

NEURAL-NETWORK-LIKE BIOMACHINOGENESIS VIA SEMEIOGENESIS : A UNIFIED THEORY ON THE ORIGINS AND EVOLUTION OF GENETIC CODES AND OTHER SEMEIOTIC SYSTEMS

Koji Ohnishi¹, Shouken Hokari¹, Hiroshi Shutou¹, Daiji Kanbe¹, Madoka Ohshima¹,
Hajime Sawamura², Naotaka Furuichi³, Katuei Shibuki⁴, and Masaki Goda²

¹ Faculty of Science, ² Faculty of Engineering, and ³ Faculty of Agriculture, Niigata University,
Ikarashi-2, Niigata 950-2181, Japan (E-mail¹: ohnishi@sc.niigata-u.ac.jp)

⁴ Brain Research Institute, Niigata University, Asahi-machi, Niigata, 951-8585, Japan.

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(Abstract)

Genetic codes were found to have emerged as semeiotic culture of hierarchical tRNA-riboorganismic society in early intracellular micro-environment ("semeiotic culture theory" or "poly-tRNA theory" on the origin of genetic codes). Well-made biomachines such as bee super-organism (= bee eusociety consisting of queens and workers), animal body (= super-organism consisting of germ-line and somatic-line unicell diploid animals), and genetic apparatus were found to have evolved by neural-network-like machinogenesis via queen-worker-like hierarchical sociogenesis. Every of these socio-machinogenesis depends on the society's own specific semeiotic system which is considered to be the society's "semeiotic culture". Origins and evolution of cognitive and autopoietic characters of various biosystems were discussed, with special emphases on intracellular riboorganismic societies (RNA societies), multi-cellular societies (= multicellular animal body), and multi-individual iso-species society (= interbreeding population or "specia"), as well as on various semeiotic culture systems including genetic codes, bee-dance language, hormones (in multi-cellular society = animal body, etc.) and pheromones (in "specia"), and primate language systems. We have reached a new concept that every life is, most plausibly, some kind of autopoietic (self-improving) cognitive system, which can well explain "why organisms behave and evolve 'actively' or 'autopoietically'". Lamarck's "use-disuse phenomenon" was found to be elegantly explained by active selection of gene-sets derived from the previous generation's germ-line (queen)-cells by somatic worker-cells of the present generation. A new finding of the roles of germ-line and somatic cells was made, i.e., somatic cells play in "active gene-selection", whereas germ-line cells in "gene-transmission to the next generation". 20th century's biology was wrong in the interpretation of Lamarckian use-disuse theory. Discussions were made towards establishing "Unified Theory on the origins and evolution of general bio-systems".

(Key words)

Origin of mRNA and genetic codes, tRNA, Ribo-organismic society, Hierarchical society, Bee eusociety, Super-organism, Multicellular animal-body, Self-learning neural-network machine, Semeiogenesis, Autopoietic evolution, Active evolution, Use-disuse theory, Unified evolutionary theory

1. Introduction

Since the era of Descartes and de La Mettrie [1], biotic organisms have long been said to be well-made machines. However, how and by whom such well-made bio-machines have been made throughout evolution is yet an important unsolved problem in biology, as have been discussed by Dawkins [2]. Very roughly speaking, in the so-called synthetic theory, evolution is generally considered to have occurred mainly via random mutations and passive selection of the genes by environment [3]. Relatively few studies have been done for searching the reason why organisms tend to behave and evolve actively and/or autopoietically. Recent representatives of them are Maturana and Varela's autopoiesis theory [4], Eigen's hypercycle theory [5], Griffin's animal-thinking theory [6,6a], Life-as-thinking-machine theories [7-9], Arita's concept of artificial life and biosystems [10], and other concepts in evolutionists [11-12]. New trends in the studies of biotic systems from the aspects of artificial life and/or complex

systems are also important and remarkable from this viewpoint.

On the other hand, Ohnishi *et al.* have recently postulated [13-16] that well-made biomachines such as animal body, bee society [= bee eusociety = bee super-organism (SO)], and intra-cellular genetic apparatus have most plausibly emerged by hierarchical sociogenesis of lower-level individuals (which are unicell animals, bee individuals, and tRNA ribo-organisms, respectively). Both bee SO and animal body are known to be altruistic kin society consisting of fertile queen individuals (queen bees, germ-line diploid uni-cell organisms) and sterile worker individuals (worker bees, somatic line uni-cell organisms), where altruistic behaviours of the latter to the former have evolved by kin selection [17-20]. In these queen-worker-type society-biomachines, typical semeiotic systems have well evolved to give the bases for the machine-functioning, as exemplified by bee-dance system (in a bee SO), neuronal signals and hormone signals (in animal body).

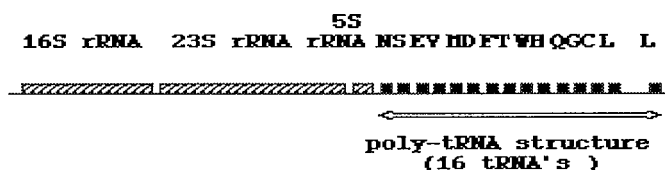
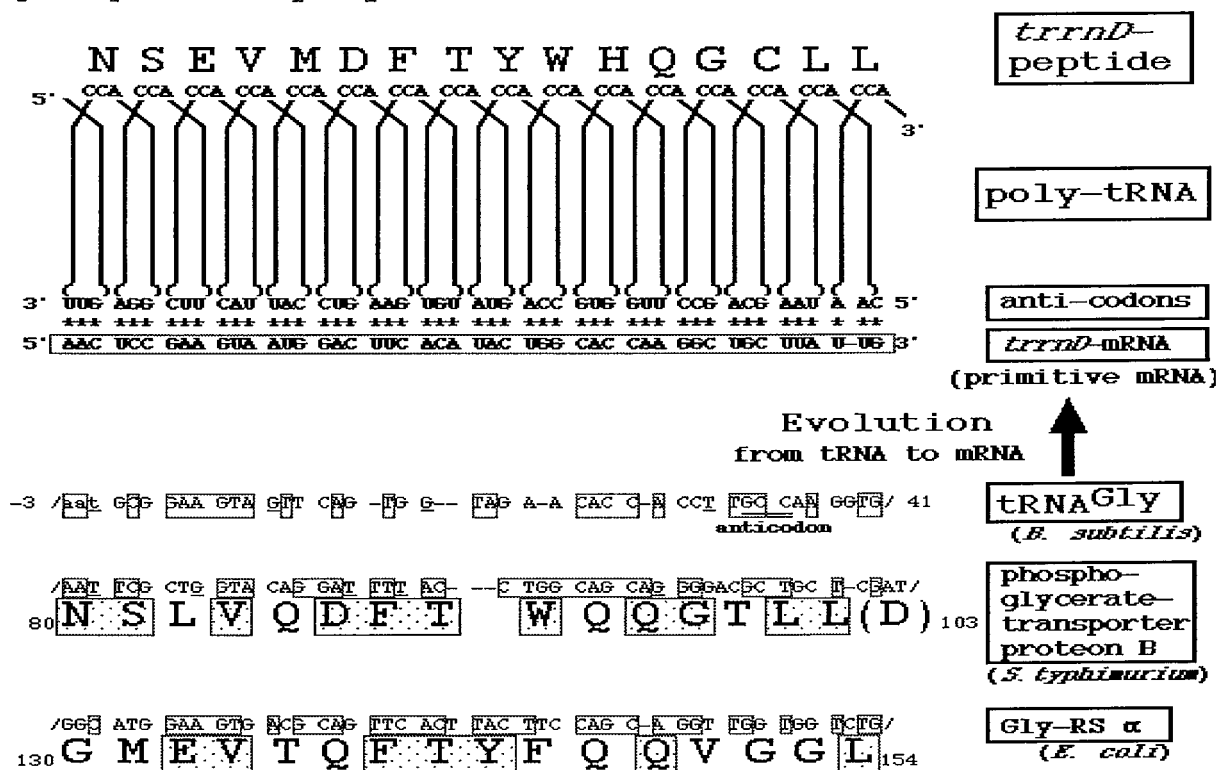
[A] *trnD* operon (*Bacillus subtilis*)[B] *trnD* poly-tRNA model

Fig. 1. A poly-tRNA model for early peptide-synthesis and the emergence of a *trnD*-type primitive mRNA (*trnD*-mRNA) from tRNA^{Gly}. The model (B) shows how primitive tRNA^{Gly} could have converted to be an earliest mRNA (*trnD*-mRNA) by interacting with the 16 (presumptive) anticodons of the tRNA-replicator riboorganisms. poly-tRNA = poly-tRNA region of the RNA transcript from the *B. subtilis* *trnD* operon shown in (A); *trnD*-peptide = a hypothetical 16-amino acid (aa)-peptide whose aa sequence is in the same order of the 16 aa specificities in the 16 tRNAs of this operon.; tRNA^{Gly} = tRNA^{Gly} gene in the *trnD*-operon.; D-3-phosphoglycerate transporter protein B = *pgtB* protein encoded by the *pgtB* gene in *Salmonella typhimurium*.

