

# Genesis of Genetic Codes and Other Semeiotic Systems by means of Neural-Network-like Hierarchical Sociogenesis and Bio-Machinogenesis

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## 1. Introduction

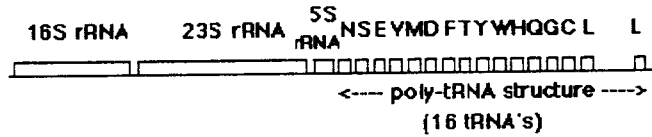
Well-made biomachines such as animal body, bee (eu-)society [= bee super-organism (SO)], and intra-cellular genetic apparatus could have most plausibly emerged by hierarchical sociogenesis of lower-level individuals (which are unicell animals, bee individuals, and tRNA ribo-organisms (RO), respectively) [Ohnishi, 1993a,b,c; Ohnishi et al., 1999]. Both bee SO and animal body are altruistic kin society consisting of fertile queen individuals (queen bees, germ line uni-cell organisms) and worker individuals (worker bees, somatic line uni-cell organisms), where altruism has evolved by kin selection [Hamilton 1964; Ross & Mathew 1989].

In the emergence of protein-synthesizing / genetic machine, early RNA replicator ROs would have evolved to be early tRNA ROs whose life cycle consists of tRNA-phase and tDNA-phase. Such early tRNA individuals would have associated together to make a co-operative tRNA society in which some of them would have co-operatively behaved to other tRNAs, and have began to behave as earliest mRNAs which assisted tRNA's peptide-synthesis (Ohnishi, 1993; Ohnishi et al., 1999).

## 2. Origin of mRNAs and Genetic codes

As shown in Fig.1 [A] [B], the RNA transcript from the *Bacillus subtilis trrnD*-operon has a structure of tandem arrangement of 16 tRNAs (trrnD-poly-tRNA), and

[A] *trnD* operon (*Bacillus subtilis*)



