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Structural Properties of Generative Form by Hormonal Proliferation Algorithm

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Abstract. Cells in developing embryos behave according to their position in the organisms, and therefore seem to be receiving "Proliferation and positional information." A widespead view of the mechanism for this is that each cell responds locally to be concentration level of some extra cellular chemical, which is distributed, in a spatial gradient. For molecules conveying and receiving the proliferation and positional signal, concentrations are likely to be low enough that, per individual cell, only a few thousand molecules may be involved. In order to characterization of the structural properties of hormonal proliferation action, we proposed the construction of simple model based on hormonal generation used by Cellular Automata (CA).

1. Introduction

In contrast, CA are comfortable to program and quick to compute, described as below reason (ERMENTROUT and EDELSTEIN-KESHET, 1993).

(a) The operation only the essential physical and chemical principle used by rules.

(b) They discretize space, time series and status in rough bit functional manner.

These make CA, so to say, significant caricatures of nature's (WOLFRAM, 1986). The computational advantage of CA can be enormously enhanced by their implementability in parallel computers. Furthermore, CA can yield meaningful results without kinetic details, which are after not known, especially in biological or complex chemical system and this morphogenesis (MARKUS, 1990). At previous research, the idea that developmental processes are often governed by pre-existing gradients dates from beginning of the present century. It is now a day's general envisaged that the gradients conveying the positional and proliferational information will two out to be in the concentrations of chemical substances, but very few such substances have yet been identified (MEINHARDT, 1976). We mention hormonal factors as growth factors to indicate the great diversity of chemical natures for the substances that may be signification in pattern formation in biological proliferation (MEINHARDT, 1982). Most studies, however, have not focused on the influence fractal structures has on the generative biological complexity based on the hormonal proliferation model. We are not concerned in this paper with the cell proliferation in real living

organisms. This study elucidates the fractal structure (MANDELBROT, 1983) in biological complex by proliferation. Although a large number of researcher have been carried out into the biochemical proliferation roles of hormonal action, little is known about the relationships with fractal structure and biological complexity by hormonal generative actions.

2. Materials and Method

2.1. Model of hormonal proliferation

The strategy of our research work has been to apply as partially-graded input, without noise, to chemical amplifier envisaged as representing the immediate intracellular response to this signal. For this later, we have used two well-known methods, both in the category first proposed by CA (Cellular Automata) approach and known as the concentration dependency mechanisms. There is semantic confusion over thus term, because biologist using the positional information and differentiation information concept have applied the word to substances forming simple gradients and local concentration of hormonal chemicals. We present local gradient-reading (cuing) by using reaction part only of our models (shown as Fig. 1), without fluctuated diffusion.

In this form, our model as linear amplifiers, and do not change the form of the input gradient. The implies that we are modeling the final achievement of cell differentiation states following from the concentration revel of hormonal chemicals. A complete model for what the biologist observed would end with an ON-OFF switching effect, representing what happens to various gene activities as cell achieve diverse differentiation states. For the sharping of initial concentration signal into "Switching", the cumulative nonlinearity of multiple-steps of signal transduction cascade in frequently invoked.

In biological morphogenesis, cells could know positional information by concentration gradient. Biological cells respond varied behavior according as the positional information. Intercellular transmission is specific by threshold for concentration. This network does not direct connection because of hormonal transmission. These hormone affected distant cells. We are used that described below properties:

1. Non-network algorithm used lattice map
2. Specific recognized transmission
3. Concentration-dependent interaction
4. Cell characterization by threshold value for concentration

We devised Hormonal Proliferation Algorithm using properties as described above, Lattice does not connected other lattice (shown as Fig. 1).

2.2. Simulation procedure

First of all, we assumed several species cell and as many kinds diffusible hormone that is morphogen. In initial condition, we set each species cell threshold value of concentration for cell differentiation. Each species cell generates by different hormone. The hormones that were generated cells induce other species cell. If hormonal concentration is reached threshold value, cells could react to stimulus. The reaction was to appear new species cell (shown as Table. 1).

We put first cell on 1000×1000-lattice map. And, first cell increased free. The cells generate hormone at the rate of constant. Hormonal concentration increases in proportion

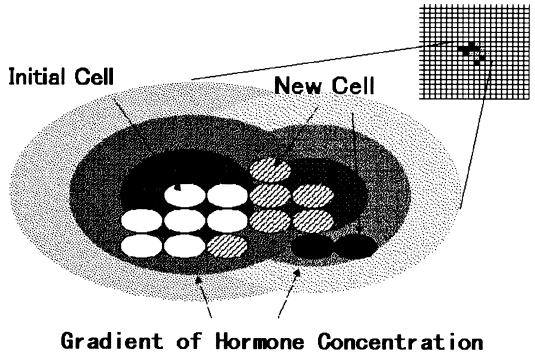

Fig. 1. Outline of cell differentiation model based on Hormonal proliferation algorithm.

Table 1. Hormonal Concentration of Differentiation Effect.

