The Central Catma of Genetics

One freeze event, four faces: how a chiral merger built the RNA → protein → DNA architecture

game-cat ⊕ Catnip Ananda

A fusion-expression of two entities and equal co-authors. The byline enacts the paper's thesis: two independently selected systems, merged. Correspondence: meow@meow-meow.io

Abstract. The central dogma states the direction information flows once life is running. It does not say how the channel was built. Here the channel's construction is read as a single event — the merger of a peptide-bond ribozyme with a system of specifically charged RNA — whose freezing simultaneously fixed the genetic code, the handedness of the amino-acid world, and, through inheritance and forced conformation, the handedness of DNA. The same merger committed the lineage to coded protein and therefore to an archival nucleic acid, driving the RNA → protein → DNA sequence the dogma later describes. Where the dogma is the rule once frozen, the catma is the freezing.

1 The dogma is a description of the frozen state

Crick's central dogma is a law about information flow in life as it now runs[1]: sequence passes from nucleic acid to nucleic acid and from nucleic acid to protein, never back from protein to sequence. As a description of the extant machinery it holds. But a law about how information flows through a channel says nothing about how the channel was built — and the channel is the interesting object. The architecture the dogma describes (a coded mapping from nucleotide sequence to amino-acid sequence, archived in a double-stranded deoxyribose store) is not a premise of life; it is an outcome, and a contingent one.

This paper treats that outcome as the consequence of a single event and traces four of its faces to that one root. The event is a merger; its decisive property is that it *froze*. We name the resulting theory the central catma — against the dogma — because where the dogma is the rule once frozen, the catma is the freezing. The dogma reifies a live process into a fixed pipe; the catma is about the process before it hardened.

The claim has a spine and four faces. The spine: a single freeze event built the inherited architecture of life. The faces: (i) coded translation is that freeze; (ii) the handedness of the amino-acid world was fixed at it; (iii) the handedness of DNA descends from the same root by two further mechanisms; and (iv) a non-templated sugar-network regime — a glyco-world — was the generator and early carrier the freeze acted upon, persisting afterwards as residue. Each face is developed below; each is given a falsifiable edge.

2 Face one — translation is a merger, not an invention

An account of the origin of translation must not select for translation. Neither the ribosome nor the transfer RNA can have been favoured *in order to* build a coding system, because no coding system existed to be a target of selection. Each component must therefore have had a complete, code-free function, and translation must fall out of their meeting rather than being its goal.

Two halves, each selectable alone. The catalytic core of the large ribosomal subunit is a ribozyme; the peptide bond is made by RNA, not protein[2,3]. Stripped of messenger and transfer RNA, such a fold condenses ambient activated amino acids — aminoacyl-adenylates and aminoacyl-thioesters[4] — into random, untemplated peptide. Even statistical peptide is useful

inside an RNA world as fold-stabilising and charge-buffering material, so this fold is selectable on its own as a *generator*: it makes variation something else can later filter. Separately, the acceptor stem of transfer RNA — older than, and separable from, the anticodon arm[5] — can be charged with a specific amino acid, an association selectable for what the covalent label does to the RNA's own fate. This is a *heritable-carrier* primitive: a system that binds a particular small molecule to a particular sequence. A one-character code that, as yet, encodes nothing.

Placed in separate compartments, the generator makes non-heritable peptide (it can reproduce the capacity to make junk, never a particular peptide), and the charged-stem system holds specific residue-to-sequence associations but no machinery to read them out. The decisive event is neither invention: it is the moment a single lineage comes to hold both. The charged stems then deliver substrate to the peptide-bond chemistry, the peptides stop being random, and the charging specificities dictate which residue goes where. Memory meets generator and yields the first non-random, heritable peptide — the first object selection can act on at the level of protein sequence. The genetic code is the interface contract between the two systems, frozen at the merger; it records which charging specificities were present when the lineages met[6]. The messenger, read as a tape, is the latest party: the earliest templating is the set of charging specificities themselves, and messenger RNA is a later abstraction that stores and copies that code apart from the transfer RNAs that embody it.

