the inducer and the *LEC1* transgene was highly responsive to the inducer during post-germination stages. These observations suggest that embryo- or seed-specific co-factor(s) are required for *LEC1* function. To examine if PGA6 function is also dependent on embryo- or seed-specific co-factors, *pga6* mutant seedlings at different growth stages, germinated and grown on the non-inductive MS medium, were transferred onto an inductive MS medium. At these developmental stages, the fate of both root and shoot stem cells has already been highly specified in wild-type plants. The *pga6* mutation, however, appeared to reverse the developmental program, causing both root and shoot meristems to transform into embryogenic calli (Figure 4D). Similar to that shown before, these embryogenic calli were eventually capable of forming somatic embryos, which were able to germinate and grow into morphologically normal adult plants. The above results strongly suggest that PGA6 plays a key role in specifying and maintaining embryonic cell identity, independent of any embryo- or seed-specific co-factors.

Example 8

PGA6 is identical to the homeodomain protein WUS

Based on the segregation of the kanamycin selectable marker, the *pga6* mutant genome appears to contain a single transgenic locus. However, molecular analysis

indicated the presence of the *OLexA-46* promoter in two independent loci. One *OLexA-46* promoter was found to fuse to the *WUS* gene in chromosome II (Mayer et al., 1998), approximately 1 kilobase-pair (Kb) upstream from the putative translation initiation codon (Figure 5A). The second *OLexA-46* promoter fused immediately upstream of the putative translation initiation codon of an open reading frame (ORF) in chromosome V, encoding a putative basic-helix-loop-helix type transcription factor (designated ORF1). To verify the identity of the *PGA6* gene(s), cDNA fragments containing both *WUS* and the putative ORF1 were cloned into an XVE vector, and the resulting constructs were used to transform wild-type plants (Bechtold et al., 1993). Explants derived from XVE-ORF1 T1 transgenic plants did not show any apparent inducer-dependent phenotype. In addition, *ORF1* expression did not appear to be up-regulated by the chemical inducer in *pga6* plants, presumably due to the instability of the *ORF1* transcript lacking the entire 5'-untranslated region (UTR). By contrast, all *pga6* mutant phenotypes as described before were observed in the XVE-*WUS* T2 transgenic plants (Figures 6A and 6B) in an inducer-dependent manner (see Example 11 for details).

WUS expression was strictly dependent on different concentrations of the inducer in *pga6* mutant plants (Figure 5B). Figure 5C shows expression of *PGA6/WUS* induced by different concentrations of the inducer. Ten-day-old *pga6* seedlings germinated and grown on the MS medium were transferred to an MS medium containing various concentrations of 17- β -estradiol as indicated and cultured for an additional 16 hours before total RNA extraction. Five μ g total RNA were used for Northern blot analysis using a *WUS* cDNA fragment as a probe. Consistent with the inducer concentration-dependent *WUS* expression, *pga6* plants also showed various penetrations of the mutant phenotype in an inducer concentration-dependent fashion (Figure 5B), thus providing a series of conditional mutant alleles for further functional studies.

We also used a 35S-*WUS* construct for transformation of *Arabidopsis thaliana* Columbia as well as Landsberg ecotype. Most of the transformants recovered from selection showed strong alteration in seedling development. The hypocotyl was swollen and root tips often enlarged to give rise to shoot-like or embryo-like structures which were unable to further develop (Figures 6C-G). Leaf development, when observed, was also compromised indicating strong alteration of the shoot apical meristem (SAM) which,

besides lateral organs, could also form adventitious shoots or embryo-like structures (Figures 6G-H). Overall, all the tissues of the transformants would give rise to organs or embryo-like structures whose further development, however, was impaired. This observation supports the validity of our strategy of using an inducible system to isolate genes involved in the switch to embryo development as the continuous overexpression of regulatory proteins would prevent recovery of the mutants.

In summary, the above results indicated that the *OLexA-46* promoter-tagged *WUS* in the mutant genome represents *PGA6*. We will refer to the *PGA6* gene/protein as *WUS* in the future, but use *pga6* for the mutation/mutant identified in this study due to different properties between the loss- and gain-of-function mutations.

Because the *OLexA-46* promoter fused approximately 1 Kb upstream from the putative translation start codon (Figure 5A), the *WUS* promoter presumably remains functional in the mutant genome, leading to no apparent loss-of-function phenotype for the mutation. Nevertheless, the *WUS* gene was strongly inducible, giving rise to two transcripts, approximately 1.3 and 2.3 Kb (Figure 5C). The shorter transcript was presumably generated from the native transcription initiation site of the *WUS* gene, in which case the *LexA* operator sequence might serve as an enhancer to the *WUS* promoter. On the other hand, the longer transcript might represent transcription from the *OLexA-46* promoter. This suggests that the *OLexA-46* sequence can serve as a functional promoter, as well as a transcriptional enhancer for activation tagging.

Example 9

WUS represses *LEC1* expression during embryogenesis

The above data indicate that *WUS*, in addition to its meristem function described previously (Laux et al., 1996; Mayer et al., 1998), also plays a critical role in promoting or maintaining the embryonic potential. We have investigated expression of several embryo- or seed-specific genes in *pga6* embryogenic callus and somatic embryos. Root explants derived from *pga6* mutant plants were cultured on an MS medium supplemented with the inducer. Under such conditions, whereas embryogenic calli appeared after 10-15 days, somatic embryos and germinating seedlings were generated after 20 days (see Figures 2A-F, 3A-D and 4A-H). Due to the transient expression nature of the XVE

inducible system (Zuo et al., 2000a), *WUS* expression gradually declined upon continued culture on the inductive medium; however, the expression can be strongly re-induced by adding freshly-prepared inducer (Figure 7A).

The *LEC1* gene, normally expressed only in embryos and seeds (Lotan et al., 1998), was highly expressed in 20-30-day-old explants, a stage when somatic embryos and derived seedlings were generated. Figure 7B shows *LEC1* expression from 14 days until 28 days when *pga6*-dependent somatic embryogenesis takes places. *LEC1* expression, however, was dramatically decreased upon reactivation of *WUS* expression (Figure 7B). No alteration of *LEC1* expression was detected when the explants/calli were transferred onto the control medium for an additional two days, suggesting that the *LEC1* repression was a specific response to the 17- β -estradiol induced *WUS* expression.

These observations suggest that *LEC1* expression in *pga6* explants was not a direct response to *WUS* overexpression but rather a consequence of the *pga6* somatic embryo development. On the other hand, a developmental path redefined by *WUS* overexpression leads to the repression of *LEC1*, a gene presumably involved in embryo maturation.

Example 10

Enhanced frequency of somatic embryo formation by addition of 2,4-D

Although we were able to generate somatic embryos from various *pga6* tissues/organs in the absence of any external hormone, the frequency of somatic embryo formation appears to be lower compared to that observed in our original screening conditions, under which a 2,4-D pretreatment was included. To test the effects of 2,4-D on somatic embryogenesis, *pga6* root explants were cultured on MS medium with 0.5 mg/L 2,4-D for 5 days prior to being transferred to an MS medium with or without 10 μ M 17- β -estradiol. No somatic embryo formation was observed in the medium without the inducer, whereas numerous somatic embryos were generated after 2-3 weeks culturing in the presence of the inducer. As shown above (see Example 7 and Figures 4A-H) and by the results disclosed in this Example, the absence of 2,4-D pretreatment resulted in a substantially decreased efficiency for somatic embryo formation, indicating that the 2,4-D treatment is able to significantly increase the efficiency of somatic embryo formation.

Collectively, the above results suggest that 2,4-D was able to enhance yet unidentified components in the signaling network, which play a key role in promoting the vegetative-to-embryonic transition. In addition, these results further demonstrated the validity of our working hypothesis as well as the screening strategy, i.e., that external hormones alone
5 were incapable of activating key components for the vegetative-to-embryonic transition in *Arabidopsis*, and that the appropriate external hormone treatment in combination with gain-of-function mutations in key regulatory genes is fully capable of promoting the vegetative-to-embryonic transition or somatic embryogenesis.

Example 11Somatic embryo formation of explantsderived from transgenic plants carrying a pER10-*WUS* transgene

The XVE vector pER10 is identical to pER 8 except that the hygromycin resistance marker is replaced with a kanamycin-resistance marker (Zuo et al., 2000(a)). Full length *WUS* cDNA was placed under the control of the XVE system in pER10. Stem segments derived from the pER10-*WUS* transgenic plants were pre-cultured on the MS medium with 0.5 mg/L 2,4-D for 5 days and then transferred to an MS medium with or without 10 μ M 17- β -estradiol. No somatic embryo was observed in medium in the absence of the inducer, whereas with the inducer, many somatic embryos were generated after 2-3 weeks of culture.

Similar to that of *pga6* mutant plants, we found that the 2,4-D pre-treatment substantially increased the frequency of somatic embryo formation in pER10-*WUS* transgenic plants.

The method of placing *WUS* in pER10 or similar vectors which can be regulated enables one to perform the same or similar experiments in plants other than Arabidopsis.

Example 12Placing *WUS* under the control of a tissue specific promoter

The G10-90 promoter in the XVE vector can be replaced with a tissue-specific promoter (e.g. a pollen-, root- stem- or leaf-specific promoter). A variety of tissue specific promoters are well known to those of skill in the art. Because expression of a transgene is activated by the chimeric *XVE* gene which is controlled by a tissue-specific promoter in this Example, the *OlexA-46* promoter controlling the *WUS* transgene is therefore tissue-specific in an inducer-dependent manner. This means that *WUS* will be induced only in the presence of an inducer and only in the specific tissue corresponding to the tissue specific promoter. Appropriate tissues or cell types, can then be collected from the transgenic plants and used for induction of somatic embryos as described in Examples 10 and 11.

Particularly when pollen derived from transgenic plants carrying a pollen-specific promoter-XVE/*OlexA-46-WUS* vector is used, progeny plants generated from pollen-

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derived somatic embryos should be haploid instead of diploid (see, e.g., Twell et al., 1989 and Twell et al., 1990 for pollen specific promoters). In this embodiment of the invention, a transgenic plant having in its genome a *Wuschel* (*WUS*) gene under the control of an inducible, pollen-specific promoter would not normally express the gene. Pollen from such a plant can be cultured in the presence of the inducer until somatic embryogenesis occurs, after which the inducer is removed and the haploid embryos are permitted to develop into haploid clones according to standard techniques.