RNAs are considered to have emerged as replicator ribozymes which are the so-called ribo-organisms [21]. Protein-synthesizing and genetic apparatus has most plausibly evolved as an intracellular co-operative society of ROs [13, 22-26], consisting of tRNA-ROs (queen-like ROs) and (tRNA-derived) RNA ROs (mRNA's and rRNAs) (worker-like ROs) [13-16]. Genetic codon-system seems to have evolved as a typical semeiotic system of the riboorganismic (RO'ic) society, meaning that the 'triplet codon system is a kind of 'generalized culture' (defined by Ohnishi [8,9,13]) of the RO'ic society.

Since the first proposal of "poly-tRNA theory" on the origin of mRNAs and genetic codes in 1993 (3-5), a considerable progress has been made in generating new aspects concerning the origins and evolution of hierarchical evolution of various types of organic individuals, and in establishing semeiotic view of socio-biomachin-ogenesis [3-9,15]. This semeiotic

view has brought about an important new finding that the genetic-codon system is also a kind of cultural semeiotic system in intra-cellular ribo-organismic society (= society of RNA replicator-organisms), which well coincides with de Saussure's definition of general semeiotic system based on *signifiant* (signifier) and *signifié* (the signified) [26a].

Thus we can now begin a new important scientific field, "general evolutionary semeiotics" concerning origins and evolution of various semeiotic systems including genetic codes, molecular semeiosis (pheromons, hormones, cell-signalling systems, inter-neuronal semeiosis, etc.), bee-dance systems, animal displays, human (and primate) language systems and other human cultural semeiotic systems. It is important to note that the finding (by poly-tRNA theory) of the detailed processes of the origin and early evolution of genetic codon system, which is an oldest, ca. 40-million-year-old semeiotic system, can elucidate truly

essential features of general semeiosis, as will be analyzed in this paper. Such important, reasonable generalization of semeiotics cannot have been evoked without considering a wide range of semeiotic systems from genetic codes to human languages. Thus the poly-tRNA theory has now revealed to be better called, "cultural semeiotic theory" on the origin of genetic codes. Every life from ribo-organism to human can associate to make a society in which semeiotic culture would emerge.

Thus we have reached a new concept that every life seems to be some kind of cognitive (possibly self-improving neural-network) biomachine, which could work as a cognitive, actively evolving bio-individual [8,9,16].

In this original-study paper, how and why various types of hierarchical bio-sociogenesis tend to give rise to biomachinogenesis and semeiogenesis was analyzed from a theoretical viewpoint of learning neural-network machine [27,28]. An important aim of this paper is to build a basis of "Unified theory on the origin and evolution of life" from a viewpoint of the new paradigm of "cognitive life".

2. Origin of early mRNAs and the genetic codon-system : Semeiotic culture (Poly-tRNA) theory

In the emergence of the earliest protein-synthesizing and genetic machine, early RNA replicator ROs would have evolved to be early tRNA ROs (possibly having been ribozyme(s) for making peptide bonds) whose life cycle consists of tRNA-phase and tDNA-phase. Such early tRNA individuals would have associated together to make a co-operative tRNA RO'ic society in which some of them would have co-operatively behaved to other tRNAs, and have began to behave as presumptive (or earliest) mRNAs which assisted tRNA's peptide-synthesis [13-16, 22-26]. As shown in Fig.1 (A, B), the RNA transcript from the *Bacillus subtilis trnD*-operon has a structure of tandem arrangement of 16 tRNAs (*trnD*-poly-tRNA), and is considered to be a relic of early RNA-machine for making a hypothesized "*trnD*-peptide", whose amino acid (aa)-sequence is in the order of the aa-specificities of the 16 tRNAs in the *trnD*-poly-tRNA [22-24]. Early tRNA^{Gly} (of the poly-tRNA) would have interacted with the 16 anticodons of the poly-tRNA (in way of two by two on the primitive A and P sites of early ribosome consisting of three rRNAs made by the operon), and base-replacement mutations generating base-complementarities between «the tRNA^{Gly}» and the (presumptive) anticodons could have been selected throughout evolution. Evolutionary relics of the hypothesized 48-base-long *trnD*-mRNA (defined as to be complementary to the 16 anticodons) were found to be significantly homologous to the DNA sequence encoding *trnD*-peptide-like regions of 3-phosphoglycerate transporter protein B (*pgtB*) and glycyl-tRNA synthetase (GlyRS) a subunit (Fig. 1 (B), Fig.2) (Ohnishi, 1998). The six-tRNA- region (for tRNA^{His}-tRNA^{Gln}-tRNA^{Gly}-tRNA^{Cys}-tRNA^{Leu}-tRNA^{Leu})

is homologous to the DNA region encoding the aa's 85-303 of the *E. coli* GlyRS a subunit [24]. F₀-ATPase (H⁺-translocating ATP synthetase F₀-sector) a subunit and *pgtB* gene were also aligned against *GlyS* gene (encoding GlyRS) and the *trnD*-poly-tRNA region (Fig. 2). F₁-ATPase g subunit genes and a C-type lectin gene (lectin Bra-3, acorn barnacle) were also aligned in this Figure.

Statistical evaluations of base-match-levels in Fig. 2 were made as follows. P_{nuc}(m,n) values in Fig.2 denote the probability by chance for giving m- or more-base-matches in an n-base-long alignment of randomly selected sequences, and gives statistical evaluation for the homology-levels of the observed m-base-matches in n-base-alignment [22]. P_{nuc}(m,n) is given by,

$$P_{nuc}(m,n) = \sum_{(i=m,n)} C_{n,i} (1/4)^i (3/4)^{n-i}$$

where $C_{n,i} = n! / [i! (n-i)!]$, and $\sum_{(i=m,n)}$ denotes summation over m to n.

In the alignment of the *trnD*-poly-tRNA region with the *GlyS* and F₀-a genes, 44.7 % (= 282/631) and 44.8% (= 215/480) base-match levels were obtained, giving $P_{nuc}(282, 631) = 0.39 \times 10^{-19}$, and $P_{nuc}(215, 480) = 0.40 \times 10^{-20}$, respectively. On the other hand, the alignment of the *GlyS* and F₀-a shows a 512 % base-match, giving $P_{nuc}(242, 473) = 0.32 \times 10^{-34}$, a strongly significant homology-level. From these results, alignment of these three sequences were concluded to show genuine homology relationship. A prokaryotic ribosomal RNA, 16S rRNA, was further aligned against these sequences, resulting in showing a significant level of base-sequence similarity to the tRNA^{Gly-Cys-Leu} region, giving a 54.9% base-match and $P_{nuc}(118, 215) = 0.97 \times 10^{-20}$, which means that 16S rRNA has evolved from the poly-tRNA region [29].

Contemporary tRNAs seem to (considerably) well conserve early characteristics of primitive tRNAs, whereas other RNAs (mRNAs, rRNAs, M1 RNA, etc.) would have rigorously changed their own poly-tRNA structures and functions [13]. It would be rather reasonable to say that mRNA/mDNAs and rRNA/rDNAs (and also M1 RNA and snRNAs) are worker-like (wl-)ROs derived from (poly-)tRNA-ROs, whereas contemporary tRNAs are queen-like (ql-)tRNA ROs. However, the most important difference between the queen-worker-type eusociety (bee SO (= eusociety) and animal body) and the intracellular hierarchical (t)RNA RO'ic society is that ql-tRNAs (= tRNAs) and wl-tRNAs (= mRNAs, rRNAs) both replicate in their DNA-phase, meaning that both types of RNAs are fertile replicators. What are the major logical and evolutionary differences between these two types of hierarchical sociogenesis which seems to have made themselves well-made bio-machines? This question will be discussed below from a viewpoint of the genesis of self-learning (SL-) neural network (NNW, NNw) machine by means of hierarchical sociogenesis of altruistic or co-operative behaviours.

Fig. 2. (Continued.)