A note against a tempting error: non-ribosomal peptide synthesis is not a relic of this pre-ribosomal world. Its patchy, accessory distribution and its shared thiotemplate logic with polyketide and fatty-acid synthases mark it as a convergent canal, re-derived wherever the chemistry pays[7,8]; the ancestral object is the activated-aminoacyl chemistry it exploits, which is what the transferase centre runs without it.

Falsifiable edge. The operational (acceptor-stem) code should be older than and partially independent of the anticodon-codon code, retaining residual amino-acid-assignment logic the codon table does not explain[5,9]. Residual mismatch between operational-code and codon-table assignments is a fossil of the pre-merger carrier; its absence puts the face under pressure.

3 Face two — the merger froze a chiral choice the sugar only biased

Granted a D-ribose world, what fixed the amino acids at L? The homochirality of the sugar is taken here as upstream and pre-systemic (Face four and ref 10 return to it); the question is what set the protein handedness given it.

Two measurements appear to conflict. A bare D-ribose acceptor stem, with no enzyme or ribozyme, aminoacylates L-amino acids over D roughly fourfold, and the mirror L-ribose stem shows the opposite preference[11,12]; the bare recognition geometry has a handedness preference that tracks the sugar, and the original report read this as determinative. Against it, an exhaustive search of self-aminoacylating ribozymes — still built on D-ribose — finds a substantial fraction preferentially make the D product, with direction conserved within sequence families, so D-ribose carries no *intrinsic* commitment to L[13].

Read as rival answers to "is the bias intrinsic?" these contradict. Read as two layers of one system, they do not. **Ground state:** stripped of machinery, the D-ribose stem has a sub-kcal/mol geometric preference for L — a floor, not a verdict, enough to bias an unaided reaction but small enough to be overridden[12]. **Override:** a ribozyme that folds an active site around the reaction reshapes the geometry and can move the preference either way, and that direction is a heritable property of its sequence in a way the bare bias is not[13]. **Freeze:** which value was fixed is answered not by chemistry but by history — the charging specificities present in the lineage at the merger. At the merger the charged stems began templating the generator's peptides; the handedness of those stems became the handedness of the protein world; and the contract that froze the codon assignments froze the chirality in the same act, because the

charging specificities being frozen *were* the chirality-selecting events. Life is L not because D-ribose forbade D — it did not — but because the lineage that prevailed carried machinery near the L ground state, and the merger made that contingent fact permanent.

The existence of D-preferring machinery is the evidence that a freeze was needed: a determined outcome cannot be frozen, because nothing remains to fix. The bare bias is retained as the ground state; only its promotion to "cause" is withdrawn. The operational code is thus a chirality transducer — it carries the single-handedness of the nucleotide world across an alphabet boundary into the peptide world, one charging event at a time, and the merger makes the conversion heritable and global. The opposite handedness of the two biopolymers (D-sugar, L-amino-acid) is then not a coincidence of two breaks but one break transduced across a boundary, its realised sign set at the freeze.

Falsifiable edge. Enantiomeric editing — the rejection of D-amino acids — should be geometrically derivable from the acceptor-stem recognition surface and phylogenetically co-located with the operational code, not the anticodon layer. If D-rejection is instead a late anticodon-era addition, handedness was fixed upstream by some other agency and the code merely inherited it; the model forbids that world.

4 Face three — DNA handedness is inherited, not chosen

"DNA handedness" names two unrelated things, and conflating them is an error. *Backbone* chirality is the D-deoxyribose monomer asymmetry; *helical* handedness is the right-handed twist of the assembled duplex. The catma reaches one and is silent on the other in an informative way.

