Translation is a merger, not an invention

Two independently selected RNA systems, neither of them for translation

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Abstract. The peptidyl transferase centre and the aminoacyl–tRNA system are treated here as two separately selected RNA-world artefacts with distinct, code-free ancestral functions. The genetic code is read as the frozen interface contract of their encounter rather than as the object either lineage was selected to produce.

1 The teleological trap

Any account of the origin of translation has to clear one hurdle before it can be taken seriously: it must not select for translation. Neither the ribosome nor the transfer RNA can have been favoured *in order to* build a coding system, because the coding system did not yet exist to be a target of selection. A satisfactory model must therefore give each component of the apparatus a complete, self-sufficient function in a world with no code, no messenger, and nothing to translate — and then show that translation falls out of their meeting as a side effect, not as a goal.

What follows separates the apparatus into two halves, assigns each a plausible pre-coding function selectable on its own terms, and identifies the decisive event not as the invention of either half but as their co-compartmentalisation.

2 The two halves, before they were paired

2.1 The peptidyl transferase centre: a generator of structural peptide

The catalytic core of the large ribosomal subunit is a ribozyme;[1,2] the peptide bond is still made by RNA, not by protein. Stripped of messenger and transfer RNA, such a fold does only one thing: it condenses whatever activated amino acids are locally available — aminoacyl-adenylates and aminoacyl-thioesters,[3] abundant in a Hadean-energetic setting — into *random, untemplated* oligopeptides.

The selective payoff requires no foresight. Even statistical peptides are useful inside an RNA world: they stabilise folds, buffer charge, present hydrophobic surface, and serve as crude cofactors. A ribozyme that captures ambient activated residues and condenses them into *any* peptide secures a local supply of RNA-stabilising material. The ancestral function of the centre is thus *peptide as a structural reagent for RNA*. Specificity is absent; the chemistry is everything. This is a **generator** — it produces variation that something else may later filter.

2.2 The charged acceptor stem: a one-character memory

The transfer RNA carries two histories. The acceptor stem — the end that is charged — is separable from, and plausibly older than, the anticodon arm (the operational-RNA-code observation).[4,5] The question is what a small hairpin that acquires a *specific* amino acid at its terminus does before any ribosome exists to read it.

The amino acid is best understood as a modification on the RNA, selected for its effect on *that RNA's own fate*: a covalent label gating replication, marking identity in a population of competing replicators, or tuning folding and stability; or a recognition and energetic adjunct for an early replicase acting on the 3′ terminus. Either way the ancestral function is *specifically*

charged RNA, selected for what the charge does to the RNA itself. This is a **heritable-carrier** primitive: a system that stably associates a particular small molecule with a particular sequence. It is a one-character code that, as yet, encodes nothing.

3 Two cells

The two functions are clearer still when placed in separate compartments.

Cell A, of the transferase lineage, makes random structural peptides from ambient activated amino acids. It is productive but its peptide output is *non-heritable*: it can reproduce the capacity to make junk peptide, never a particular peptide. It holds a generator with no memory.

Cell B, of the acceptor-stem lineage, maintains a set of RNAs each stably wearing a specific amino acid, used for RNA identity or replication. It holds *specific residue-to-sequence associations* — a memory — but no machinery that reads those associations out into a polymer. It holds a code with nothing to encode.

Each cell is selected, complete, and useful on its own terms. Neither is in any sense reaching toward translation.

4 The encounter

The decisive event is neither invention.[10] It is the moment a single lineage comes to hold both systems — by fusion, transfer, or simple arising in one compartment. At that instant the charged RNAs of the memory system become the substrate-delivery system for the peptide-bond chemistry of the generator, and the peptides stop being random. The charging specificities now dictate which residue is presented, and therefore which residue is incorporated: memory meets generator and yields the first non-random, heritable peptide — the first object on which selection can act at the level of protein sequence.

The genetic code, on this reading, is the **interface contract** between the two systems, frozen at the moment of merger.[6] It was negotiated by no one; it records which charging specificities happened to be present when the two lineages met.

4.1 The messenger is the late party

Neither half requires a messenger. The earliest templating is carried by the set of charging specificities themselves — the operational code written on the acceptor stems. Messenger RNA, read as a tape, is a later abstraction that lets that charging code be stored and copied independently of the transfer RNAs that embody it.

Two priority questions are often posed as rivals: did the chemistry of peptide formation come first, or did a non-messenger template come first? In the merger account both are satisfied, by different molecules. The transferase centre gives chemistry priority; the charged acceptor-stem code gives information priority; the messenger is neither-first. The spine of the account is the merger, not either priority taken alone.

A note on a tempting wrong turn. Non-ribosomal peptide synthesis is not the ghost of a pre-ribosomal pathway. Its patchy, accessory distribution is the signature of a convergent canal,[7,8] re-derived wherever thioester-templated chemistry pays off, rather than of a deep inherited core. The genuinely ancestral object is not the enzyme family but the activated-aminoacyl chemistry it exploits — the same chemistry the transferase centre runs without it.

5 A falsifiable edge

The account is a compass rather than a story only if it can be wrong. It predicts that the operational (acceptor-stem) code is older than, and partially independent of, the anticodon-and-codon code,[4,9] retaining residual amino-acid-assignment logic the codon table does not explain — testable against existing synthetase-recognition and transfer-RNA identity-element data. Any residual mismatch between operational-code and codon-table assignments is a fossil

of the pre-merger memory system; its absence would put the account under pressure.