[B] poly-tRNA model

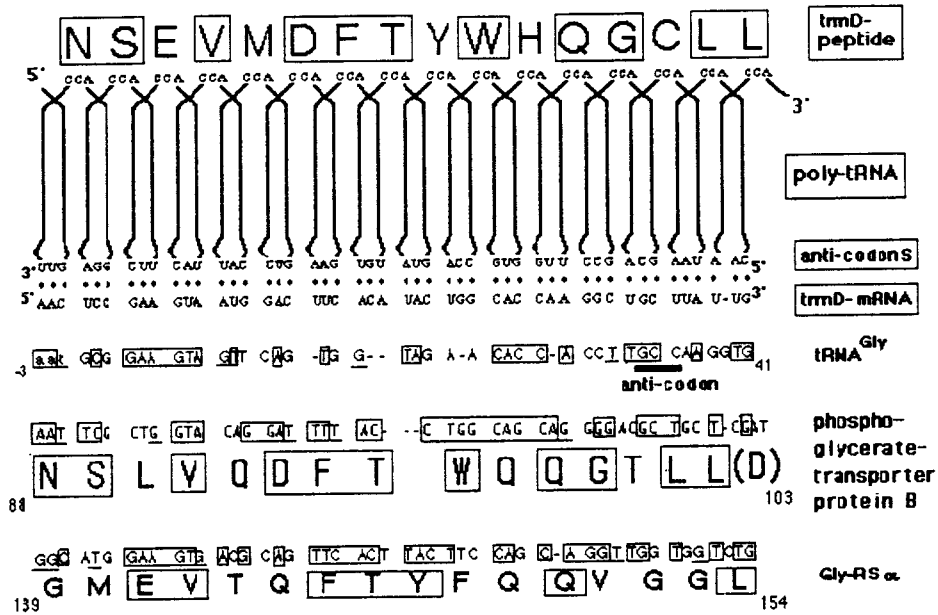
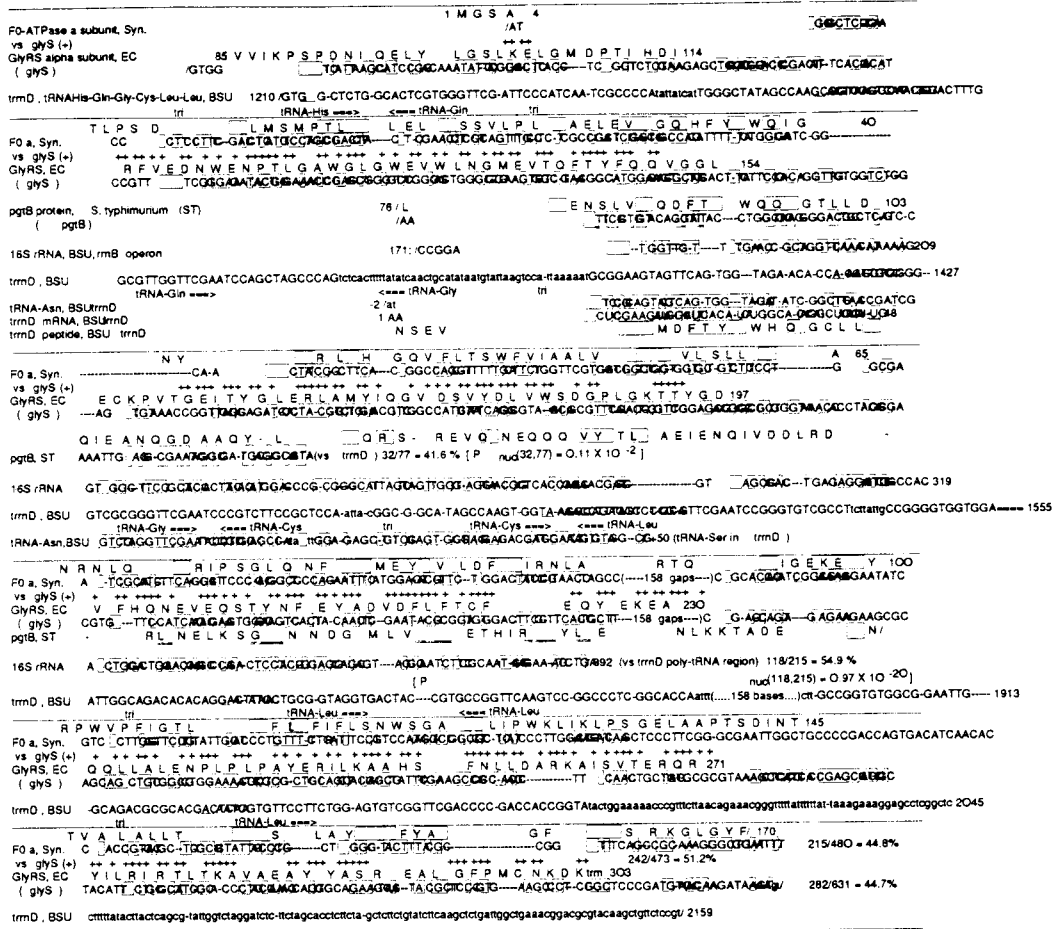
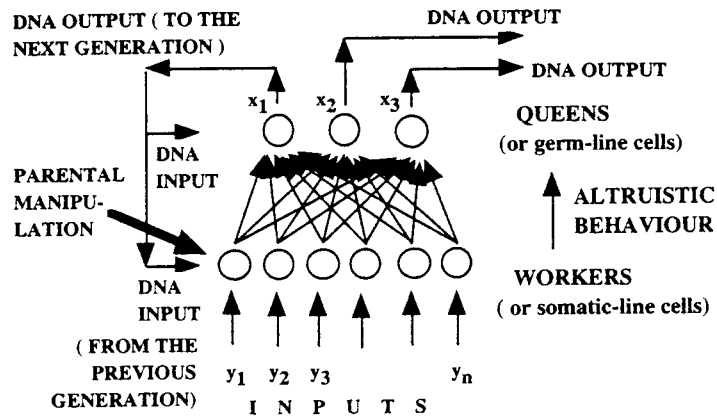


Fig. 1. A poly-tRNA model for early peptide-synthesis and the emergence of a *trnD*-type primitive mRNA (*trnD*-mRNA) from tRNA<sup>Gly</sup>. The model in [B] shows how primitive tRNA<sup>Gly</sup> could have converted to be an earliest mRNA (*trnD*-mRNA) by interactions of tRNA replicator ribo-organisms. Poly-tRNA = poly-tRNA region of the RNA transcript from the *B. subtilis trnD* operon shown in [A]. ; *trnD*-peptide = a hypothetical early 16-amino acid-peptide whose aa sequence is in the same order of the 16 aa specificities of the 16 tRNAs in this operon. ; *trnD*-mRNA = a hypothetical early 48-base mRNA complementary to the 16 anticodons of the 16 tRNAs. ; tRNA<sup>Gly</sup> = tRNA<sup>Gly</sup> gene in the *B. subtilis trnD* operon. ; phospho-glycerate transporter protein B = *pgtB* gene-encoded protein in *S. typhimurium*. ; GlyRS = glycyl-tRNA synthetase  $\alpha$  subunit (*GlyS* gene) in *E. coli*.