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3. Neural-network-like DNA-information flow in hierarchical behavioral network of altruistic kin societies

Why such hierarchical societies could have evolved to be well-made (bio)machines? A possible answer would be that hierarchical altruistic behavioural and DNA-information-flow networks could make a (self-)learning-NNW machine shown in Fig.3 (I). The major features of the NNW-machine (NNwM) are as follow; (1) Workers are units of an input-layer of NNwM, and queens are unit(s) of an output-layer. (2) Final output of the NNwM is queen's outputs of DNA-information to the next generation, based on which the next generation's SO (eusociety) comprising workers and queens will be reproduced. (3) An altruistic behavioral flow from workers to queens is partially equivalent to the DNA-information flow from workers to queens, because altruism increases final DNA-output from queens to the next generation, and the queen's DNAs share a great portion (r) with the DNAs of workers in this kin society, i.e., $r = 3/4$ in bee eusociety and $r = 1$ in multicellular animal body, where r denotes «co-efficient of (genetic) relatedness» defined by Hamilton [17]. (4) The final DNA-output from queens to the next generations is achieved via "gametes" (i.e., newly grown queen bees in bee-SO, or ovum in animal body). (5) Therefore, the DNA-flows (3) and (1) make a feedback DNA-flow from "queen(s)" (of the previous generation) to "workers" (of the present generation), or else, from "queen-niches" to "worker-niches". (6) Another important

feedback would be "(parental) manipulation by the previous generation" exemplified by the suppressive effect of queen-bee's (maternal) behaviour or substance(s) to worker's fertility, and by maternal mRNA (*bicoid*, *nanos*, and *torso* mRNAs), which cause early somatic (worker) cell differentiation in the fruitfly, *Drosophila* (Gilbert [30], p.548). This close parallelism between bee-SO and animal-body elucidates a common underlying evolutionary logic by which hierarchical society tends to become a SO, an upper-level individual.

These features (1) - (5) would most plausibly cause the kin societies to be well-made leaning -NNwMs (L-NNwM's) [27] capable of self-improving in every generation towards evolutionary bio-machinogenesis. The teacher signal of such L-NNwM would probably be often possessed by the own NNW system, since every element of this system is a cognitive bio-individual, such as a uni-cell animal. This means that the L-NNwM would work as a self-learning NNwM capable of self-improving in every generation.

In these altruistic societies, since the value of r between worker and queen is relatively high, the workers can output their own DNA base-sequence information to the next generation, not by their own DNAs, but by the DNAs of newly grown fertile individuals (=queens), to whom workers altruistically behave. Structural elements of this system are cognitive bio-individuals. This means that the L-NNwM would work as a cognitive self-learning NNwM capable of self-improving in every generation.

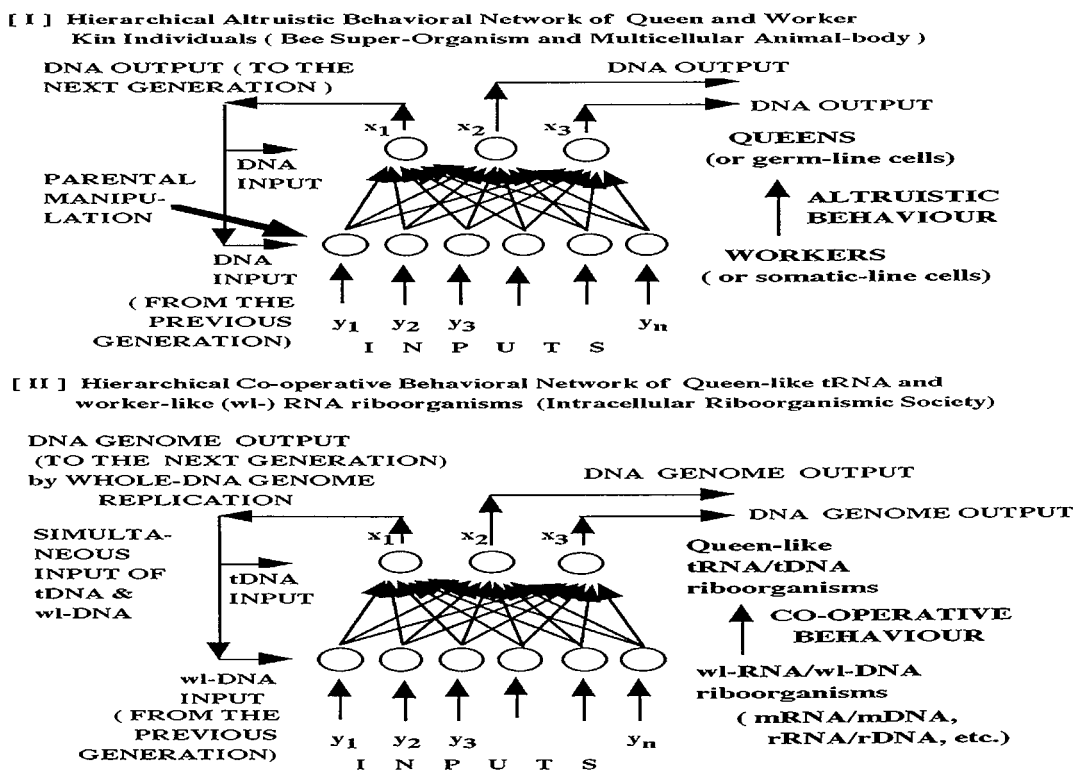


Fig. 3. Learning-neural network models I and II for sociogenesis and bio-machinogenesis

The quantity ($O_w(Q_i)$) of the sum of DNA outputs from all workers to the next generation through the i -th queen is given by,

$$O_w(Q_i) = \sum_{(j=1,N)} r_{ij} A(W_j), \quad [\text{Eq.1}]$$

where $\sum_{(j=1,N)}$ denotes summation over $j = 1$ to N (the number of workers), and $A(W_j)$ denotes the increase of the i -th (newly grown) queen's DNA-output to the next generation caused by the j -th worker's altruistic behaviour to the i -th queen. r_{ij} denotes the coefficient of genetic relatedness representing the ratio of DNA information quantity shared by the i -th queen and the j -th worker.

The r_{ij} in [Eq.1] would make some portion of the connection weight c_{ij} in NNW theories such as the back propagation method (BPM) [27,28], and thereby the DNA information of the workers would be accumulated to queens (fertile females) by the high r value (by Eq. 1), and further outputted to the next generation via queens (or gametes). If the DNA-information of the worker j is more adaptive (which tends to increase $A(W_j)$), then such DNA sequence would be more effectively transmitted to the next generation via altruism by Eq. 1. Mutations of DNA-information in queens or germ-lines would slightly change the so-called «connection weights» of the NNwM of the next generation. DNA-sequence-mutations occurred in the queens (diploid germ-line cells) of the previous generation can be outputted from previous generation's biomachine, and further inputted to the present generation's biomachine, in which workers (or somatic cells) can express and use the (mutated) genes (obtained from the previous generation's queen) by their own altruistic behaviour, resulted in active or auto-poietic selection of better (more adaptive) genes. The selection of better genes can be achieved by increasing the survival of the biomachines giving more DNA-outputs to the next generation. However, such selection depends on intra-biomachine (altruistic) behavioral network of constituting worker- and queen-individuals. Thus we can conclude that autopoietic selection by the «cognitive faculty» of self-learning NNwM would occur, resulting in active, cognitive, and autopoietic evolutionary improvements in biomachinogenesis throughout evolution.

4. New interpretation of Lamarck's use-disuse theory

This logic can well explain how Lamarck's use-disuse theory could work in living biosystems. Germ-line (diploid) queen-cells work in transmitting genetic information to the next generation. On the other side, somatic-line cells work in selecting better and neutral genes «by using (i.e., expressing) them». Twentieth century's genetics has not clearly pointed out this important selectionary function of «somatic worker-cells», from which major mis-understandings of the use-disuse theory would have arisen. Thus the «use-disuse theory» does not need any «somatic mutation», and only needs mutations of DNA-

information occurred in the previous generation's germ-line (queen-) cells [16, 31].

Based on such altruistic behaviours of workers, the queen-worker-type NNwM can auto-poietically evolve and self-improve by the cognitive faculty of the network system.

In conclusion, the queen-worker type hierarchical altruistic society (Fig. 3 [II]) can satisfy conditions of a cognitive learning-NNw-machine, which accepts environmental and internal input information, and finally outputs DNA-information from queens to the next generation. This is a kind of cognitive process, since the NNwM can recognize «environment information», and better DNA-outputs from queen can be made by hierarchical network of DNA-information-flow.