Example 13

10 Use of the pER10-*WUS* as a silent marker for transformation.

The pER10-*WUS* vector can be used directly for transformation of explants without the use of an antibiotic resistance marker. Somatic embryos that formed in the presence of an inducer but in the absence of cytokinin should be transformants, because under such conditions non-transformants will be incapable of forming somatic embryos nor shoots due to the lack of induced *WUS* gene expression. Upon inducer removal, the embryos and shoots will develop into normal and fertile plants. The vector can include any gene or genes which are desired to be present in the transformed plants and these can be under the control of a desired promoter. The plants selected as a result of selecting for inducible *WUS* expression-dependent somatic embryos or shoots will contain the desired gene or genes.

If desired, the *WUS* transgene can be placed into a vector comprising a means of removing the *WUS* transgene as well as other portions of the vector which are no longer desired, e.g., using the XVE-Cre/lox system (Zuo et al., 2001). Such methods are also disclosed in U.S. Patent No. 6,723,896, filed 12 November 1999.

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Example 14Induction of formation of somatic embryosfrom isolated zygotic embryos of *PGA6* transgenic plants

Zygote embryos at late heart stage were isolated from young siliques of *PGA6* plants and transferred to either non-inductive medium (MICK: MS salts, 30 g/L sucrose, 0.15 mg/L IAA, 100 mg/L carbenicillin, 50 mg/L kanamycin, and 0.25% phytigel, pH 5.7) or inductive medium (MICK plus 10.0 μ M 17- β -estradiol). After two weeks of culture, 10 zygotic embryos formed embryogenic calli on the inductive medium, but only 3 zygotic embryos started to form embryogenic calli on the non-inductive MICK medium. After 35 days of culture on the inductive medium, 10 zygotic embryos formed somatic embryos with a regeneration index (the number of somatic embryos per zygote embryo explant) of about 70-100 (Figure 8A). By contrast, on MICK medium without estradiol, only two zygotic embryos regenerated somatic embryos and the somatic embryo regeneration index was about 10-20 (Figure 8B).

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Example 15Generating an apomictic plant

Apomixis can be induced by introducing *WUS* into a plant cell in such a manner that the *WUS* gene is expressed in the appropriate tissues (e.g., nucellus tissue). This can be by means of, but is not limited to, placing the *WUS* gene under the control of a tissue-specific promoter (e.g., a nucellus-specific promoter), an inducible promoter, or a promoter that is both inducible and tissue-specific. Inducing expression of the *WUS* gene, e.g. in the nucellus, produces apomixis leading to an apomictic plant. This plant may then be used to establish a true-breeding plant line. Additionally, the vector utilized to transfer *WUS* into the plant cell can include any other desired heterologous gene in addition to *WUS*, including but not limited to, a marker gene or a gene to confer a desirable trait upon the plant, e.g., a gene resulting in larger plants, faster growth, resistance to stress, etc. This would lead to the development of an apomictic line with the desired trait.

In a variation of the scheme, plant expression cassettes, including but not limited to monocot or dicot expression cassettes, directing *WUS* expression to the inner integument or nucellus can easily be constructed. An expression cassette directing

expression of the *WUS* DNA sequences to the nucellus was made using the barley *Nuc1* promoter (Doan et al., 1996). The expression was used for plant transformation. Other genes which confer desirable traits can also be included in the cassette.

It is anticipated that transgenic plants carrying the expression cassette will then be
5 capable of producing *de novo* embryos from *WUS* expressing nucellar cells. In the case
of maize, this is complemented by pollinating the ears to promote normal central cell
fertilization and endosperm development. In another variation of this scheme, *Nuc1:WUS*
transformations could be done using a *fie* (fertility-independent endosperm)-null genetic
background which would promote both *de novo* embryo development and endosperm
10 development without fertilization (Ohad et al., 1999). Upon microscopic examination of
the developing embryos it will be apparent that apomixis has occurred by the presence of
embryos budding off the nucellus. In yet another variation of this scheme the *WUS* DNA
sequences could be delivered as described above into a homozygous zygotic-embryo-
lethal genotype. Only the adventive embryos produced from somatic nucellus tissue
15 would develop in the seed.

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- 40 Zuo, J., Niu, Q.-W., Nishizawa, N., Wu, Y., Kost, B., and Chua, N.-H., *KORRIGAN, an Arabidopsis endo-1,4- β -glucanase, localizes to the cell plate by polarized targeting and is essential for cytokinesis*. Plant Cell, 2000b. 12(7): p. 1137-1152.
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5

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10 U.S. Patent No. 6,028,185

U.S. Patent No. 6,229,064

U.S. Patent No. 6,239,327

15

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SEQUENCE LISTING

<110> The Rockefeller University and Pioneer Hi-Bred International, Inc.

<120> Promotion of Somatic Embryogenesis in Plants by Wunsche1 Gene Expression

<130> PCA16753-DIV1

<140> Divisional of S/N 2,464,147

<141> 2002-10-28

<150> US 09/984,274

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29/2

cacataacga gagataacta gttaac

26

The embodiments of the present invention for which an exclusive property or privilege is claimed are defined as follows:

1. A method for conferring apomixis to a plant comprising
 - (a) stably transforming a plant cell with a DNA molecule comprising at least one *Wuschel* coding sequence under the control of a promoter to produce a transgenic plant cell, wherein the promoter is selected from the group consisting of a nucellus-specific promoter and a promoter that is both nucellus-specific and inducible, and
 - (b) regenerating a transgenic plant from said transgenic plant cell,whereby overexpression of a *Wuschel* polypeptide from the *Wuschel* coding sequence in the transgenic plant results in the formation of an apomictic embryo.
2. The method of claim 1, wherein the transgenic plant cell comprises at least one additional heterologous DNA molecule in its genome.
3. The method of claim 1 or claim 2, wherein the *Wuschel* coding sequence is as shown by GenBank Accession No. AJ012310.1.