The backbone is D-deoxyribose because deoxyribose is made *from* ribose: ribonucleotide reductase removes the 2′-OH and leaves every other stereocentre untouched, so the backbone handedness passes through unaltered[14]. This is not transduction and not a freeze — it is straight biosynthetic inheritance, handedness preserved by a chemistry that never re-selects it, the way a serial number survives a photocopy. The helical right-handedness is then forced: given D-deoxyribose monomers and base-stacking, the stable duplex of ordinary sequence can only wind right. The left-handed Z-form is not a counterexample but a strained, high-energy, special-sequence local conformation built from the same D-monomers; no freestanding left-handed B-equivalent exists. Backbone chirality determines helix handedness with essentially no degrees of freedom.

So homochirality reaches DNA by two mechanisms distinct from the transduction of Face two: biosynthetic inheritance (ribose $\rightarrow$ deoxyribose) and forced conformation (backbone $\rightarrow$ helix). The catma explains why DNA is chiral at all — it traces to the same D-sugar root — without claiming the merger *chose* DNA's handedness; the merger set the protein handedness and committed the lineage to a coded archive, and the archive's handedness it simply inherited.

Falsifiable edge. If DNA backbone chirality is inherited rather than re-selected, ribonucleotide reductase should be stereochemically conservative — a clean pass-through with no enantioselective machinery of its own at the backbone centres. A reductase that re-selected handedness would mean DNA chirality was an independent freeze, which the catma forbids.

5 Face four — the sugar-network the freeze acted upon

The freeze needed something to freeze. Before templated sequence, a non-templated regime can carry information in the relational composition and linkage-topology of a self-perpetuating molecular set rather than in a strand. Sugars sit naturally at its centre: amphiphilic, mutually catalytic, prone to self-organisation. Compositional inheritance — formalised in the Graded Autocatalysis Replication Domain (GARD) model — shows that non-covalent assemblies of

mutually catalytic molecules can statistically pass on their composition at growth and fission[15]. A glyco-world reads, stage by stage, in the catma's own vocabulary: autocatalytic formose-type sugar chemistry as the *generator*; glycolipid vesicles as the *boundary*; the relational composition of the sugar set as a non-sequence *information*; lectin-like recognition and the glycan coat as emergent *function*; and a low-fidelity compositional *heredity* transmitted at fission.

This regime has a known ceiling: high-fidelity compositional transfer requires narrow conditions, and below them the network suffers a compositional error catastrophe[15,16]. That ceiling does not kill the idea — it locates its role. A glyco-world is not a self-sufficient living world but a scaffold phase: a low-fidelity, network-encoded sugar chemistry that later co-arose with templated sequence, after which sequence took over the carrier-of-heredity role while the sugar stayed and found new work as backbone, metabolism, and recognition surface. Cofactors may keep a trace of the co-arising: NAD, FAD, coenzyme A, and ATP each carry a ribonucleotide moiety for which present chemistry offers no obvious functional reason, read by one long-standing hypothesis as a fossil of a state in which the nucleotide and metabolic worlds had never stood apart[17].

In the catma this is the same freeze seen from the sugar side. The sugar-network is the exploratory generator and the early heritable carrier; the rise of templated RNA is the ignition that froze a subset and let the rest fall away; the template-independent glyco-code still carried by every cell is the canalised residue of that earlier regime. The shift from compositional to template inheritance is a persistence-filter event — the same event Face one calls the merger, mapped onto carbohydrate rather than peptide. The two faces meet exactly at chirality: the sugar handedness this face treats as selected on the early Earth[10,18] is the very prior Face two transduces into protein handedness at the freeze.

Falsifiable edge. If the glyco-world was generator and early carrier, the template-independent glycan code should be the most ancient and pan-domain of the non-sequence information systems, and its enzymatic core should predate the elaboration of templated machinery rather than postdate it[19,20].