5. Hierarchical DNA-flow in intracellular (t)RNA society

In case of hierarchical (t)RNA (RO'ic) society consisting of ql-tRNAs and wl-RNAs, the (genetic) relatedness of ROs is not so strong as can be seen between queens and workers in hymenopteran eusocieties or in clonal kin unicell-society making animal body. Thus, Hamilton's kin selection rule would not have effectively worked throughout evolutionary machinogenesis of genetic apparatus, even if it might have some importance in the earliest emergence of weakly hierarchical structures. The DNA-information flow in the queen-like/worker-like hierarchical RNA society is schematized in Fig. 3 (II). In the case of Fig. 3 (I), the DNA flow from worker to the next generation can be achieved by high genetic relatedness and altruistic behaviour. However, in the case II, wl-RNAs also output their own DNA information to the next generation via their own DNA-replication. How the wl-RNAs output their own information to the next generation? And how does the feedback of DNA information occur? Since wl-RNAs are fertile (i.e., replicable in their wl-DNA phase), hierarchical machinogenesis will not successively evolve unless ql-tRNAs appropriately control worker's behaviours. Transfer-RNA genes (tDNAs) would most plausibly be more important and essential than other DNA genes in initiating DNA/genome replication. The feedback control of worker's DNA information seems to be achieved by the mode of DNA replication. The wl-DNAs do not replicate independently of ql-DNA's replication, but replication of all DNA genes occurs as a replication of the whole genome DNA(s). Such simultaneous replication of all wl- and ql-DNAs would have caused efficient evolution of cooperation of different wl-DNAs. In case of independent random replication in intracellular RNA/DNA society, better combination of two or more mutations would soon disappear, and efficient machinogenesis seem to be difficult to evolve. In other words, wl-DNA informations can be directly outputted to the next generation via replication of DNA genome. Notwithstanding the capability of wl-DNA's

replication, the hierarchy of tRNA ROs seems to constitute some kind of self-learning NNwM.

Thus we could reach an entirely new viewpoint that genetic code-system would have evolved as an semeiotic culture of hierarchical tRNA riboorganismic society. Evolution from hierarchical society to NNw-like machine needs efficient flow of information. Such needs or « Darwinian fitness of SO » would have worked as a selection pressure on accerated maturation of genetic code-semeiotic system.

6. BPM Computer-Simulation of a learning-NNW model

Various NNw models are known [27,28], among which hierarchical NNw-machines are well-known to really exist in mammalian neuronal networks in brain, and are worth studying by simulation tests in the present theoretical modellings of hierarchical sociogenesi and machinogenesis in Fig. 3. Learning process of simple hierarchical NNw-machine is easily simulated by the BPM (back propagation method) [28].

The mathematical logic of BPM is elegant , and plausible to work in biosystems.

Accordingly, in order to analyze learning process of the NNw-model I in Fig. 3, a simple computer simulation was made by BPM. A most simple two-layered hierarchical L-NNw consisting of one queen (an output-layer unit) and two workers (input-layer units) shown in Fig. 4(A) was considered. The input informations (at time t) to the input layer units are randomly selected values of $y_1^{(t)}$ and $y_2^{(t)}$ ($0 < y_i^{(t)} \leq 1$) which correspond to points in the category (pattern) 2 area indicated in Fig. 4(B), and the input to the queen is given by $z^{(t)} = c_1^{(t)} y_1^{(t)} + c_2^{(t)} y_2^{(t)}$, where $c_i^{(t)}$ denotes conection weight (at time t) between the queen and the i -th worker. The discrimination between category 1 and category 2 is determined by a straight line (or a hyperplane in n -dimensional euclidean space, if inputs are y_1, y_2, \dots, y_n) given by the same equation, $z^{(t)} = c_1^{(t)} y_1^{(t)} + c_2^{(t)} y_2^{(t)}$, as shown in Fig. 4(B). In case of n inputs, the discrimination boundary is given by a hyperplane, $z^{(t)} = c_1^{(t)} y_1^{(t)} + \dots + c_n^{(t)} y_n^{(t)}$.

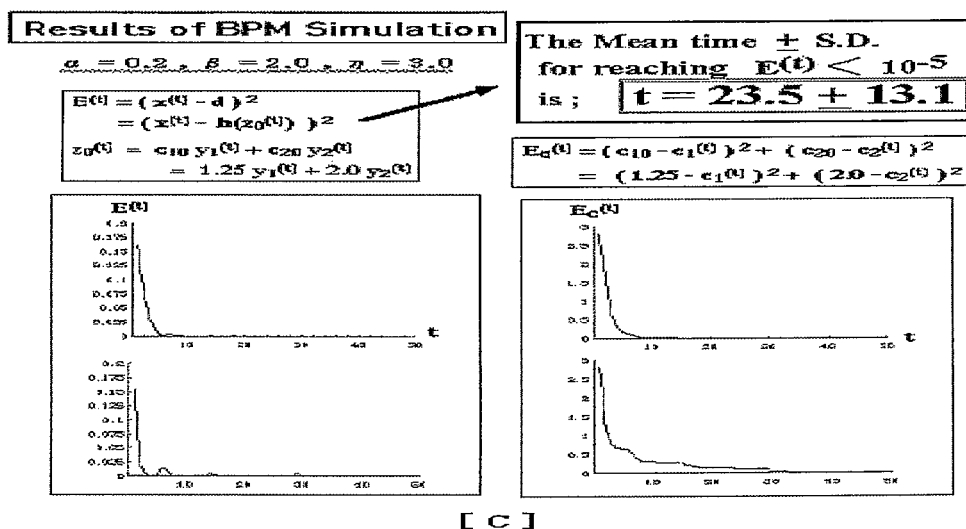
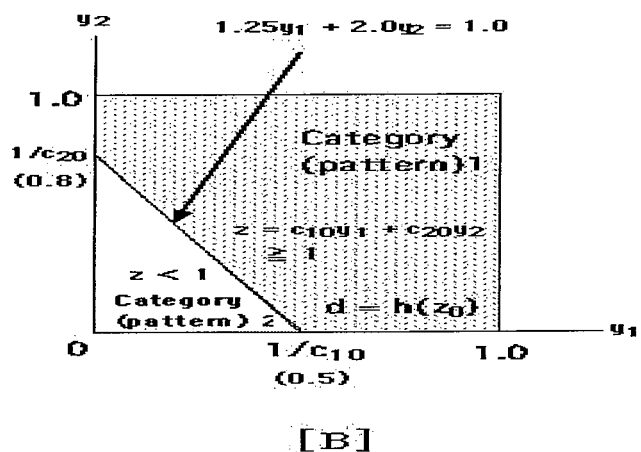
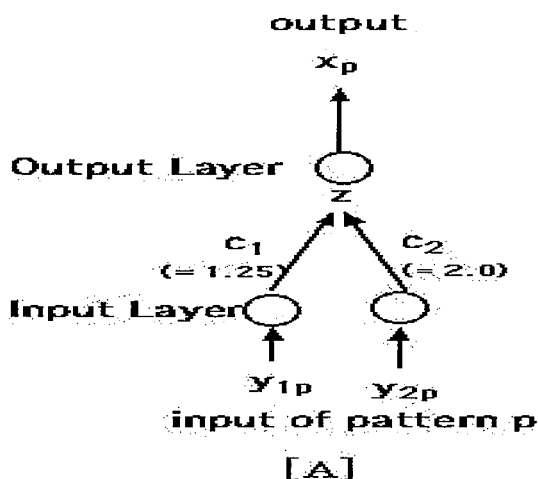


Fig. 4 BPM simulation of pattern-recognition learning by a simplest two-layered NNw-machine consisting of one queen-element and 2 worker-elements. See text for further details

This discrimination between patterns 1 and 2 corresponds to Yes/No-type or 1/0-type cognitive decision process in real bio-cognitive and/or intra-computer cognitive system. Combinations of many 1/0-type decisions will generate a more complex cognitive decision process.

The output from the queen is given by $x^{(t)} = h(z^{(t)}) = 1 / \{ 1 + \exp[-\beta(z^{(t)} - \theta)] \}$, where $h(\cdot)$ denotes a sigmoid function ($x = 0.5$ for $z = \theta$).

Here, the sigmoid function $h(\cdot)$ corresponds to the well-known firing threshold determination in neuronal system.