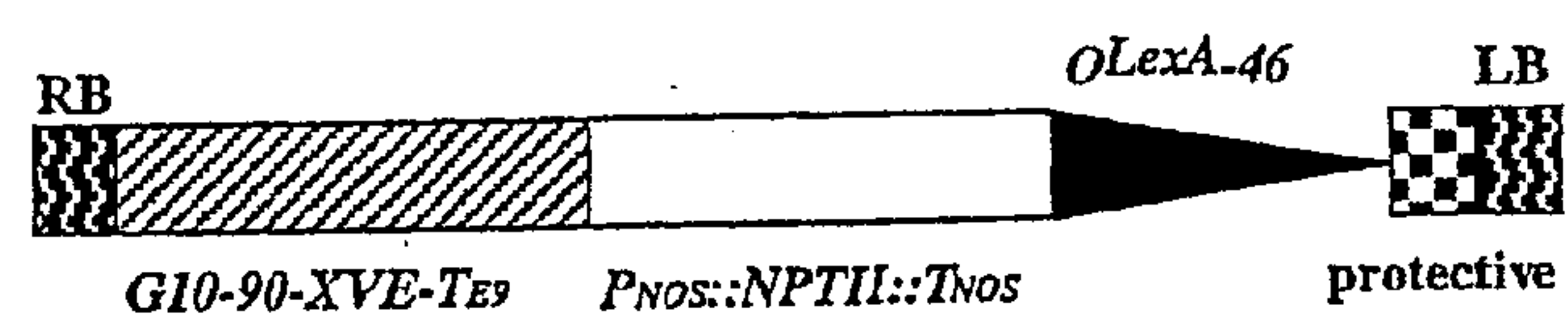


FIGURE 1

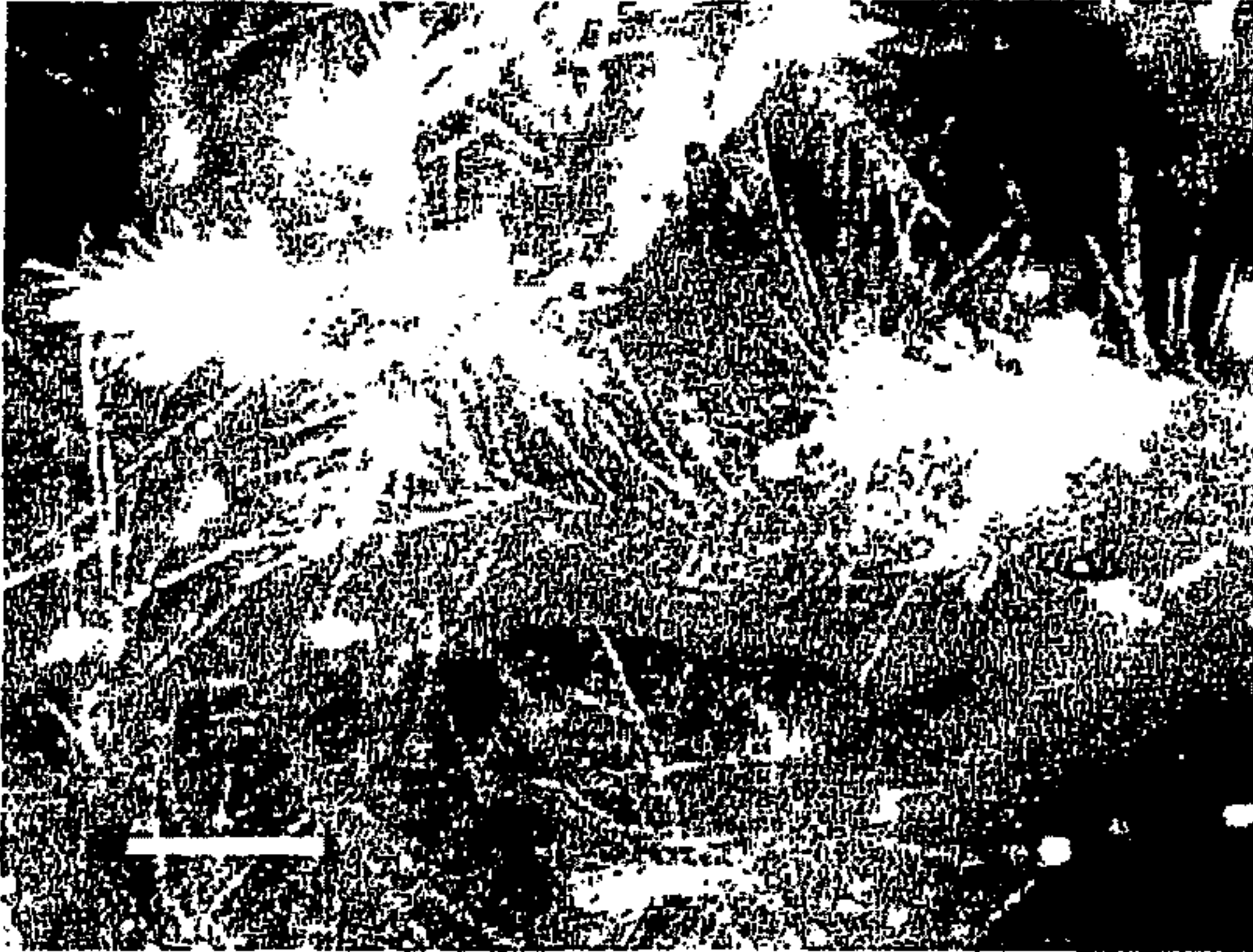


FIGURE 2A

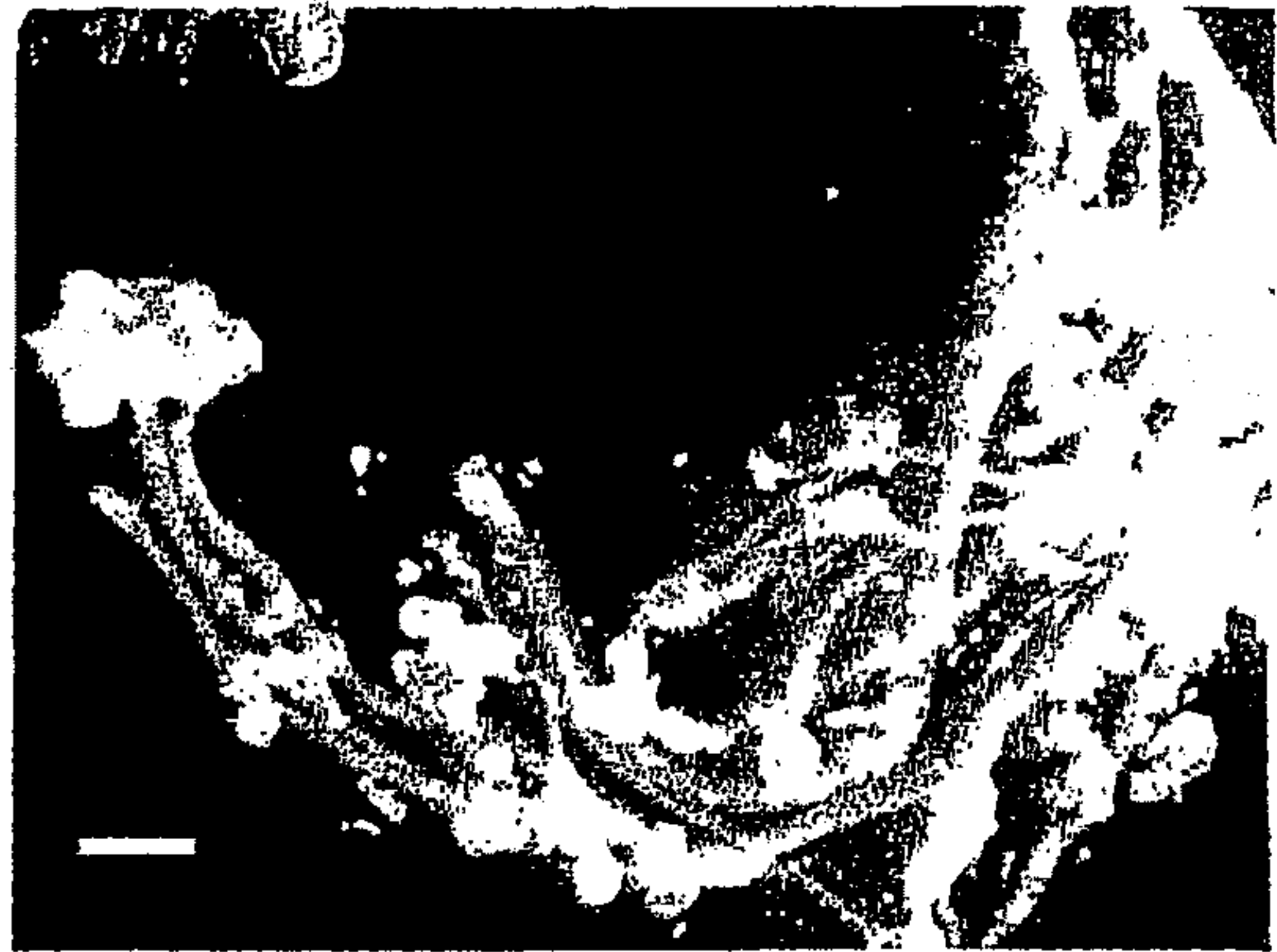


FIGURE 2B

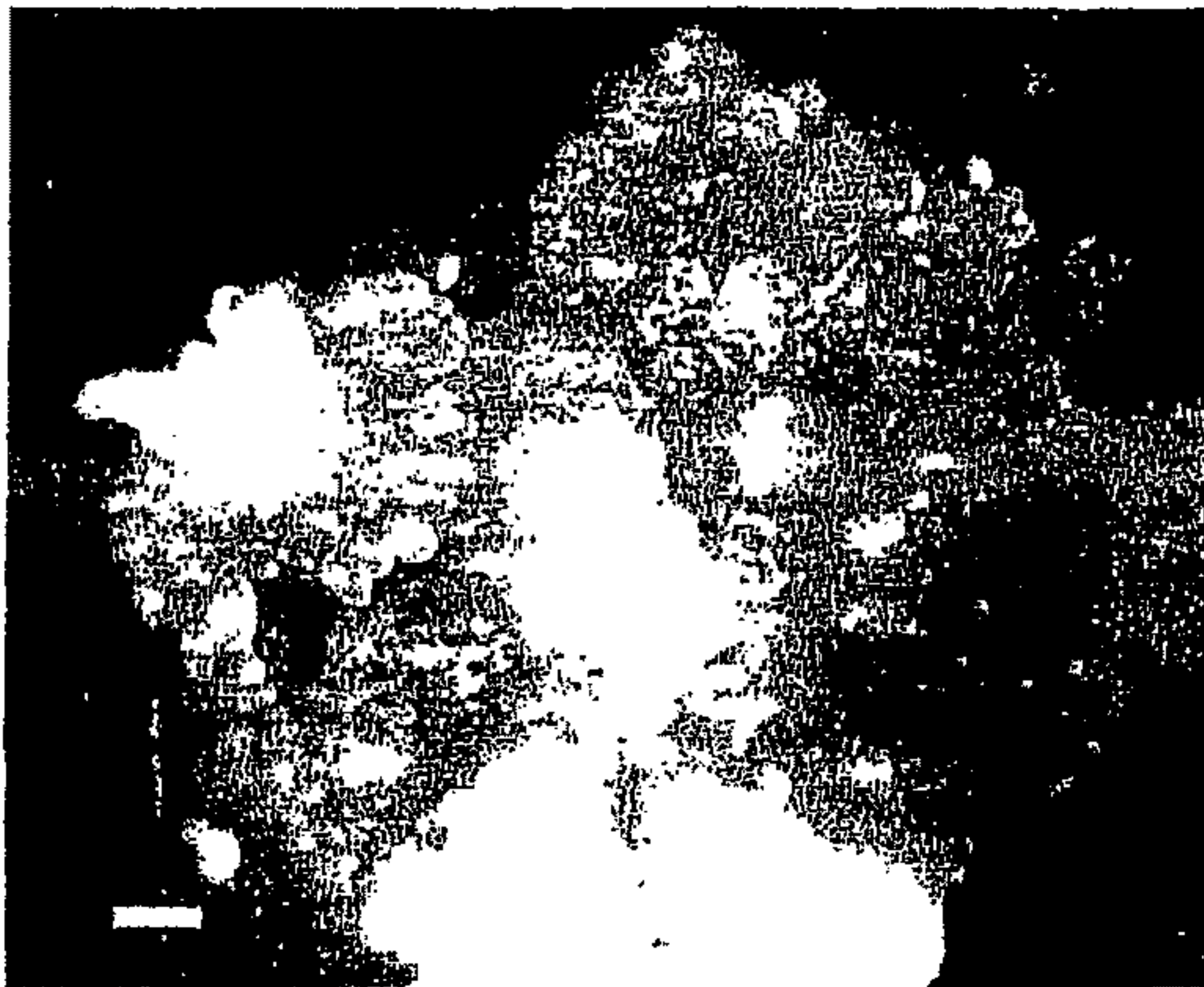


