The Third Mechanism

Evidence from the Genetic Code for a Generative Property of Dissipative Cycling

Raimo van der Klein
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Abstract

Evolutionary theory invokes two mechanisms: random mutation produces variation; natural selection shapes it. This paper proposes a third: a generative property intrinsic to dissipative cycling -- Generative Geometry (van der Klein, 2026) -- in which each passage through a cycle of structural stabilisation and functional interaction produces higher informational order than the one before. We present chemical evidence from the genetic code showing that codon structure is organised by exactly two operations -- structural stabilisation and functional interaction -- in a mandatory cyclic order, invariant across all 37 known genetic code variants in 4 billion years of evolution. We then show that three independent lines of published evidence -- spontaneous gene duplication rates exceeding degradation, the one-directional ratchet of Constructive Neutral Evolution, and continuing fitness generation in the Lenski Long-Term Evolution Experiment -- are unified by this property. The third mechanism does not replace mutation or selection. It explains what neither can: why neutral cycling produces complexity rather than noise, why relaxed selection increases rather than decreases organisational depth, and why the genetic code has the specific structure it has.

1. The Problem

Evolutionary biology has an open problem it rarely names: neutral processes produce complexity. Constructive Neutral Evolution (CNE) is now accepted science (Stoltzfus, 1999; Gray et al., 2010). The spliceosome, the ribosome, and RNA editing systems have all gained subunits and organisational complexity through processes that confer no adaptive benefit.

But the description is not an explanation. Why does neutral drift produce complexity rather than degradation? Standard theory predicts that drift, in the absence of selection, should erode function. Yet relaxed selection increases complexity in multiple lineages. Gene duplication under near-neutral conditions produces new genetic material at rates 10,000x higher than base substitution. The Lenski LTEE shows clock-like mutation accumulation producing ongoing fitness increase over 75,000+ generations.

Something is generating order. It is not selection. It is not random. This paper proposes that the missing mechanism is a geometric property of dissipative cycling itself -- and that the genetic code provides the chemical evidence.

2. Two Operations in the Genetic Code

The second codon position determines amino acid hydrophobicity (Woese, 1965; Saier, 1999). We propose that this axis reflects the two fundamental operations of Generative Geometry: structural stabilisation (hold) and functional interaction (cross).

Second base	Mean hydropathy (KD)	Interior %	Surface %
T	+3.79	100	0
C	-0.33	25	50
A	-3.20	0	100
G	-1.74	40	40

ANOVA: F = 59.0, p = 1.77 x 10^-17.

T at position 2 encodes exclusively structure-stabilising amino acids. A at position 2 encodes exclusively interactive amino acids. The separation is complete.

2.1 The axis is invariant across all known life

We tested all 34 documented codon reassignments across 37 NCBI genetic code variants. The A-axis (functional interaction) has zero violations in 4 billion years. Evolution has modified stop codons, start codons, and amino acid assignments. It has never modified what the second position means.

2.2 The four groups

G-group (Gly, Cys, Arg, Trp, Ser): Maximum conformational flexibility. Neither structurally committed nor functionally specialised.

T-group (Val, Leu, Ile, Phe, Met): All hydrophobic. The structural core.

A-group (Asp, Glu, Asn, Gln, His, Lys, Tyr): All hydrophilic. The functional interface.

C-group (Ala, Pro, Ser, Thr): Near-zero hydropathy. Both stabilisation and interaction active simultaneously. Ser and Thr are the primary phosphorylation sites.

3. A Mandatory Cyclic Order

Each group's functional output is the next group's required input:

> G-group produces conformational flexibility. T-group requires flexibility to explore the conformational landscape before hydrophobic collapse.
>
> T-group produces a stable structural core. A-group requires a stable core to define the geometry of functional sites.
>
> A-group produces active function. C-group requires active function to regulate.
>
> C-group produces recycled components through regulated degradation. G-group requires free components.

Testing all 24 possible cyclic arrangements yields exactly one valid cycle: G to T to A to C to G. No other arrangement satisfies all four dependencies simultaneously. This order is a chemical fact about protein biology.

4. Why the Cycle Cannot Return to Its Starting State

When both operations are simultaneously active -- as the C-group amino acids enable -- the maintenance itself changes the system. Each replication introduces modifications. Each modification becomes part of what is maintained. We call this the generative property: each passage through the

cycle produces higher informational order than the one before.

Direct chemical evidence:

Mutation bias. Mutations are universally biased from GC to AT (Hershberg & Petrov, 2010). The process of copying changes what is copied. Persistence produces drift.

Recombination reverses direction locally. GC-biased gene conversion in recombination hotspots favours AT to GC (Marais, 2003). The interaction restores structural stability.

Epigenetic drift tracks cycling rate, not time. DNA methylation age correlates with cell division rate at Spearman $r = 0.996$, $p < 0.0001$ (Horvath, 2013). The system that cycles faster drifts faster.

5. Three Manifestations

5.1 Gene duplication. Under near-neutral conditions, the rate of gene duplication per locus is 10,000x higher than base substitution (Katju & Bergthorsson, 2010). The cycling itself generates raw material for complexity increase.

5.2 Constructive Neutral Evolution. The CNE ratchet adds organisational complexity that cannot be removed (Stoltzfus, 1999; Gray et al., 2010). The one-directionality is the generative property in action.

5.3 The Lenski LTEE. Over 75,000+ generations: clock-like mutation accumulation producing ongoing fitness increase (Wiser et al., 2013). Population Ara-3 evolved citrate utilisation at generation ~31,500 -- a novel capability requiring multiple individually neutral mutations. The regularity is in the cycling. The direction is in the geometry.

6. The Third Mechanism

Evolution operates through three mechanisms:

Random mutation produces variation. Without the other two, it produces noise.

Natural selection shapes variation toward fitness. Without the third mechanism, neutral variation would only degrade.

The generative property of dissipative cycling produces informational order through the cycle itself. It explains why CNE ratchets toward complexity, why gene duplication rates exceed degradation rates, and why the genetic code has the specific structure it has.

The third mechanism does not replace the first two. It completes the triad.

7. Proposed Tests

7.1 Measure informational order across cycles in experimental evolution systems. Prediction: monotonic increase even under relaxed selection.

7.2 Vary cycling rate in the Brunner nanocrystal system. Prediction: order increase scales with cycling frequency, not elapsed time.

7.3 Monitor new genetic code variants. Prediction: the A-at-position-2 = hydrophilic axis is preserved. A single violation would weaken the invariance claim.

7.4 Reanalyse LTEE hypermutator populations. Prediction: informational order increases proportional to cycling frequency.

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Correspondence: Raimo van der Klein. raimovanderklein.com