Category p input-information ($p = 1, 2$) were defined by $z_{p0} = c_{10} y_{1p} + c_{20} y_{2p}$ ($c_{10} = 1.25$, $c_{20} = 2.0$), satisfying $z_1 \geq 1$ and $z_2 < 1$, respectively, as shown in Fig. 4(B). Teacher signal for category 1 is given by $d_1 = h(z_{10})$, and error function is given by $E(c) = (1/2)(x_1 - d_1)^2$.

Teacher signal corresponds to a desirable or adaptive value of z , and $d_1 = h(z_{10})$ corresponds to the case where the system itself can use the $h(\cdot)$ or the like by some appropriate process. Error function given by $E(c) = (1/2)(x_1 - d_1)^2$ denotes squared difference between the two values. The smaller $E(c)$ is, the better the system is adapted for cognition.

In the next step, connection weight at $(t + 1)$ -th time is modified by

$c_i^{(t+1)} = c_i^{(t)} - (1 - \alpha)\eta [\partial E / \partial c_i]_t + \pm (c_i^{(t)} - c_i^{(t-1)})$ [Eq. 2] where $[\partial E / \partial c_i]_t$ denotes $\partial E / \partial c_i$ at $c_i = c_i^{(t)}$, and $\alpha(c_i^{(t)} - c_i^{(t-1)})$ is an item of inertia.

Eq. 2 gives a feedback system for refining the connection weights for better cognition.

Repetition of computation by Eq. 2 was continued up to $t = t_{\text{end}}$, where $E(c^{(t)}) < 10^{-6}$. Simulation for 40 trials by Eq. 2, employing $\alpha = 0.2$, $\beta = 2.0$, and $\eta = 3.0$, resulted in (mean \pm S.D. of t_{end}) = 23.5 ± 13.1 (Fig. 4(C), left). Corresponding error function of $c = (c_1, c_2)$, defined by $E_c^{(t)} = (c_1^{(t)} - c_{10})^2 + (c_2^{(t)} - c_{20})^2$, was also found to have rapidly reduced to be $< 10^{-6}$ (Fig. 4(C), right), meaning that learning for discriminating category 1 and 2 was very rapidly achieved. Thus it is concluded that even a simplest two-layered NNW in Fig. 4(A) can work as a L-NNWM capable of achieving an efficient «linear-division recognition».

In the real cases of the NNW-model (in Fig. 3), it is important to note that every units in both layers are biotic individuals (queens and workers) which themselves are most plausibly learning-NNW-biomachines. Therefore, even if every elements of the simplest 2-layered NNW in Fig. 4(A) are simplest 2-layered NNW-bioindividuals (such as hypothetical simplest queens and workers), then the simplest machine in Fig. 4(A) can work as an at-least-4-layered NNW possessing at-least two «hidden layers», as shown in Fig. 5, meaning that this machine can discriminate the so-called «non-linearly separable datasets». This seems to explain why «well-made biomachines» tend to have emerged via queen-worker-

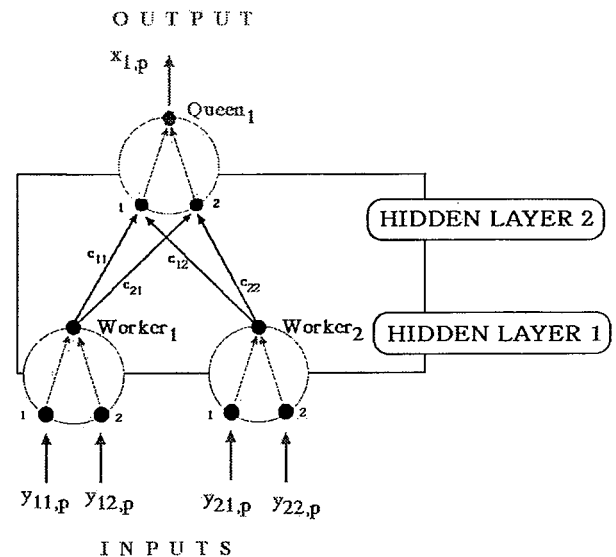


Fig. 5. Hidden- layers in a double-2-layered NNW-machine consisting of one queen and 2 workers which are also cognitive NNwM- individuals.

type or queen-worker-like hierarchical sociogenesis. It would be suggested that early two-layered (queen-worker-type) sociogenesis could have rapidly acquired a feature of L-NNwM by this «hidden-layer-logic». Since the teacher signal, d_1 , can be considered to be possessed by the bio-system (or the hierarchical society) itself, or by the constituting biotic individuals (queens and/or workers), the L-NNwM would most plausibly function as a «self-learning NNwM». Thus we can conclude that the queen-worker-type NNwM was made by self-improving and self-making process based on the function of the self-learning NNwM.

Accordingly, even if mutations occur randomly, mutated genes which are more adaptive would have been actively selected by the self-learning NNwM. Essential basic similarity between model I and model II in Fig. 3 suggests that genetic apparatus would have been made in essentially similar evolutionary logic. The self-learning NNWs in I and II in Fig. 3 strongly suggest that machine-making by self-learning and self-machinogenesis throughout evolution in NNW-models I (or II) is a kind of generalized "thinking" process. Human thinking by brain (which is often accompanied by "consciousness") is a special case of these generalized thinking phenomena. These results well coincide with the previously proposed concept of "generalized thinking" and "generalized culture" [8,9].

These theoretical considerations reveal that how and why active and/or autopoietic evolution have occurred and resulted in adaptive and neutral evolution. Random mutations and random/passive selections could explain evolution of adaptive and neutral genes. However, if biosystems are cognitive NNW-like biomachines, then more effective autopoietic and/or active selection of adaptive and neutral mutations would have been achieved. Adaptive and neutral mutations can be actively selected by the cognitive faculty of the NNW-like biosystem. In case of multi-cellular animals, adaptive and neutral mutations occurred in the germ-

line queen-cells of the “previous generation” can be selected by the altruistic behaviours of the “cognitive” somatic worker-cells (because worker-cell itself is a cognitive NNwM). This view can well explain the real logical mechanism of adaptive evolution, especially the mechanism of “**Lamarck’s use-disuse phenomenon**” [32-34]. Somatic-cells are gene-selectors, and germ-line cells are gene-transmitters to the next generation. This division of work can efficiently work, based on the clonal kinship and genome-identity between somatic and germ-line cells.

7. Diploid species as a cognitive NNw-machine functioning as a unit of autopoietic and/or active selection

Mayr [35,36] defined “diploid species” as “groups of actually or potentially inter-breeding natural populations which are reproductively isolated from other such groups”. This definition well coincides with a new hypothesis, proposed here and schematically

shown in Fig. 6, that diploid species is an entity of a probabilistic self-learning NNwM (SL-NNwM), in which females and males are input-layer elements, and zygotes (fertilized eggs) are output-layer elements, where each zygote accepts an input egg and an input sperm from one female and one male, respectively, and where the zygotes re-constitute the next generation by means of feed-back information flow from zygotes to the input-layer elements, males and females. Thus “species” or “isospecific interbreeding population (deme or Mendelian population or isospecific society)” is also a hierarchical SL-NNwM which recognizes or accepts information or stimuli from outer (extra-specific) and inner (intra-specific) environments, and outputs zygote-derived multi-cellular individuals to the input-layer in the next generation. Prenuptial displays and pheromones, which are semeiotic signals for successful mating, would generate better connection-weights for improving the hierarchical NNwM shown in Fig. 6.