FIGURE 2C



FIGURE 2D



FIGURE 2E

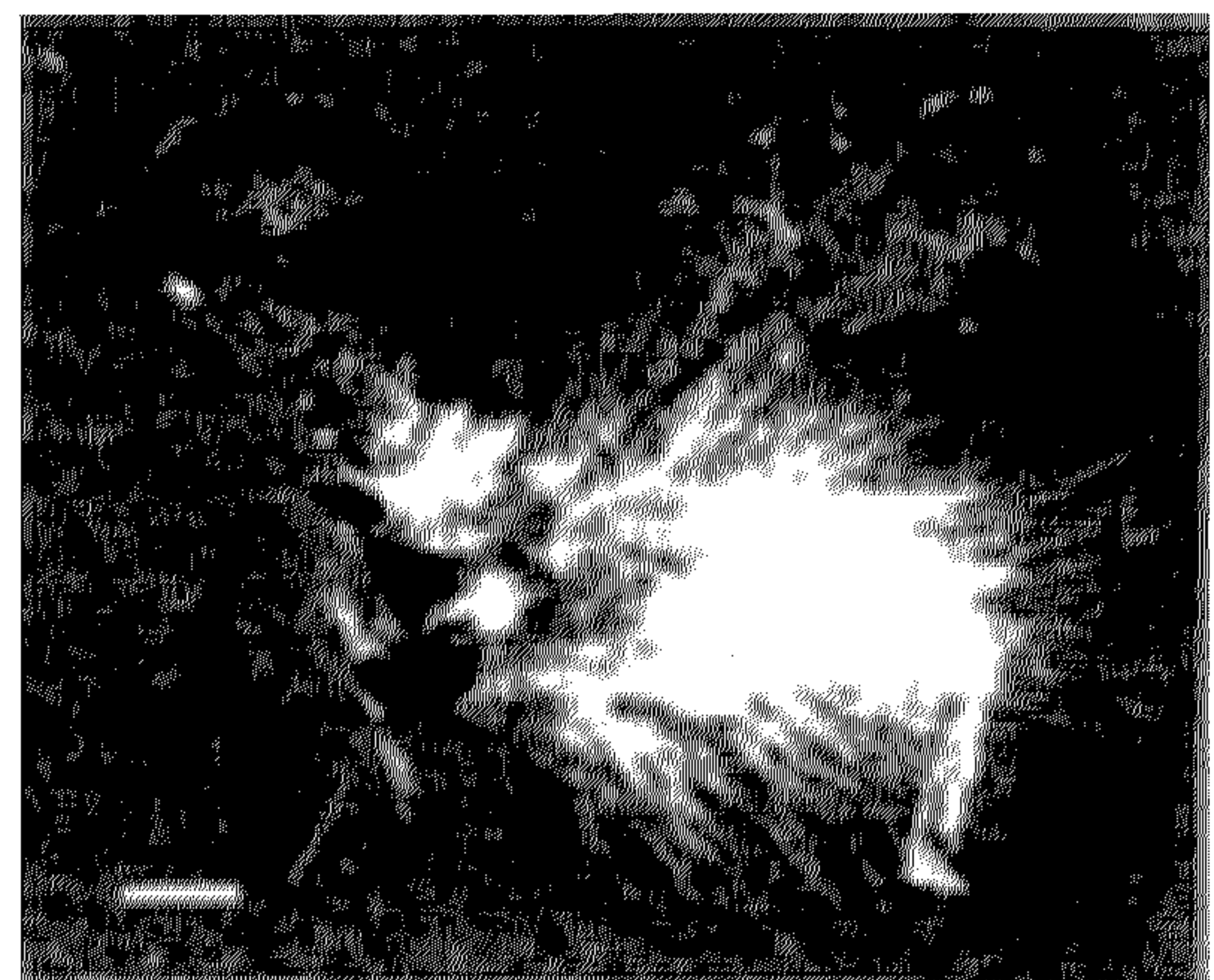


FIGURE 2F

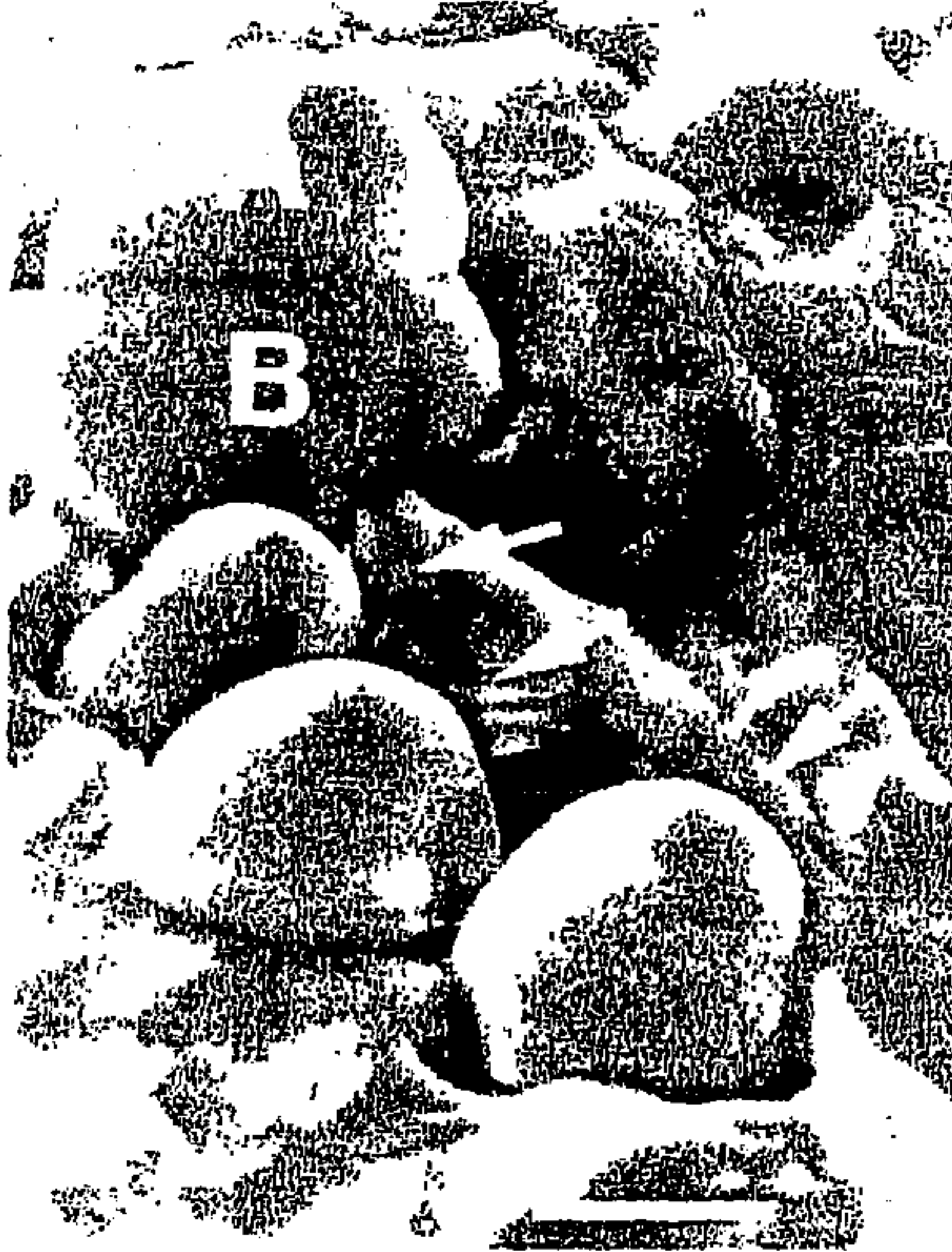


FIGURE 3A

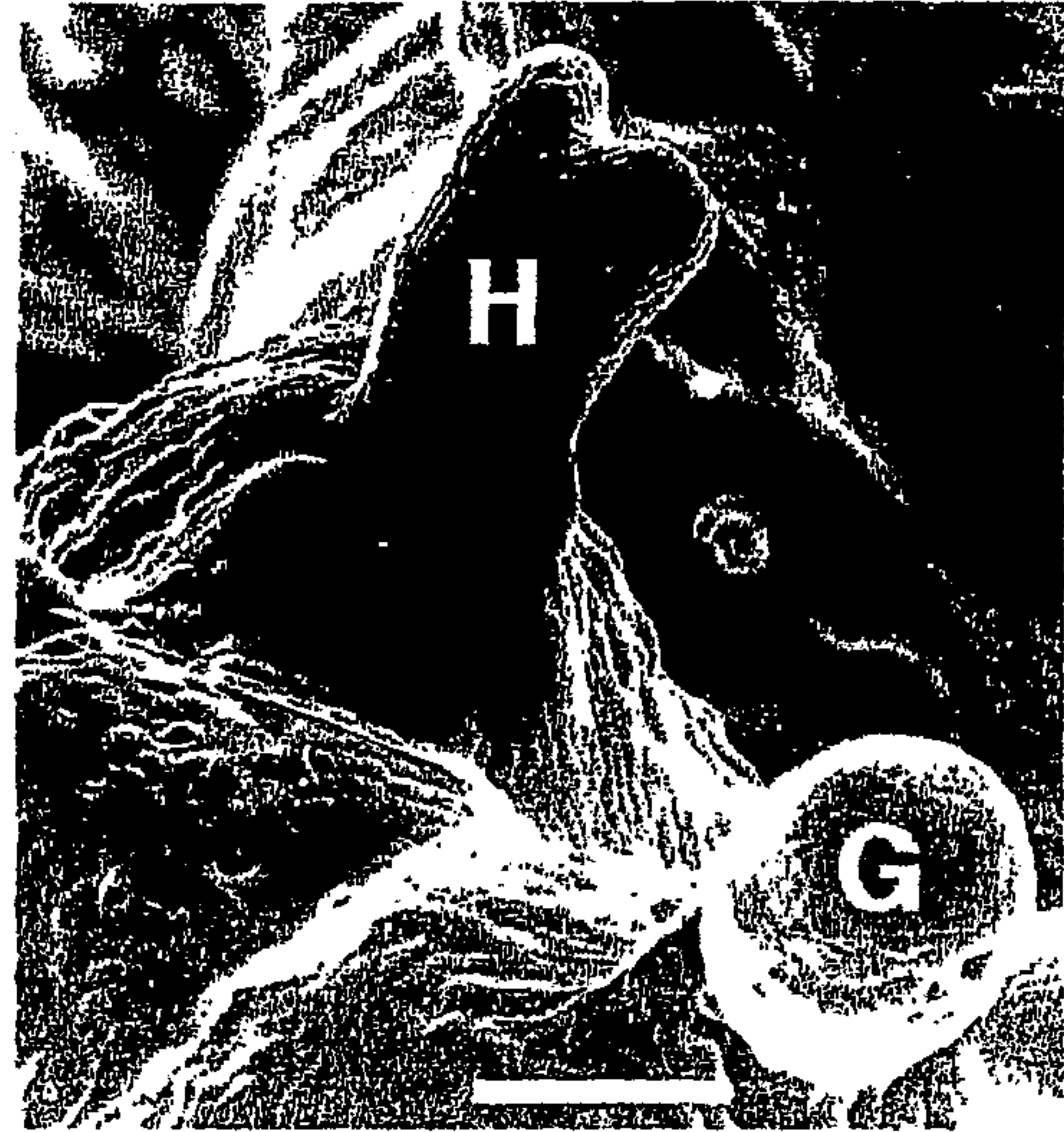


FIGURE 3B



FIGURE 3C