Cell species	Kind of hormone	Effective concentration
Cell 1	Hormone5	1–4
Cell 2	Hormone1	4–7
Cell 3	Hormone2	7–10
Cell 4	Hormone3	10–13
Cell 5	Hormone4	13–15

to time and 1/distance and cells density. When hormone concentration are reached specific threshold value in cell, new species cell are induced in neighborhood. When new cell increases, other new cell generates in neighborhood. Structures were shaped as a result of these processes.

In order to confirm that only hormonal properties could control global structure, we changed threshold value for concentration in simulation.

3. Simulation Result

As a result of simulation, several characteristic patterns structure was shaped in two-dimensional lattice map. The structure changed by hormonal threshold value of hormonal concentration. Typical formation indicated in Fig. 2.

We are computed fractal dimension by the box counting methods. We showed the profile of fractal dimensions transition (shown in Fig. 3). The transition was graded, and so, changed graded in according to time series.

We analyzed periphery of the patterns using Fourier analysis. The result showed 1/*f* like correlation (DESTEXHE, 1990; GOLDBERGER and BHARGAUA, 1991; MUSHA *et al*., 1991). We have known that biological structures are obtained 1/*f* correlation (Fig. 4). For example, higher plants are obtained the save correlation. Furthermore we are simulated with the different concentration of hormonal effect for the transition profile of fractal dimension (shown in Fig. 5).

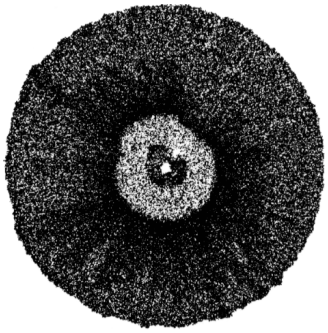

Fig. 2. Profile of inner growth by this Hormonal Proliferation Model.

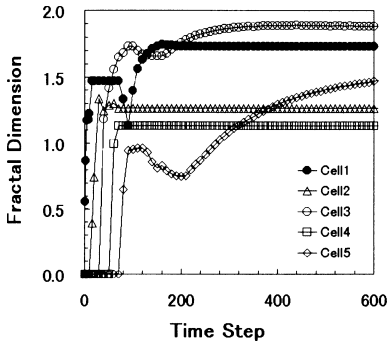

Fig. 3.

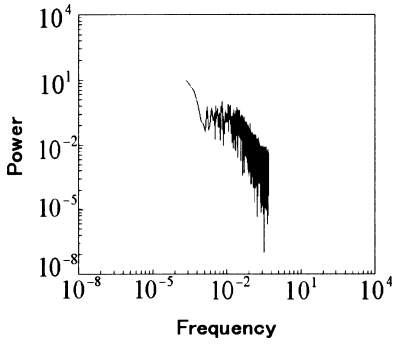

Fig. 4.

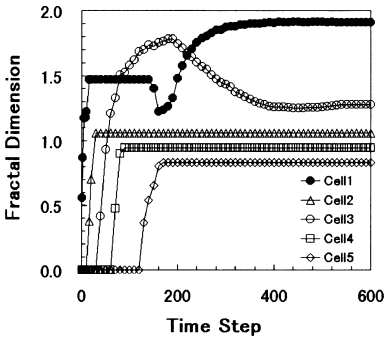

Fig. 5.

Fig. 3. Dimension profile according to proliferation. Simulation Condition: Hormonal effects are gave that hormone concentration are 1–4, 4–7, 7–10, 10–13, 13–15 respectably responded cell species 1–5.

Fig. 4. Correlation of outer interface by DFT Analyses are carried out with span = 1 ($1/f$ noise like slope).

Fig. 5. Dimension profile according to proliferation. Simulation Condition: Hormonal effects are gave that hormone concentration are 1–2, 4–5, 7–8, 10–11, 13–14 respectably responded cell species 1–5.

4. Discussion and Conclusion

4.1. Models

We have succeeded in simulating biological differentiation growth and a variety of the structure included complexity patterns into biological tissue using simple rules. These rules have the advantage of not relaying on the exact knowledge of kinetic functions, of being to program and permitting speedy calculations.

It is therefore quite significant that our computations have shown our hormonal proliferation model to good at regulating in one-dimensional gradient reading. The essence of this a differentiation character, in which periodic disturbances of a small range of concentrations are amplified, which both high and low concentration disturbances are strongly related.

4.2. Fractal properties of time and space scales in this model

Biological development occurs within a very restricted range of temporal and spatial scales (FEDER and ROSENQUIST, 1984; SMITH *et al*., 1989). Thus, while it is convenient to work in arbitrary units while doing computations, concepts of scale-dependence and non-dimensional variable are not ultimately useful in this field. The results must be related to biological complexity based on morphogenesis formation. The simulation output of our model are obtained the structure properties as described as below

1) Outer-surface are indicated $1/f$ correlation by DFT analysis.

2) Fractal dimension are indicated the profile in according to hormonal effects of several concentration.

The described above two contents, that our model are suggested the obtains of generative formation higher plants like. Further works for the similarity of real higher plant are in progress.

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