**Fig.2.** Alignment of the *E. coli* (EC) glycyL-tRNA synthetase (GlyRS) alpha subunit gene (*GlyS*), the *Synechococcus* sp. F0-ATPase a subunit gene (*a*), and the *Salmonella typhimurium* phospho-glycerate transporter protein B gene (*pgtB*) against the poly-tRNA region (tRNA<sup>His</sup>-Gln-Gly-Cys-Leu-Leu region) from *Bacillus subtilis* (BSU) *trmD* operon. Amino acid sequences of the *Synecho-coccus* sp. Statistical evaluation of base-match levels was made by computing  $P_{nuc}(m,n) = \sum C_{n,i} (1/4)^i (3/4)^{n-i}$ , (where  $C_{n,i} = n! / [i! (n-i)!]$ ), and  $\Sigma$  denotes summation over  $i = m$  to  $n$ ), which denotes matching probability by chance giving the observed  $m$  or more base-matches in the  $n$ -base alignment. Data are from GenBank Database. Base-matches to the *trmD* poly-tRNA region and deduced amino acid matches to GlyRS are boxed. Base and amino acid matches to *GlyS* / GlyRS are boxed, and/or indicated by "+".

[ I ] Hierarchical Altruistic Behavioral Network of Queen and Worker Kin Individuals ( Bee Super-Organism and Multicellular Animal-body )



[ II ] Hierarchical Co-operative Behavioral Network of Queen-like tRNA and worker-like (wl-) RNA riboorganisms (Intracellular Riboorganismic Society)

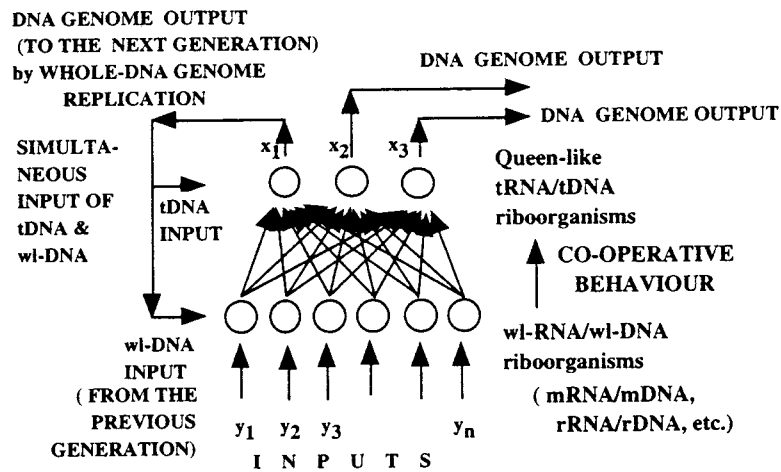


Fig. 3. Learning-neural network models I and II for sociogenesis and bio-machinogenesis.

is considered to be a relic of early RNA-machine for making a hypothesized "*trrnD*-peptide", whose amino acid (aa)-sequence is in the order of the aa-specificities of the

16 tRNAs in the *trrnD*-poly-tRNA. Early tRNA<sup>Gly</sup> (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 the base-complementarities between tRNA<sup>Gly</sup> and (presumptive) anticodons could have been selected throughout evolution. Relics of the hypothesized *trrnD*-mRNA (complementary to 16 anticodons) are significantly homologous to the DNA sequence encoding *trrnD*-peptide-like regions of 3-phospho-glycerate transporter protein B (*pgtB*) and glycyl-tRNA synthetase (GlyRS)  $\alpha$  subunit (Fig. 1, [B], Fig.2). The six-tRNA- region ( tRNA<sup>His-Gln-Gly-Cys-Leu-Leu</sup>) is homologous to the DNA region encoding the aa's 85-303 of the *E. coli* GlyRS  $\alpha$  [Ohnishi 1993c]. Fo-ATPase a subunit and *pgtB* gene were also aligned against *GlyS* gene and the *trrnD*-poly-tRNA region (Fig. 2). An prokaryotic ribosomal RNA, 16S rRNA, was also found to show significant level of base-sequence similarity to the tRNA<sup>Gly-Cys-Leu</sup> region, as shown also in Fig. 2. Statistical evaluations of base-match-levels elucidated that the aligned pairs in in Fig. 2 are mostly based on genuine homology relationship.

Contemporary tRNAs seem to well conserve early characteristics of primitive tRNAs, whereas other RNAs (mRNAs, rRNAs, M1 RNA.) would have rigorously changed their own structures and functions [Ohnishi et al. 1999]. It would be rather reasonable to say that mRNA/mDNAs and rRNA/rDNAs are worker-like (wl-) ROs derived from (poly-)tRNA-ROs, whereas contemporary tRNAs /tDNAs 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 society is that ql-tRNAs and wl-mRNAs 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 biomachines? This question will be discussed below from a viewpoint of the genesis of self-learning neural network (NNW) machine.