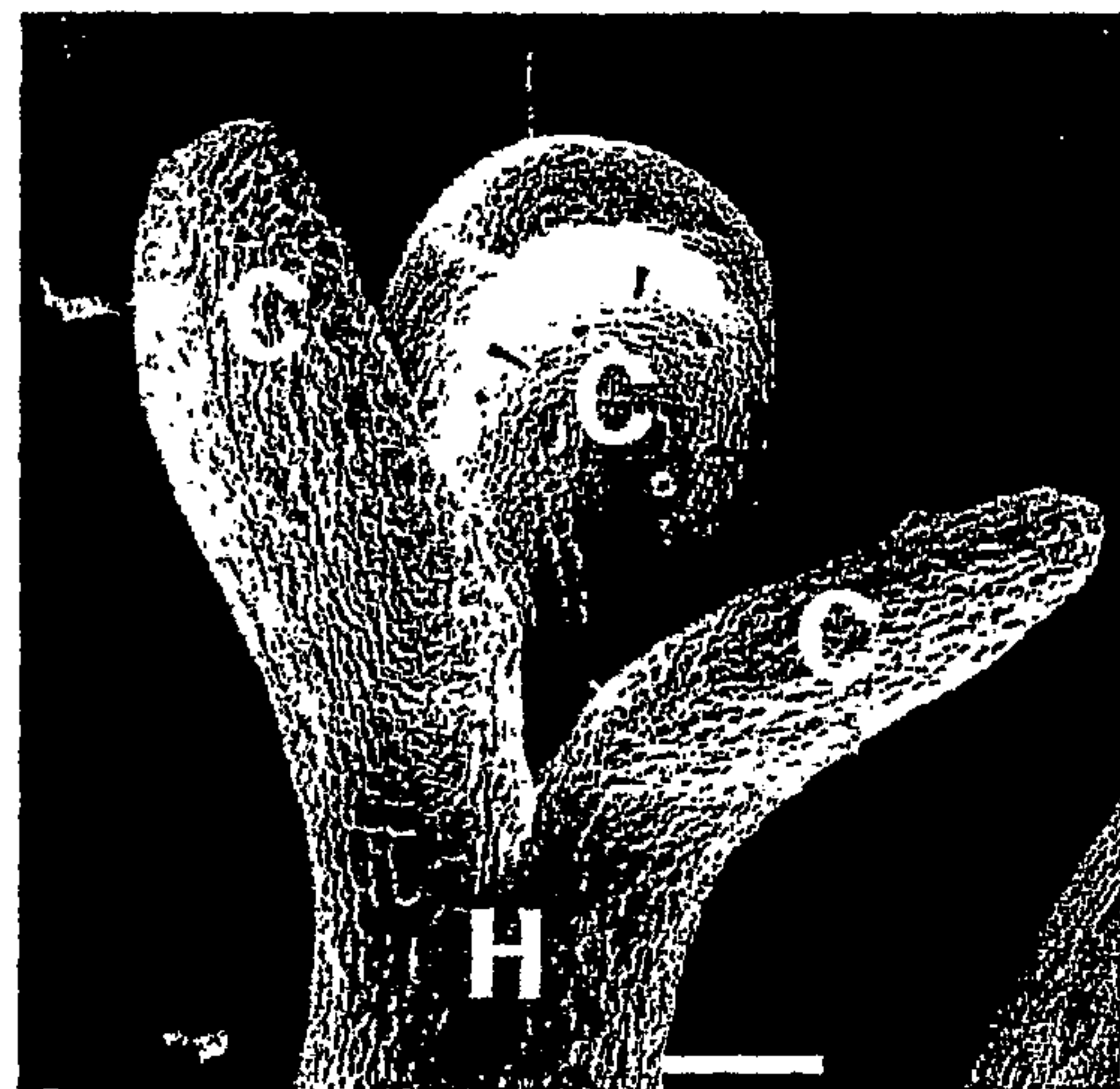


FIGURE 3D

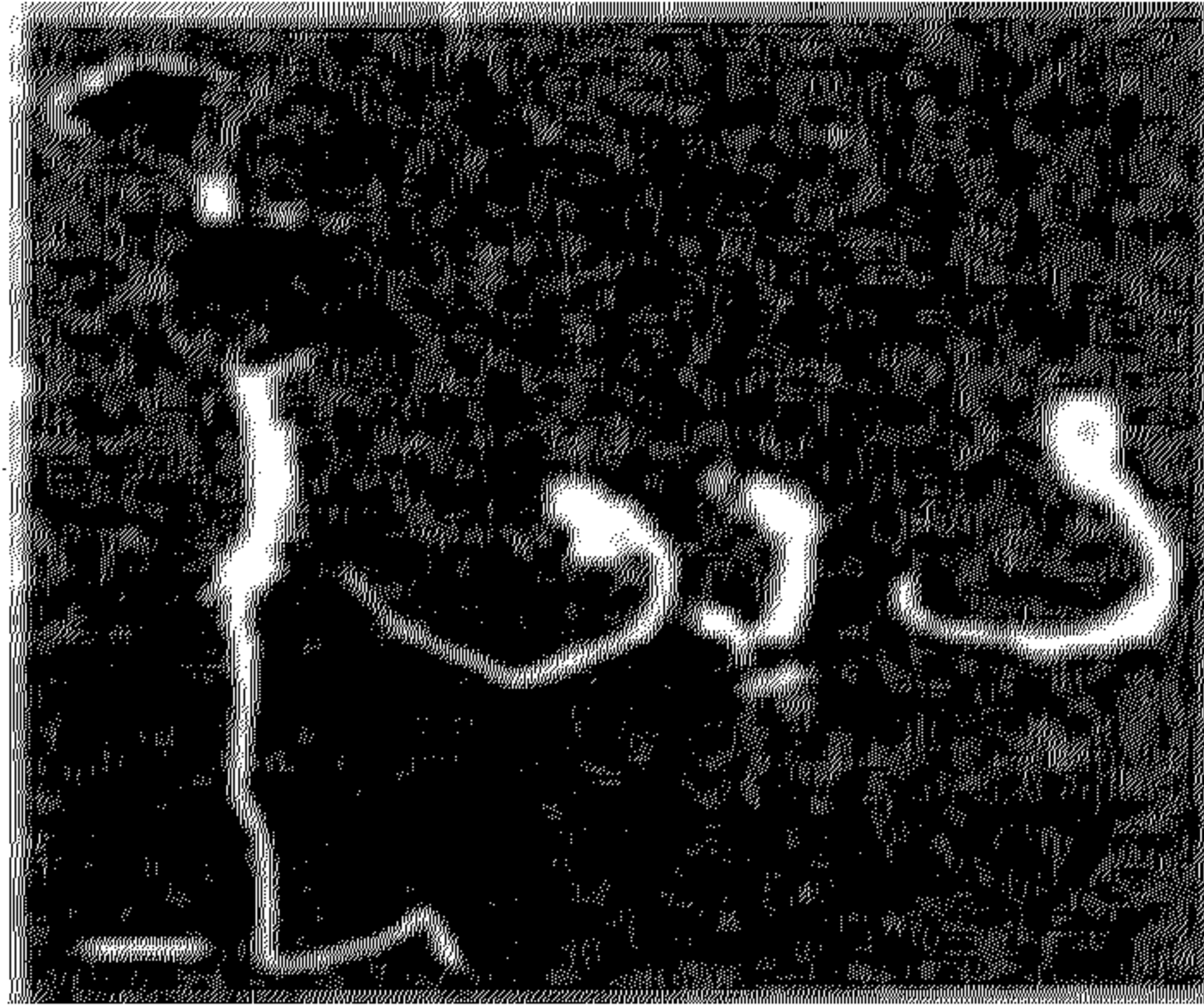


FIGURE 4A



FIGURE 4B



FIGURE 4C



FIGURE 4D

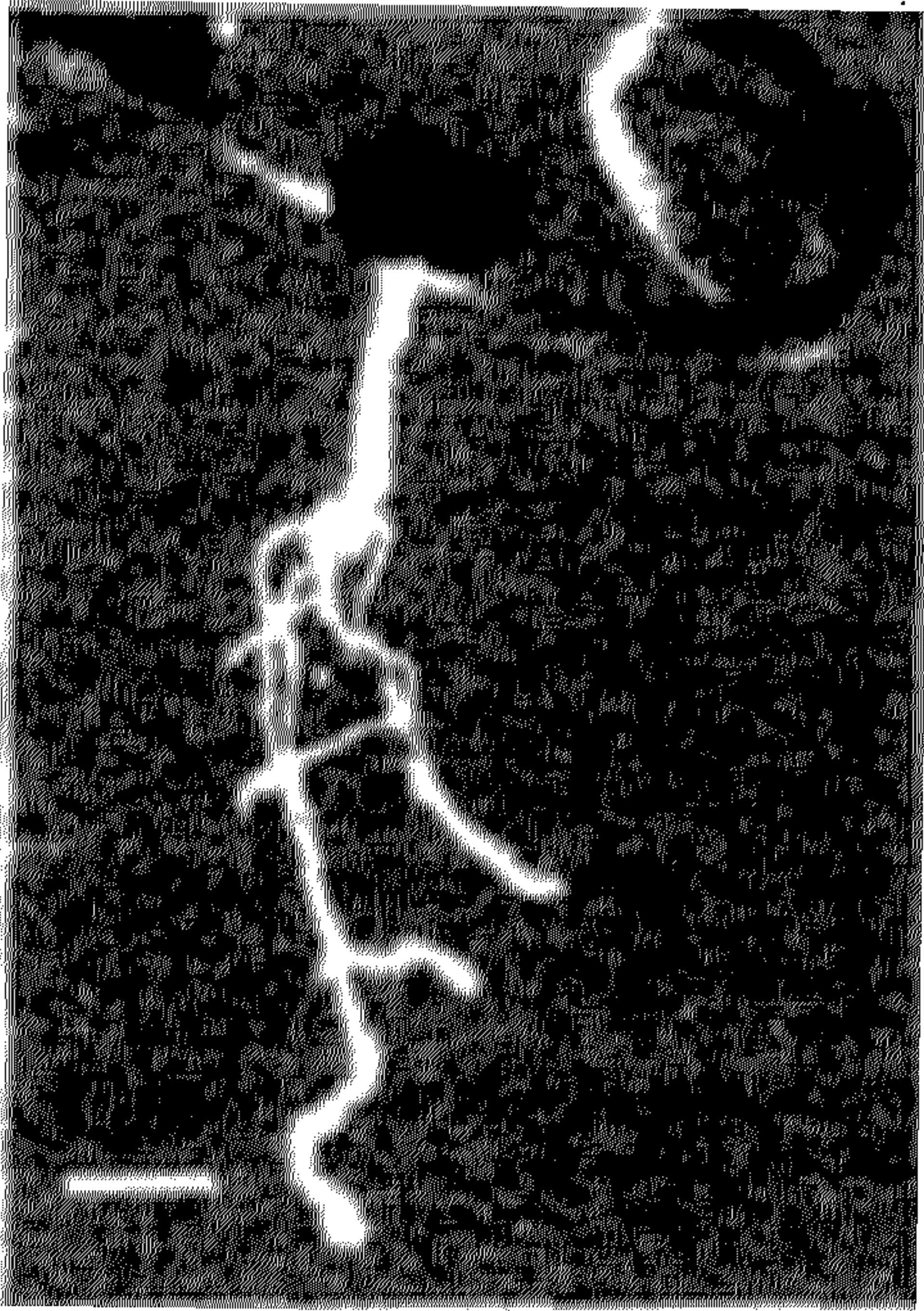


FIGURE 4E



FIGURE 4F