6 References

[1] Nissen P., Hansen J., Ban N., Moore P.B., Steitz T.A. (2000). The structural basis of ribosome activity in peptide bond synthesis. *Science* 289:920–930.

[2] Cech T.R. (2000). The ribosome is a ribozyme. *Science* 289:878–879.

[3] de Duve C. (1991). *Blueprint for a Cell: The Nature and Origin of Life*. Neil Patterson, Burlington NC. (Thioester-world / activated-aminoacyl chemistry preceding the RNA world.)

[4] Schimmel P., Giegé R., Moras D., Yokoyama S. (1993). An operational RNA code for amino acids and possible relationship to genetic code. *Proc. Natl. Acad. Sci. USA* 90:8763–8768.

[5] Eriani G., Delarue M., Poch O., Gangloff J., Moras D. (1990). Partition of tRNA synthetases into two classes based on mutually exclusive sets of sequence motifs. *Nature* 347:203–206.

[6] Crick F.H.C. (1968). The origin of the genetic code. *J. Mol. Biol.* 38:367–379. (Frozen-accident hypothesis.)

[7] Wang H., Fewer D.P., Holm L., Rouhiainen L., Sivonen K. (2014). Atlas of nonribosomal peptide and polyketide biosynthetic pathways reveals common occurrence of nonmodular enzymes. *Proc. Natl. Acad. Sci. USA* 111:9259–9264.

[8] Fischbach M.A., Walsh C.T. (2006). Assembly-line enzymology for polyketide and nonribosomal peptide antibiotics: logic, machinery, and mechanisms. *Chem. Rev.* 106:3468–3496.

[9] Rodin S.N., Ohno S. (1995). Two types of aminoacyl-tRNA synthetases could be originally encoded by complementary strands of the same nucleic acid. *Orig. Life Evol. Biosph.* 25:565–589.

[10] Hartman H., Smith T.F. (2019). Origin of the genetic code is found at the transition between a thioester world of peptides and the phosphoester world of polynucleotides. *Life* 9:69. (Closest prior art — see note below.)

[11] Higgs P.G., Pudritz R.E. (2009). A thermodynamic basis for prebiotic amino acid synthesis and the nature of the first genetic code. *Astrobiology* 9:483–490.

[12] Trifonov E.N. (2000). Consensus temporal order of amino acids and evolution of the triplet code. *Gene* 261:139–151.

7 Claim--source verification table

Each row pairs a claim made in the text with the reference(s) that support it, and notes whether the reference establishes the claim outright or is cited as supporting context for a step that is the author's own.

Claim (as stated in text)	Ref.	Standing
The peptidyl transferase centre is a ribozyme; the peptide bond is made by RNA, not protein.	[1], [2]	**Established.** Crystal structure shows the catalytic site is entirely RNA.
Activated amino acids (aminoacyl-adenylates / -thioesters) are the ancestral peptide-bond substrate and predate the coding system.	[3]	**Supports.** Thioester-world chemistry is de Duve's; the priority-over-coding framing is the author's.
The acceptor stem is aminoacylated specifically, independent of the anticodon — an "operational RNA code".	[4]	**Established.** Minihelices lacking anticodons are charged sequence-specifically.
Aminoacyl-tRNA synthetases fall into two structurally unrelated classes of ∼10 each.	[5]	**Established.** Class I / Class II partition by mutually exclusive motifs.
The two synthetase classes may derive from complementary strands of one ancestral gene (the "twofold-of-ten" duplication signal).	[9]	**Supports.** Rodin–Ohno sense/antisense hypothesis; cited as the real result behind the "10 duplications" claim.
The genetic code is a contract "frozen" at a particular moment and thereafter near-unchangeable.	[6]	**Established (concept).** Crick's frozen accident; the "interface contract of a merger" reading is the author's.

Claim (as stated in text)	Ref.	Standing
NRPS is a derived, modular, patchily-distributed convergence (shared thiotemplate logic with PKS/FAS), not an ancestral pre-ribosomal relic.	[7], [8]	**Established.** Distribution and shared assembly-line mechanism; "convergent canal, not relic" is the author's inference from it.
The code began with ∼10 prebiotically-abundant amino acids and accreted the rest stepwise.	[11], [12]	**Established.** Consensus early set (Ala, Asp, Glu, Gly, Ile, Leu, Pro, Ser, Thr, Val) converges across spark-discharge, meteorite, and codon-chronology evidence.
The operational (acceptor-stem) code is older than and partially independent of the codon code — the falsifiable prediction.	[4], [9]	**Supports / open.** Consistent with the operational-code and complementarity literature; the specific residual-mismatch test is the author's and is not yet settled.
Core thesis: translation is the merger of two independently selected RNA systems (generator + memory), neither selected for translation.	[10]	**Partial prior art.** Hartman & Smith independently argue a thioester-peptide / phosphoester-polynucleotide *transition*; the generator/memory framing and the "code = frozen interface contract" move are the author's.

Note on prior art and priority. The strongest overlap is with Hartman & Smith (2019) [10], who also cast the origin of the code as the coupling of a peptide world to a polynucleotide world. The contribution that reads as distinct here is threefold: (i) the explicit *generator / heritable-carrier* decomposition of the two halves, each given a complete code-free function; (ii) the "two cells" individuation that makes the merger the unit of explanation rather than either component; and (iii) the falsifiable operational-code-priority test in §5. These three are the parts worth timestamping before external circulation; the remainder is consensus and is cited as such above.