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

A possible answer to this question would be that hierarchical altruistic behavioral and DNA-information-flow networks could make a (self-)learning-NNW machine shown in Fig.3 [I]. The major features of the NNW are as follow ; (1) Workers are units of an input-layer of NNW, and queens are unit(s) of an output-layer. (2) Final output of the NNW-machine (NNWM) is queen's outputs of DNA-information to the next generation, based on which the next generation's workers and queens will be reproduced. (3) altruistic behavioral flow from workers to queens, where the behavioral flow is partially equivalent to DNA flow from workers to queens (because altruism increases final DNA-output from queens to the next generation, and the queen's DNA information share a great portion ( $r$ ) of DNA sequences with workers of this kin society, i.e.,  $r = 3/4$  in bee eu-society and  $r = 1$  in multicellular animal body.), where  $r$  denotes 'co-efficient of (genetic) relatedness' [Hamilton, 1964].

(4) The final DNA-output from queen to the next generation 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 cell differentiation in the fruitfly, *Drosophila* [Gilbert 1997, p.548].

These features (1)-(5) would most plausibly satisfy the conditions by which the kin societies could evolved as learning neural-network machines (L-NNWMs) (Dracopulos, 1997) capable of self-improving in every generation towards biomachinogenesis. The teacher signal of such L-NNWM would probably be possessed by the own NNW system itself, since every element of this system is a cognitive bio-individual. This means that the L-NNWM would work as a self-learning NNWM capable of self-improving in every generation.

In case of hierarchical (t)RNA (RO'ic) society consisting of ql-tRNAa and wl-RNAs, the relatedness of ROs is not so strong as can be seen between queen and workers in hymenopteran eusocieties or in clonal kin unicell society making animal body. The DNA-information flow in the ql-/wl- hierarchical RNA society is schematized in Fig. 3 [I]. In the Fig. 3 [I] case, the DNA flow from worker to the next generation can be achieved by high genetic relatedness and altruistic behaviour would efficiently evolve. However, in the case [II], wl-RNAs also output their own DNA information to the next generation via their own DNA-replication. Since wl-RNAs are fertile (i.e., replicable in their wl-DNA phase), hierarchical machinogenesis will not successively evolve unless some appropriate control of wl-RNA's behaviours by ql-tRNAs. tRNA genes (tDNAs) would most plausibly be more important and essential than other DNA genes in initiating DNA genome replication. The feedback control of wl-individuals' 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 finally makes a DNA-information-flow network closely resembling to the case [I] model in Fig. 3.

Thus the both cases [I] and [II] are considered to generate functional self-learning NNMs. 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 informations to the next generation, not by their own DNAs, but by the DNAs of newly grown fertile individuals (= queens), to whom workers altruistically behave. The elements of input and output layers in this system are cognitive bio-individuals. This means that the L-NNWM would work as a self-learning NNWM capable of self-improvement in every generation throughout evolution.

#### 4. BPM Computer-Simulation of a learning-NNW model

In order to analyze learning process of the NNW-model I in Fig. 3, a simple computer simulation was made by BPM [Rowe 1997]. A most simple two-layered hierarchical L-NNW consisting of one queen (an output-layer unit) and two workers

is given by  $d_1 = h(z_{10})$ , and error function is given by  $E(\mathbf{c}) = (1/2)(x_1 - d_1)^2$ . Connection weight at  $(t + 1)$ -th time is modified by

$$c_i^{(t+1)} = c_i^{(t)} - (1 - \alpha)\eta \left[ \frac{\partial E}{\partial c_i} \right]_t + \alpha (c_i^{(t)} - c_i^{(t-1)}) \quad [\text{Eq. 2}]$$

where  $\alpha(\cdot)$  is an item of inertia. Repetition of computation by [Eq. 2] was continued up to  $t = t_{\text{end}}$ , where  $E(\mathbf{c}^{(t)}) < 10^{-6}$ . 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  $t_{\text{end}}$ ] = 23.5  $\pm$  13.1, meaning that learning for discriminating category 1 and 2 was very rapidly achieved. Thus it is concluded that even a simplest two-layerd NNW can work as a L-NNWM capable of achieving an efficient linear-division recognition. In real case of the NNW-model I (in Fig. 3), every units in both layers are biotic individuals which themselves are most plausibly L-NNWMs. Since the teacher signal,  $d_1$ , can be considered to be possessed by the biotic individuals (queens and/or workers), the L-NNW would most plausibly function as a self-learning NNWM. Thus the queen-worker-type NNWM is concluded to have been made by self-improving and self-making based on the function of the self-learning NNW. 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. 32 strongly suggests 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 coincides well with the previously proposed concept of "generalized thinking" and "generalized culture" [Ohnishi 1990]. Further discussions from the aspect of generalized semeiology is given in Ohnishi et al., 2000a,b.

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