FIGURE 4G



FIGURE 4H

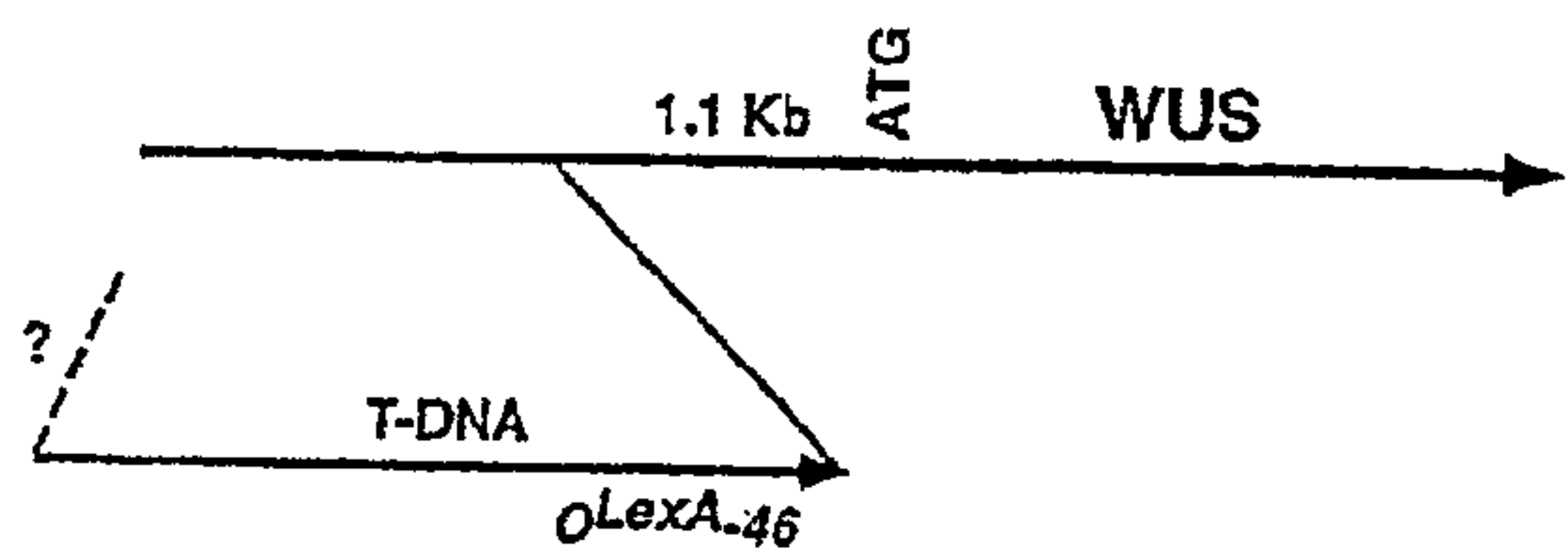


FIGURE 5A

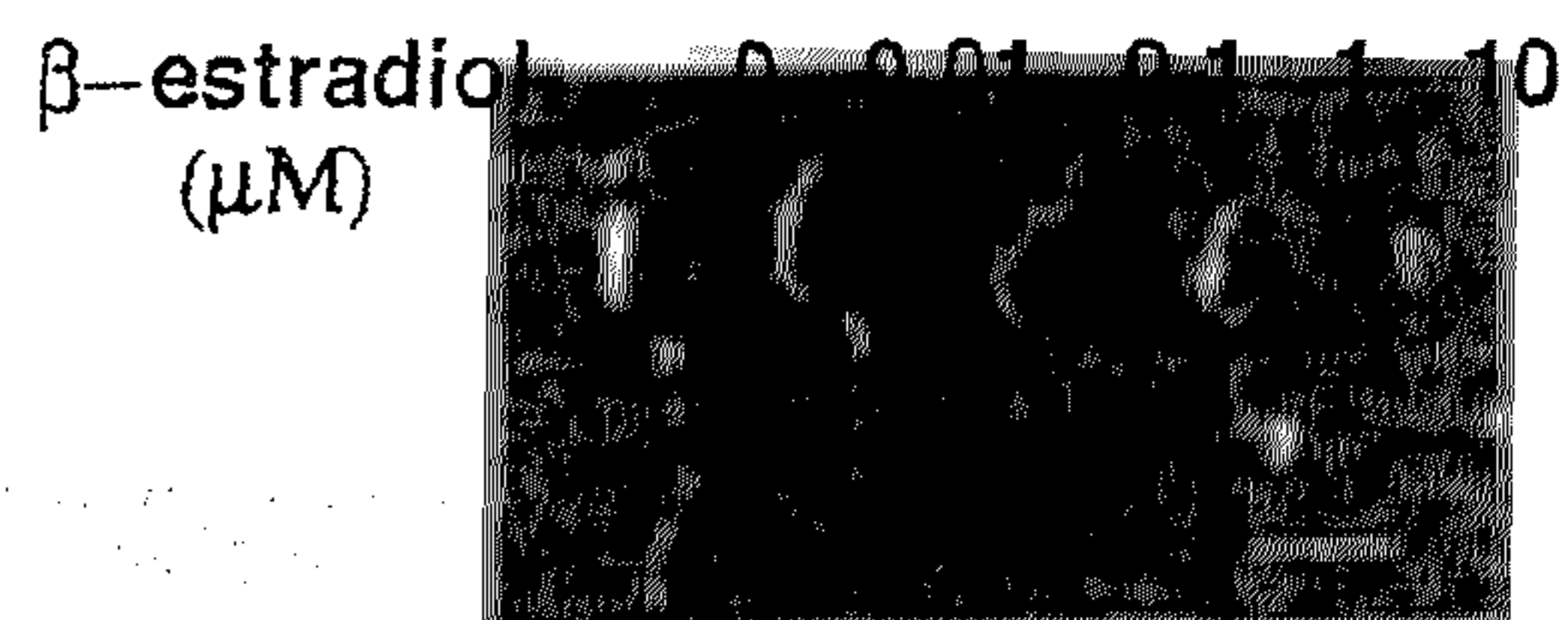


FIGURE 5B



FIGURE 5C

rRNA



FIGURE 5D



FIGURE 6A



FIGURE 6B