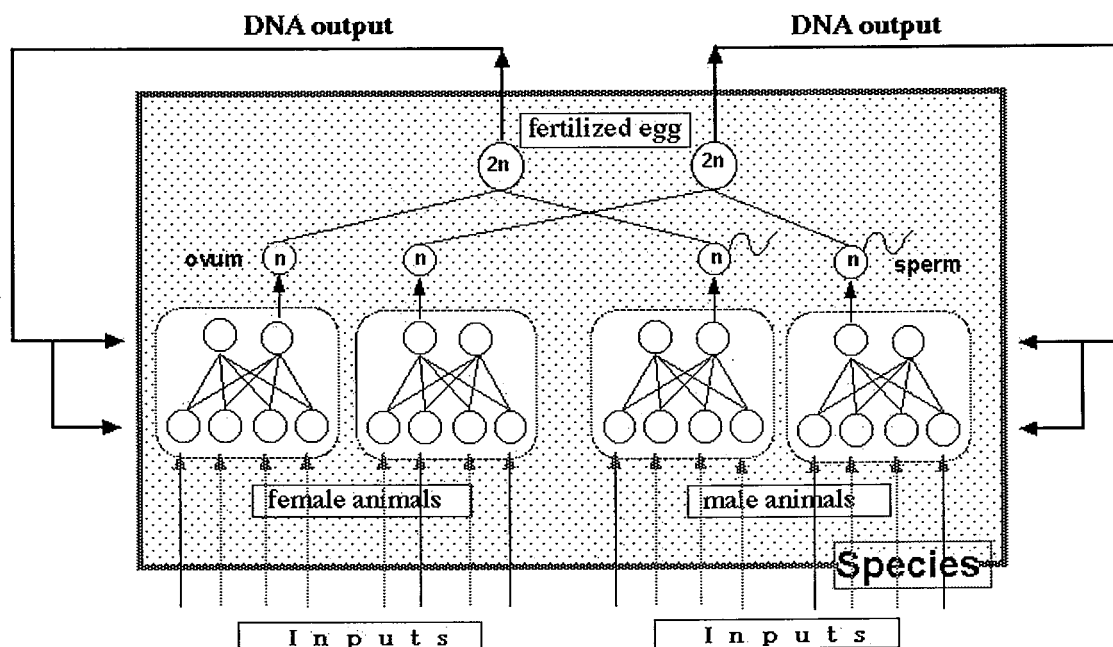


Fig. 6. Species-society (= “specia” = iso-specific society) as a possibly (self-)learning, probabilistic hierarchical NNwM.

This NNW-view of isospecific society (species-society well coincides with proposed theories for “species as an existing entity”, such as Imanishi’s “specia” proposed as “society consisting of the same-species individuals (37). Ghiselin’s (1974) proposal of “species as an individual” means “a single, unanalyzed, genealogical entity”. The NNW-view of diploid species would shed new light to the long-discussed (unsolved?) problem concerning the existence of “species”. This also well coincides with Ohnishi’s theory [8,37] on the origin of diploidy and diploid species in which diploid cell would have had emerged by co-operative associative behaviour of two kin unicell organisms, and the homologous

chromosome-pairing in meiosis is kinship-recognizing behaviour of the two constituting haploid unicell organisms [8].

Different species-societies (iso-specific societies, or specias) interact with one another to build an upper-levelled entity, which would correspond to some kind or some definition of “eco-system”. Whether ecosystem could be some kind of cognitive NNwM is a principal interest from the NNwM-aspects in this paper. If intra-specific network in ecosystem can constitute some kind of NNwM capable of recognizing input information from outside and inside of the ecosystem, and finally outputs some information (including DNAs) to the next ecosystem-generation and some of

the outputs contribute in reconstructing the next-generation ecosystem, then such ecosystem would work as autopoietic cognitive network-machine capable of evolving and self-improving. Theoretical studies for analyzing cognitive NNW structure of ecosystems seem to bring about interesting knowledge concerning species evolution.

8. Bee-dance language system as a nerve-like cognitive semeiotic system of the bee-superorganism

In the well-known *Aplysia* simple nervous system, a sensory neuron (which connects to siphon and inputs water-flow information) makes a direct synapsis onto the motor-neuron (which connects to gill-muscle, and outputs muscle-contracting information), with a feedback connection by an interneuron (28). This sign (or semeiotic) system is capable of making habituation and sensitization. This can be considered to represent an earliest evolutionary step of the brain or brain-like “thinking system”. This simple neural system consists of neuronal worker-cells, and works not only as adaptive sensory system of multi-cellular animal (= super-organisms (SO) of unicell animals), but also as altruistic behaviour to germ-line queen unicells for making more gametes.

If we compare this system with the bee-dance language system, striking similarities can be ruled out,

as shown in Fig.7. In the bee-SO, some worker-bees (here called “sensory-bees”) find food (or flower), and the information concerning the site of food (direction and distance from hive) is transmitted to other worker-bees (“motor-bees”) by doing the so-called “bee-dance” and the motor-bees recognize the information, and fly to the food-site. Sensory-bees and motor-bees are worker-bees of the queen-worker-type NNw-bio-machine in Fig. 3 I, which are comparable to sensory and motor neurons (worker-unicell animals) in the multi-cellular *Aplysia* SO. This striking parallelism strongly suggests that “bee-dance system” would have evolved as a “sensory-motor nerve-like system” of the bee-super-organism for efficiently finding and obtaining foods. This highly matured semeiotic sign system must have evolved by the selection pressure of adaptability of “bee-SO (= eusociety) ”, and not by the simple selection pressure (conventional Darwinian fitness) of bee-individuals. Accordingly, it is almost undoubtedly concluded that the semeiotic maturation of the bee-dance system would have had evolved by selection pressure of Darwinian fitness of bee-SO. This conclusion tells us important features concerning the origin and evolution of socio-machinogenesis accompanied by maturation of semeiotic system(s). .

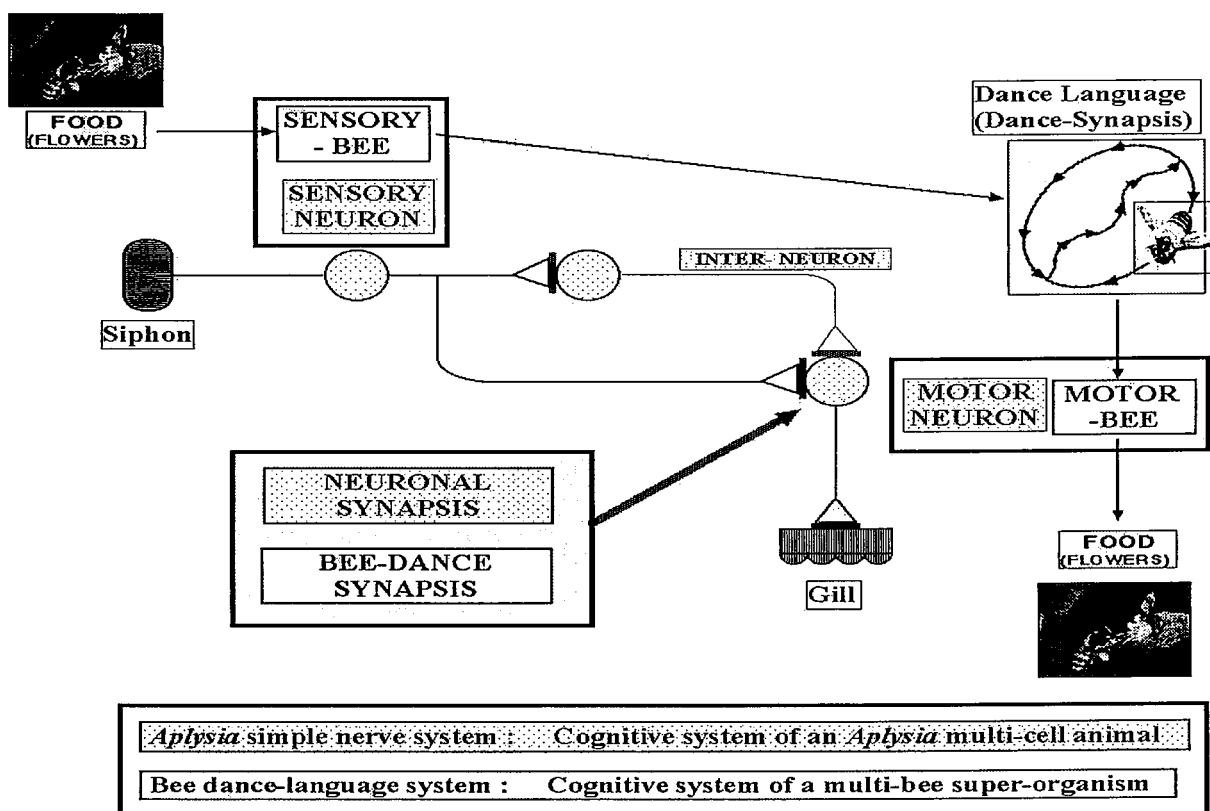


Fig. 7. Close similarities between the *Aplysia* simple neuronal system and the bee-dance language system.

An example is as follows; During war-periods of human societies, various kinds of semeiotic or sign systems tend to arise and have more important roles in making a hierarchical military system, than in ordinary society-system in peace-periods. Such military system is a transient socio-machinogenesis adaptive for generating higher probability of the society's survival. This suggests that even in human society, transient socio-machinogenesis via semeiotic maturation could occur.