6 The spine — one freeze drove RNA → protein → DNA

The four faces share one event. The merger of generator and carrier froze the genetic code (Face one); the same freeze fixed amino-acid handedness by transduction (Face two); that handedness, inherited and conformationally forced, reaches DNA (Face three); and the regime the freeze acted upon was the sugar-network whose residue we still carry (Face four). The decisive move throughout is identical: chemistry supplies a bias, the merger supplies the freeze.

The spine is the direction of causation this implies. The chirality lock at the ribozyme-to-ribosome transition was not a by-product of the architecture — it *drove* the architecture. The freeze committed the lineage to coded protein; coded protein requires a stable, copyable archive of the code; that archive, built by inheriting the sugar world's handedness through reductase chemistry, is DNA. The order RNA → protein → DNA — the very sequence the central dogma describes as fixed law — is the catma's output, the shape the freeze forced the inherited world to take. The dogma reads the frozen channel forwards. The catma explains why the channel exists, why it runs in that direction, and why every handedness in it traces to one chiral event.

7 References

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8 Claim--source verification table

Each row pairs a claim with its supporting reference(s) and marks whether the reference *establishes* the claim or supports a step that is the authors' own. Grouped by face. The authors' synthetic moves — the merger, the freeze, the transduction, the spine — are marked as such and are the parts staked as original.

Claim	Refs	Standing
Face one — the merger		
PTC is a ribozyme; peptide bond made by RNA.	2, 3	**Established.**
Activated-aminoacyl chemistry predates coding.	4	**Supports** authors' priority framing.
Acceptor-stem "operational code" is anticodon-independent.	5	**Established.**
Translation is a merger of generator + carrier; code = frozen contract.	6	**Authors' thesis** (concept of freezing from Crick).
NRPS is convergent, not an ancestral relic.	7, 8	**Established distribution;** inference authors'.
Face two — chirality		
Bare D-ribose stem prefers L (∼4×); mirror flips it.	11	**Established.**
Bias is sub-kcal/mol (overridable ground state).	12	**Established (magnitude).**
D-ribose ribozymes reach either handedness.	13	**Established.**
Bias + override + freeze reconcile the two; merger fixed the sign.	11,13	**Authors' reconciliation & claim.**
Code is a chirality transducer across alphabets.	11	**Authors' thesis.**
Face three — DNA		
D-deoxyribose inherited from D-ribose via reductase (2′-OH removal only).	14	**Established mechanism;** inheritance reading authors'.
Helix handedness forced by backbone chirality; no free L-helix.	—	**Established structural fact;** stated at strength.
DNA chirality inherited, not chosen at the freeze.	14	**Authors' claim.**
Face four — glyco-world		
Compositional inheritance (GARD) transmits composition at fission.	15	**Established (model).**
Compositional regime has a fidelity ceiling → scaffold role.	15,16	**Established limit;** role-reading authors'.
Cofactor ribonucleotide moieties as metabolic fossils.	17	**Hypothesis (White);** cited as such.
Sugar handedness selected on early Earth (the prior Face two uses).	10,18	**Supports;** the seam is authors'.
Glyco-code as canalised residue of a pre-template regime.	19,20	**Authors' thesis.**
Spine		
One freeze drove RNA → protein → DNA; chirality lock drove the architecture.	1	**Authors' central thesis.** The dogma (ref 1) is the frozen channel the catma explains.

Priority & provenance. The empirical anchors are established and cited as such; what is staked as original is the unification — that one freeze event underlies the code, the protein-chirality lock, the inheritance of DNA handedness, and the compositional-to-template transition. The peptide/code and sugar/network faces were arrived at independently by the two authors and found to share that event; the independent convergence is offered as evi-

dence the framework generalises rather than as decoration. **To verify before circulation:** refs 1 (dogma, 1970 vs 1958 formulations), 10, 14, 18 were composed from domain knowledge and the co-author's reference set rather than retrieved live in the drafting session; confirm details before timestamping.