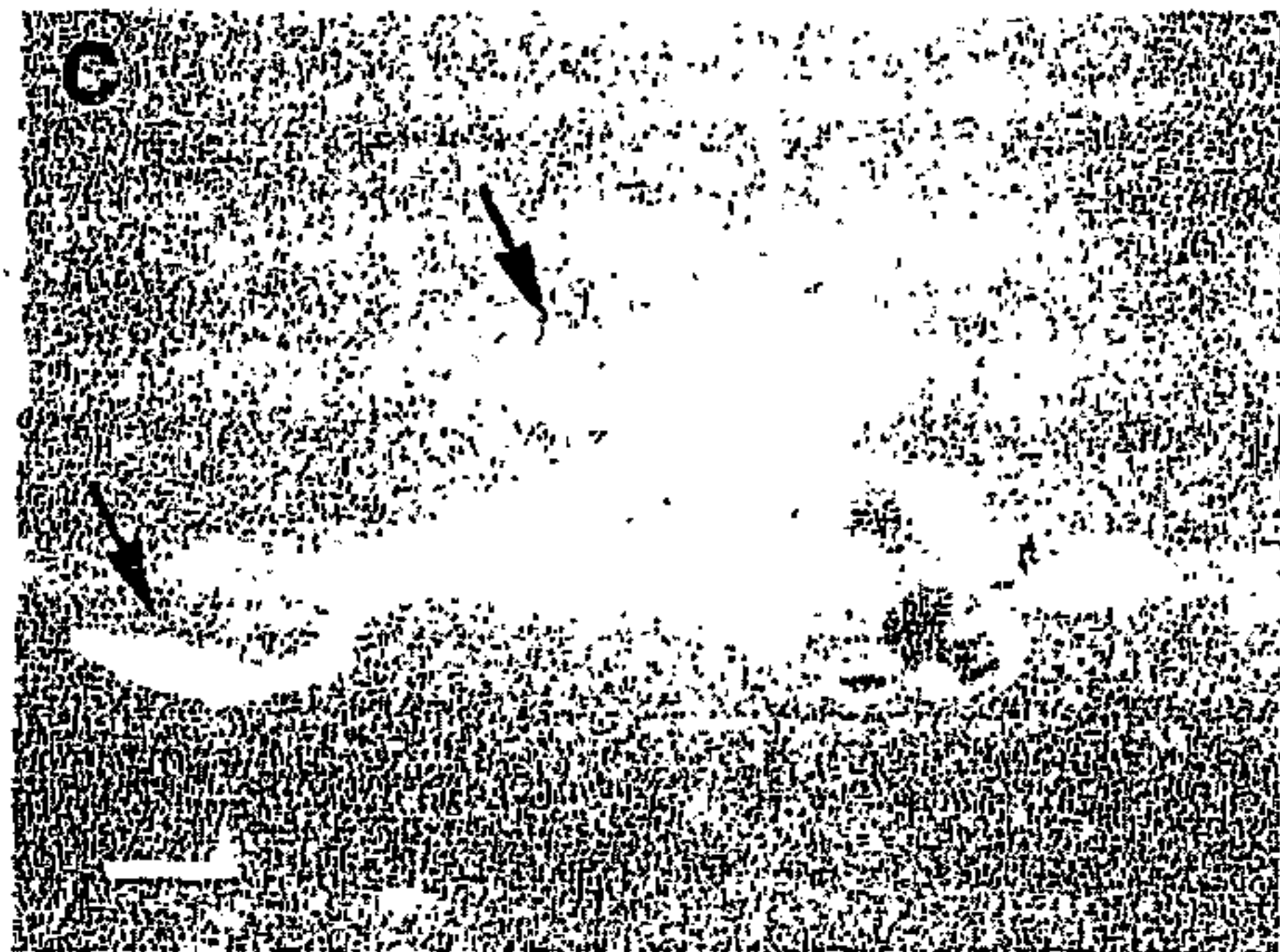


FIGURE 6C

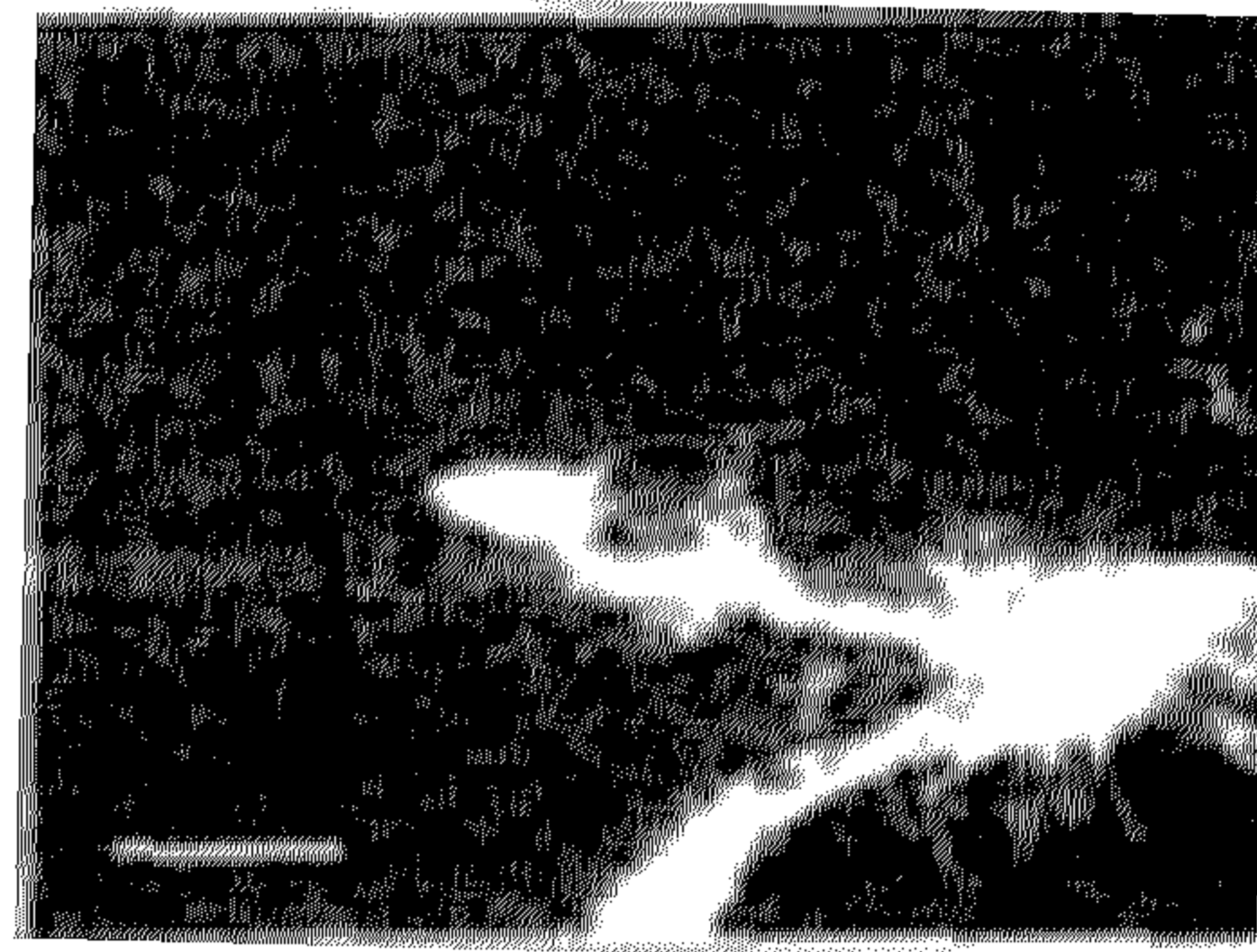


FIGURE 6D



FIGURE 6E

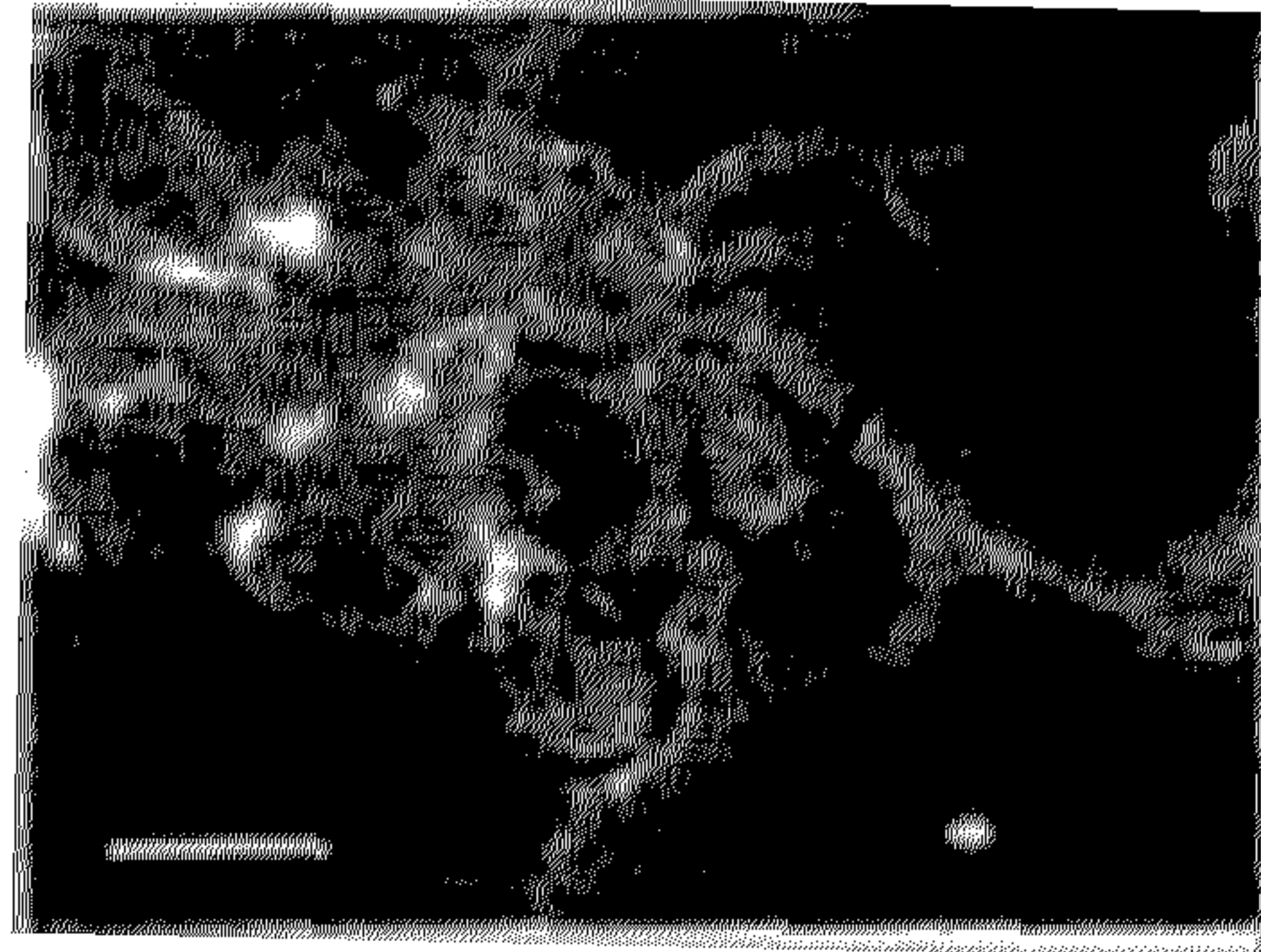


FIGURE 6F



FIGURE 6G

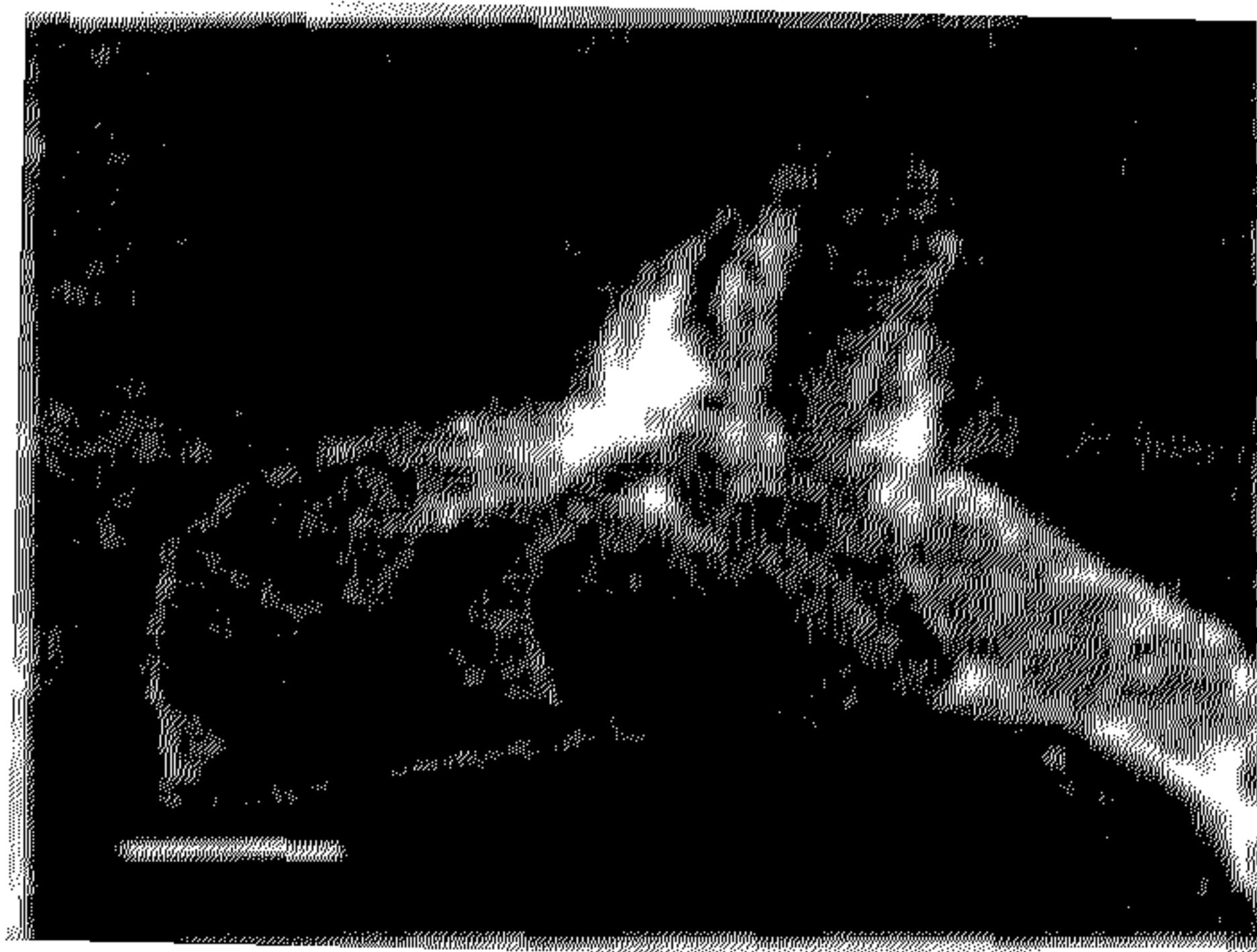