In every of these machinogenetic processes of hierarchical societies, communications among constituting individuals tend to be replaced by sign-systems which ensures rapid and exact (non-erroneous) transmission of information. The constituting individuals then tend to lost free-living capabilities and become specific elements of the society-machine, which would be a most important and essential feature in socio-machinogenesis and the survival of the machine-like society.

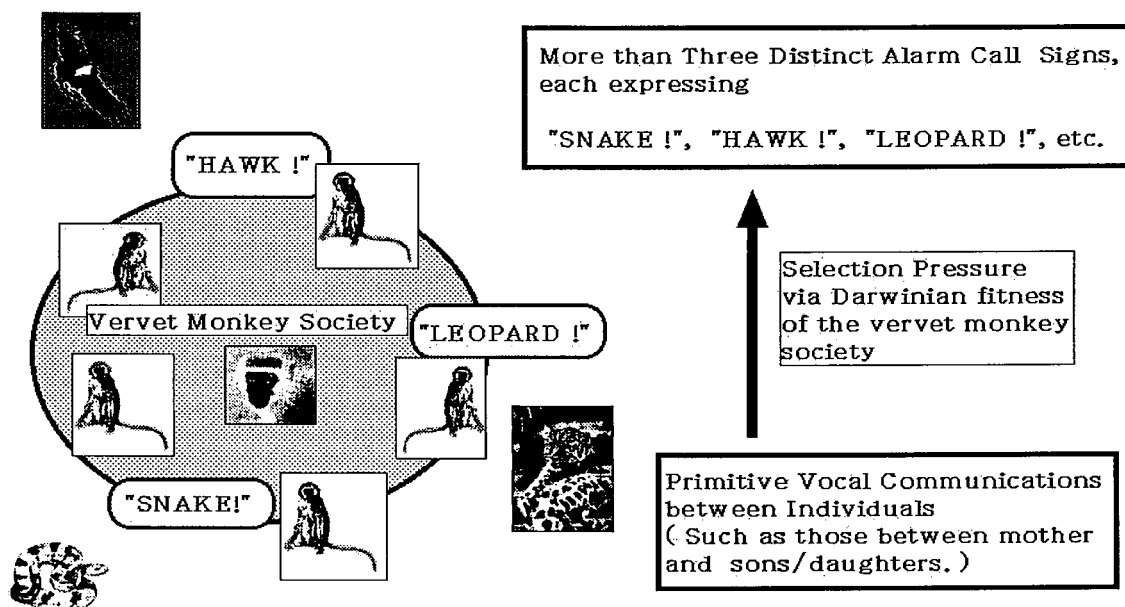


Fig. 8. An alarm-voice sign system, a possible earliest primate-language system in vervet monkey society.

10. Signifian and signifié in general semeiotic systems

10.1. General viewpoint of semeiotic systems

In every of the hierarchical societies hitherto discussed, mature semeiotic systems are observed, as summarized in Table 1, which are; human language system, synaptic signs between sensory and motor neurons, dance-language synopsis between "sensory-bee" and "motor-bee" [13], and triplet codon rules between anticodon (sensory organ or "image" or "signifian" in de Saussure's terminology) and specific amino-acid-accepting ability (amino acid specificity) ("concept" or "signifié") of tRNA-riboorganism (Table 1) [28a].

9. Origin(s) of primate language system

A hypothesis has been proposed that the vervet monkey society possessing three different alarm voice-signs (each corresponding to "snake", eagle" and "leopard", respectively) is an earliest stage having the origin of the primate language system (Cheney & Seyfarth, 1982). In this case, as schematically shown in Fig.8, the society is a SO-like quasi-individual (or transient upper-level individual), and the alarm-making monkey works as a sensory organ (or "sensory-monkey" comparable to "sensory-bee") of the society, whose alarm sign is efficiently transmitted to other society-members (= "motor-monkeys" in analogy to "motor-bee"). The semeiotic maturation would have been achieved by selection pressure to the society (quasi-Individual), rather than to the monkey individuals. The basic logical rule in the emergence and maturation of alarm-sign system is considerably similar to the bee-dance system discussed above.

de Saussure's terminology of semeiology seems to be very well applicable to the semeiotic systems discussed in this paper. In case of human language system, a typical semeiotic system functioning in human society, sounds of uttered word make an intra-brain "acoustic image", which de Saussure call "signifian". In semeiotic phenomenon (semeiosis) in language system, the acoustic image is corresponded to some specific "concept" which have been stored as some kind of memory in the brain. The most important feature of this signifian-signifié correspondence is its "arbitrariness". For example, acoustic image of "hound" in English or "Hund" in German corresponds to "concept of (some kind of) dog". However any native speaker does not know

Table 1. Arbitrary or possibly arbitrary correspondences between signifiant and signifié in generalized cognitive system. [AC] denotes arbitrary correspondence between signifiant and signifié. Every of these correspondences is maintained by the culture or cultural consensus of the respective society. Abbreviations: RO'ic=riboorganismic, ARS= aminoacyl-tRNA synthetase.

(1) HUMAN LANGUAGE (in human society)		
Signifian		
UTTERED WORD	===== [ACOUSTIC IMAGE] =====>	[AC] [maintained by cultural consensus of human society]
OBJECT	<===== [CONCEPT] =====	Signifié
(2) tRNA RIBO-ORGANISM (in intracellular ribo-organismic society)		
Signifian		
CODONS(on mRNA)	===== [ANTICODON] =====>	[AC] [maintained by ARS machines which are cultural products of ribo-organic society]
Amino Acid	<===== [Amino Acid-SPECIFICITY] =====	Signifié
(3) Aplasia SIMPLE NEURONAL SYSTEM (in SUPER-ORGANISM= hierarchical society of unice ll animals)		
[worker unice ll organism]		
STIMULATION to SIPHON	=====SENSORY NEURON=====>	SYNAPSIS [maintained by the semeiotic cultural consensus of somatic-cell subsociety]
MOVEMENT of GILL	<===== MOTOR NEURON =====> (worker unice ll organism)	
(4) FOOD -COGNITIVE SYSTEM of BEE SUPER-ORGANISM(= bee-eusociety)		
(worker bee)		
FOOD, FLOWER	=====SENSORY BEE =====>	DANCE LANGUAGE [maintained by the semeiotic cultural consensus of bee-eusociety]
	<===== MOTOR BEE =====> (worker bee)	
(5) Hormonall semeiotic systems		
Signifian		
HORMON MOLECULE	===== SIGNAL-STRUCTURE=====>	[AC]
GENE EXPRESSION	<===== hormon-SPECIFICITY=====	[maintained by the semeiotic cultural consensus of bee-eusociety]
	Signifié (hormon-RECEPTOR)	

why the signifiant can correspond to the "dog" concept, and such arbitrary correspondence is maintained only by accepted consensus of the society of native speakers.

Close similarities between bee-dance system and the *Aplysia* simple nerve system capable of making habituation and sensitization (Fig. 7 and Table 1) strongly suggests that the bee-dance is the signifiant or «image» in de Saussure's definition, and the faculty (or knowledge) of motor-bees to understand or interpret the meaning of the image would be the signifié or «concept» in his terminology. Semeiotic process is the interacting behaviour (dance-synapsis) of the sensory-bee and motor-bee.

de Saussure's definition of signifiant and signifié might not have been widely accepted in the field of modern brain science, since the definition does not exactly based on clearly defined real substance or matter. The above-mentioned comparison of human language system and bee-dance system would elucidate more exact semeiotic relationship between these two systems. In case of the comparison of bee-dance with the *Aplysia* simple nerve-system, the relationship is more clear and evident, suggesting that sensory-neuron carries and expresses signifiant (or

image) which is a kind of (ontogenetically acquired and/or genetically determined) memory, and the motor neuron possesses signifié' (or concept) which is some kind of (long-term? and/or genetically inherited) memory.

de Saussure pointed out that the arbitrary correspondence is maintained by "cultural consensus" within the society. Thus the correspondence of the "bee-dance" (image of the food-site) and its corresponding concept or set of motor-bee's knowledge would have been ontogenetically and/or phylogenetically obtained memory as cultural evolution of the bee-eusociety.

Similarly, the language system of humans would or might have evolved as an adaptive function of human society, rather than a mere communication system among human individuals. In vervet monkey society, «motor-monkey» carries and expresses «image» or vocal signs of enemies, and «motor monkeys» can interpret the image and behave adaptively.