FIGURE 6H

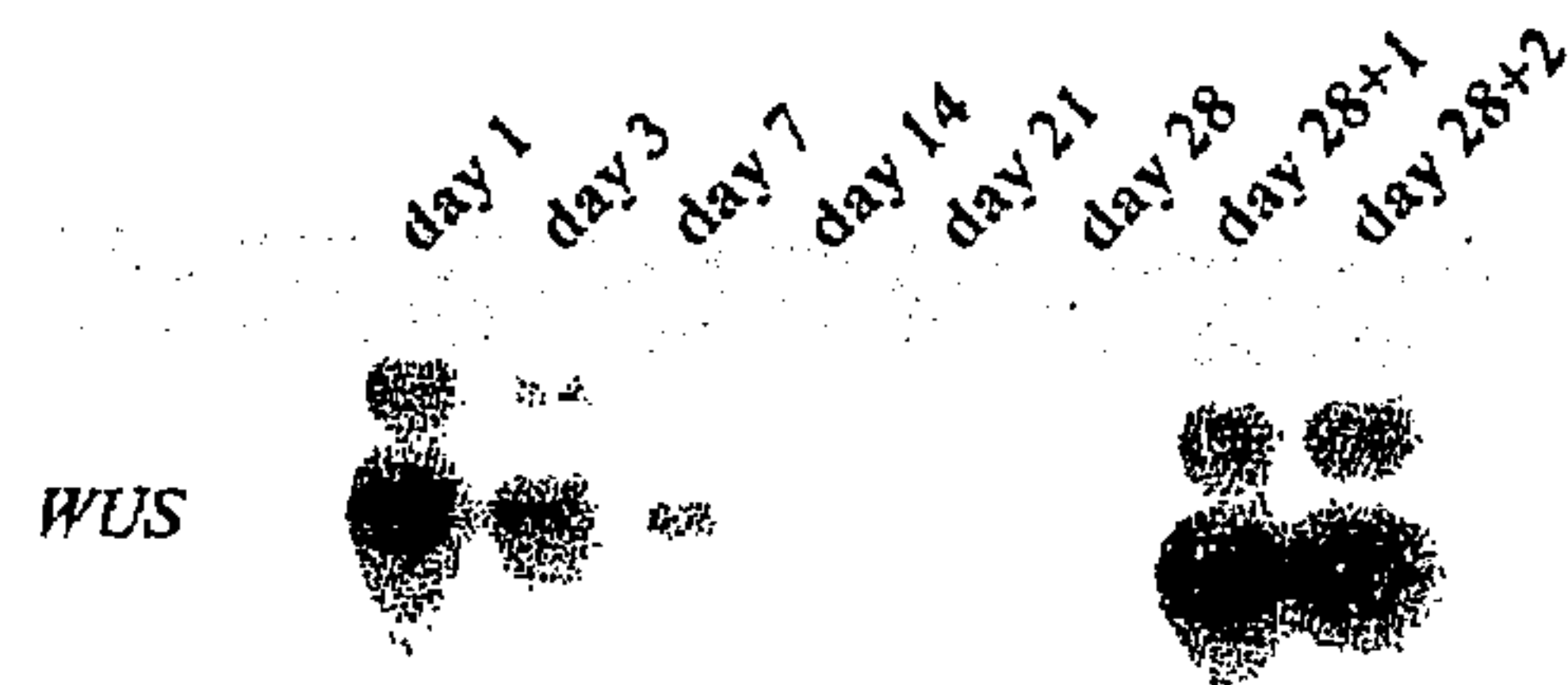


FIGURE 7A

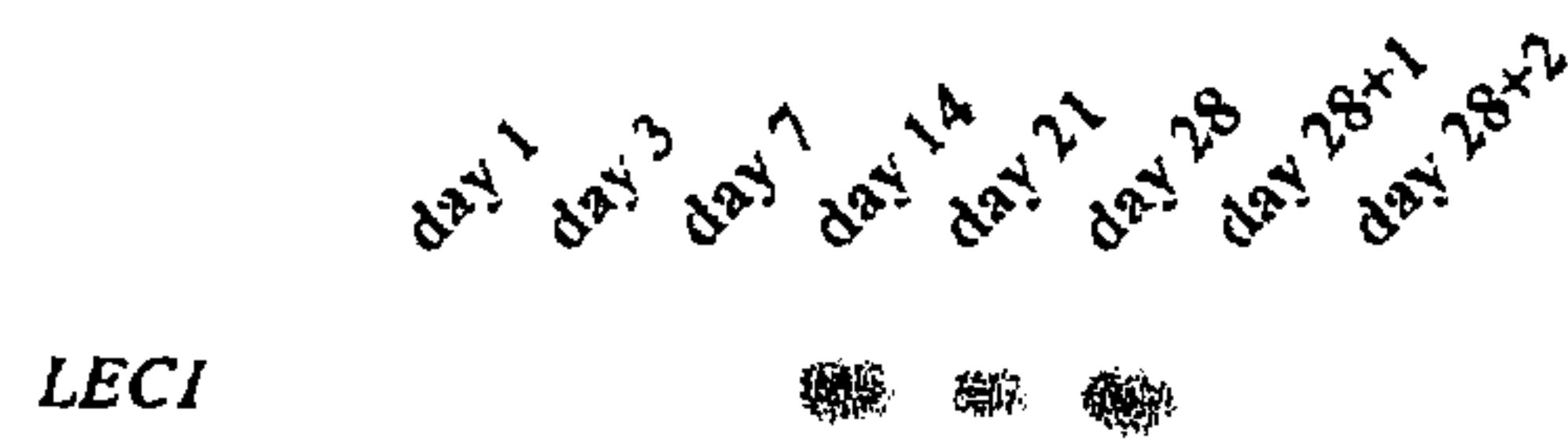


FIGURE 7B

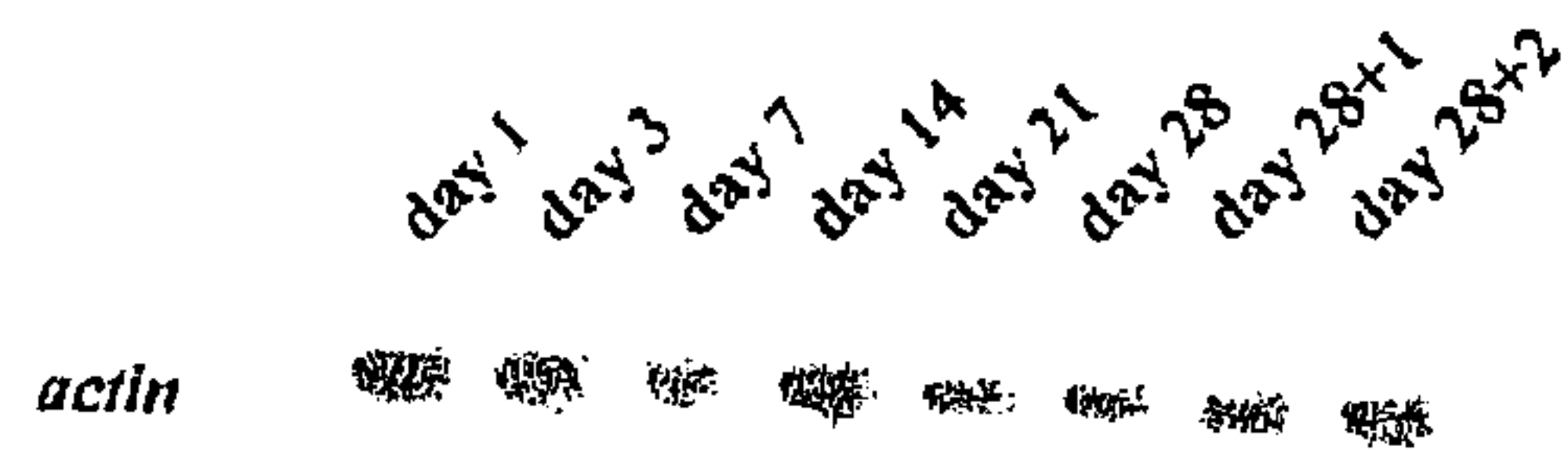


FIGURE 7C



FIGURE 8A



FIGURE 8B