In the case of (t)RNA riboorganismic society (Compare (1) and (2) in Table 1) [13], a tRNA-molecule is a cognitive.living-organism possessing an anticodon (receptor or sensory organ for recognizing correspondong codons on mRNA) and an amino-acid-accepting capacity (phylogenetically obtained

molecular memory for accepting the specific amino acid). The correspondence between anticodon (signifian) and the corresponding amino acid-binding capability (signifié) is known to be mostly arbitrary, and the exact corresponding between anticodon and the amino acid-specificity is maintained by the function of specific «aminoacyl-tRNA synthetase» which is a «cultural product» (as a protein-machine) of the hierarchical tRNA-society consisting of queen-like tRNAs and worker-like (t)RNAs (which are mRNAs and rRNAs).

10.2. Origin of arbitrary correspondence between signifian and signifié

Comparative analyses of various biotic semeiotic systems seem to shed light to the origin of de Saussure's "arbitrariness".

In case of "hound"/"Hund" system, the correspondence between the acoustic image and its corresponding "dog" image is felt arbitrary for contemporary native speakers. However, "hound" in English, "Hund" in German, as well as "can-is" in Latin have derived from a common proto-Indo-European word *kwan- "dog". If *kwan- was an onomatopoeic word, then its correspondence to "dog" is not arbitrary, and depends on "corresponding reason". The arbitrariness would evolve in such a way that the correspondence tends to be maintained not on the original logical reason, but on the newly developed cultural reason capable of maintaining the "pre-established" correspondence. In this case, the original correspondence would have been an "onomatopoeic" correspondence (if *kwan- was an onomatopoeic word) and the correspondence in modern European languages would have evolved by the historical change of the correspondence-maintaining mechanism from onomatopoeic relationship to cultural consensus.

Similar consideration seems to work in the genesis of genetic anticodon system, the oldest typical semeiotic system hitherto known. Origin of tRNA-amino acid correspondence would have been some kind of stereochemical relationship such as key-keyhole relationship, since proto-tRNA was most probably a kind of ribozyme capable of making peptide-bond for synthesizing di- and/or oligo-peptides (probably by using ATP). Stereochemical relationship is most widely observable bases for generating ribozyme specificity in many cases. In this step of specificity, the correspondence between tRNA-structure and tRNA's amino-acid-binding specificity ("specific amino acid-concept" of tRNA) is "stereochemical" like "onomatopoeic". Hierarchical interactions occurred during the genesis of poly-tRNA stage of early peptide-synthesizing mechanism shown in Fig. 1, the presumptive anticodon-triplet region of the tRNA had evolutionarily acquired the ability to bind complementary (presumptive codon) triplet region of some worker-like tRNA (which was the ancestor of the earliest mRNA). Thus, the triplet had changed to be an anticodon or "tRNA-RO's sensory organ" for

finding and binding to the corresponding codon, by which arbitrary correspondence between codon and anticodon would have evolved based on simultaneous evolution of aminoacyl-tRNA (protein-)enzyme, which is a cultural product of the hierarchical tRNA society. This means that the arbitrary correspondence between anticodon and amino acid have evolved by evolutionary replacement of the correspondence-maintaining mechanism from stereochemical (onomatopoeic-like) relationship to cultural relationship (using a highly developed protein-machine made by the anticodon-dependent semeiotic culture). Accordingly, the arbitrary correspondence between anticodon and amino acid is also a result of cultural relationship in the tRNA-hierarchical society, which very well parallels with cultural relationship maintaining arbitrary signifian-signifié correspondence in the human language system. In conclusion, the anticodon-amino acid corresponding semeiotic system have emerged as a cultural evolution of intracellular hierarchical riboorganismic (RO'ic) society.

This conclusion very well explains the reason why such a typical mature semeiotic system exists intracellularly. This problem would not be solved even in future, without considering from a viewpoint of the culture of RO'ic society. The genetic anticodon- (or codon-)system is a result of cultural evolution in RO'ic society, and therefore its origin cannot have been solved by the ordinary analyses of molecular biology and molecular genetics. Only cultural analyses can answer and solve the question.

Similar consideration in other semeiotic systems would give rise to new viewpoints corresponding to the respective biomachine-systems. For example, hormon-system in multi-cellular animals is a semeiotic system for making proper cell-to-cell communications necessary in ontogenetic building of animal body (called embryogenesis or morphogenesis). Thus embryogenesis/morphogenesis is considered to have evolved as a "sociogenetic culture" of the hierarchical society comprising germ-line unicell queen animals and somatic unicell worker-animals. This viewpoint very well coincides with my previous definition of "generalized culture" in various levels of biotic societies (Ohnishi, 1990), where animal embryogenesis/morphogenesis has been defined as a generalized culture of the multi-cell society.

Accordingly almost identical logic of semeiogenesis as a essential basis for bio-machinogenesis and/or socio-machinogenesis would underlie evolution of various biotic systems ranging from RO'ic societies to human societies. Based on this logic, it would be possible to build a unified theory for the origin and evolution of life- or organic systems.

11. Conclusions : Unified theory for the origin and evolution of biosystems

All findings hitherto discussed strongly suggest that biosystems are some kind of neural network(NNw)-like cognitive system capable of autopoietically self-

improving and actively evolving. Genesis and proper maturation of semeiotic system is necessary for the biosystem to evolve as a well-made bio-machine. Active and autopoietic features of biotic systems would be most plausibly generated by cognitive faculties of some kind of NNwM-type biosystem, or by cognitive behaviour of the lower-level individuals constituting the upper-level biosystem. Lamarck's (1809) use-disuse phenomenon can also be explained from this cognitive NNwM-viewpoint based on such as the queen-worker-type self-learning NNwM-structure of animal body.

Biosystems discussed in this paper are mostly considered to be some kind of hierarchical (self-)learning NNwM capable of self-improving based on possibly intra-systematically possessed teacher-signals. Further considerations allow us to propose that the most important characteristics of living systems is the cognitive property generated by some kind of its NNwM structure. Both hierarchical NNwM and Hopfield-NNwM are kinds of (fully-)connected NNwM, suggesting that various types of (fully)connected NNwM seem to work as various types of contemporary biosystems [27,28].

An important example would be the origin and evolution of network-like metabolic pathways. Some kind of simple early metabolic network-like pathways might have worked as a kind of cognitive NNwM, which had begun to succeed in autopoietic and/or self-improving cognitive evolution based on its cognitive abilities.

3-Phosphoglycerate (3-PG)-transporter protein B (pgtB protein) was found to conserve the most primitive, *trnD*-peptide-like structure (11 out-of-16 amino acids are shared). A question asking why pgtB protein has conserved the oldest amino acid sequence is critically important. The answer would be that pgtB was needed for modifying 3-PG for making various 3-PG-derived biomolecules. This is probably because 3-PG is located in the most critical and central branching point in the metabolic map. Various essential metabolic pathways (for bio-synthesizing riboses, nucleic-acid bases, amino acids and so on) have their respective starting points at and around 3-PG. Evolutionary selection of L-amino acids and D-riboses might have been achieved by «cognitive faculty» of some early metabolic and/or chemical reaction network capable of functioning as learning-NNwM.

The most general scheme of cognitive NNwM capable of self-evolving is shown in Fig. 9. Various biosystems are candidates for some kind of cognitive (fully-)connected NNwM systems. The future conclusion to be reached must answer the question that "Is every life some kind of cognitive NNwM?" A most typical answer which might be rather possible is that every life is a cognitive entity capable of behaving actively based on its own NNwM-based cognitive faculty. Most plausibly, cognitive behavior would be an essential feature of life on the earth.

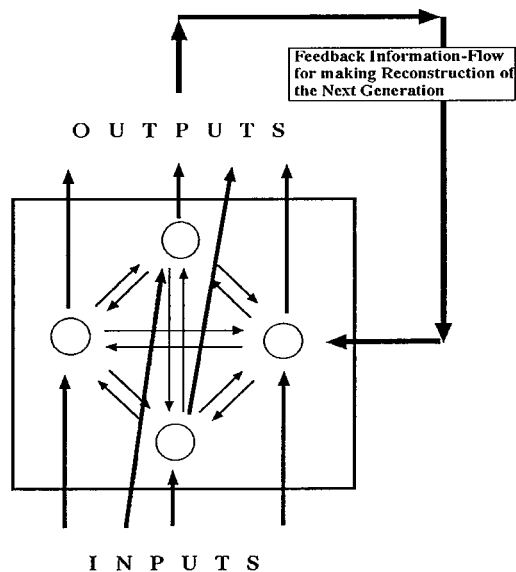


Fig. 9. Generalized scheme of (fully-)connected NNwM as autopoietic cognitive living system.

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