The merger froze a chiral choice the sugar only biased

Homochirality as transduction, not determination

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Abstract. A bare D-ribose acceptor stem aminoacylates L-amino acids in preference to D, without protein or ribozyme; engineered self-aminoacylating ribozymes built on the same D-ribose backbone reach either handedness. Both observations are treated here as measurements of different layers of one system: a ground-state bias set by sugar geometry, and a charging machinery able to override it. The realised handedness of life is read as neither sugar-determined nor machinery-determined but frozen — at the same event, and for the same reason, that froze the genetic code.

1 A companion claim

This note is a companion to a prior account in which translation is read as the merger of two independently selected RNA systems — a peptide-bond ribozyme (the generator) and a system of specifically charged acceptor stems (the memory) — with the genetic code as the frozen interface contract of their encounter.[1] That account left chirality untreated. The question taken up here is whether the same merger that froze the code also fixed the handedness of the amino acid world, and if so, what it fixed it *from*.

The upstream symmetry break — the homochirality of the sugar itself — is assumed, not explained. D-ribose is taken as the prior substrate on which both systems run; why ribose went D rather than L is the nucleotide-world chirality problem and is out of scope.[2] The claim made here begins one layer above it.

2 Two measurements that look like a contradiction

A short RNA helix built from D-ribose, presented with activated amino acids and no enzyme or ribozyme of any kind, condenses L-amino acids onto its terminus in preference to D — roughly fourfold for several residues, with the mirror-image L-ribose helix showing the opposite preference.[3,4] The bare recognition geometry has a handedness preference, and that preference tracks the sugar. The original report read this as determinative: the chirality of proteins was set by the chirality of RNA.[3]

Against this stands a later result. An exhaustive search of self-aminoacylating ribozymes — catalytic RNAs, still built on D-ribose, that charge themselves — finds that a substantial fraction prefer to produce the D-amino-acid product, that the preferred direction is conserved within sequence families, and therefore that D-ribose carries *no intrinsic* commitment to L: L-proteins need not emerge from a D-RNA world.[5]

Read as rival answers to one question — "is the D-to-L bias intrinsic?" — these results contradict. Read as measurements of two different layers, they do not.

3 Bias, override, freeze

The resolution is to stop treating "intrinsic bias" and "either handedness" as competitors and treat them as successive layers of one mechanism.

The ground state. Stripped of all machinery, the D-ribose acceptor stem has a geometric preference for L. This is a floor, not a verdict: a sub-kcal/mol transition-state difference, enough

to bias an unaided reaction but small enough to be overridden by any apparatus that reshapes the active site.[4] The bare-minihelix result measures this floor.

The override. A ribozyme that folds an active site around the charging reaction reshapes that geometry and can move the preference in either direction. The either-handedness result measures the override.[5] Crucially, the override is heritable in a way the bare bias is not: the bare geometry recurs identically for every D-stem, carrying no information, whereas a ribozyme's charging direction is a property of *its sequence* and is inherited by its descendants. The moment charging is done by an evolvable molecule, handedness becomes a heritable trait that can take either value.

The freeze. Which value got fixed is then not a question chemistry answers. It is a question the *history* answers — specifically, the charging specificities present in the lineage at the moment the memory system merged with the generator. At that merger the charged stems began templating the generator's peptides; the handedness of those charged stems became the handedness of the protein world; and the interface contract that froze the codon assignments froze the realised 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 won the merger happened to carry charging machinery sitting near the L ground state rather than an overriding D, and the merger made that contingent fact permanent.

3.1 What this does to "determination"

The bare-minihelix bias is real and is retained in full; only its *interpretation* changes. It is demoted from the cause of biological homochirality to the ground state over which the cause — a frozen historical choice — operated. The existence of D-preferring machinery is what forces this demotion: if the sugar had determined the outcome, no freezing event would be needed to explain why life is L, and the reachability of D would be a paradox rather than a clue. The D-preferring ribozymes are not an embarrassment to the transduction picture; they are its evidence. A determined outcome cannot be frozen, because there is nothing left to fix.

4 Transduction, stated

Homochirality is not independently invented in the amino acid world. It is carried there, across an alphabet boundary, by a recognition surface that is itself single-handed because the sugar is. The operational code is a chirality transducer: it converts the homochirality of the nucleotide world into the homochirality of the peptide world, one charging event at a time, and the merger makes the conversion heritable and global. The long-standing puzzle of why the two biopolymers carry *opposite* handednesses — D-sugar, L-amino-acid — loses its mystery on this reading: the pairing is not a coincidence of two independent symmetry breaks but the signature of a single one transduced across a boundary, with the realised sign set at the freeze.[6]

5 A falsifiable edge

The account stands or falls on a structural and phylogenetic prediction, and it is sharper than mere correlation. If handedness was transduced through the operational code and fixed at the merger, then the machinery that *discriminates* against the wrong enantiomer — the editing and rejection of D-amino acids — should be geometrically derivable from the acceptor-stem recognition surface and should sit, phylogenetically, with the oldest operational-code machinery, not with the later anticodon-reading layer. The direction of override in a given lineage should track its charging machinery, not its codon table.

This is testable against existing minihelix-geometry and synthetase editing-domain data, and it discriminates cleanly. If D-rejection proves to be a deep acceptor-stem-associated function, transduction-then-freeze holds. If it proves to be a late anticodon-era addition, then handedness was fixed upstream by some agency other than the code — mineral surface, polarised light, parity violation — and the code merely inherited an already-settled choice. The model

forbids that second world; finding it would end the model.

Scope. Two breaks, kept separate. The sugar break (why D-ribose) is upstream, pre-systemic, and assumed. The amino-acid break (why L-protein) is downstream, systemic, and owned here: biased by the sugar, realised by the machinery, fixed by the merger. Conflating the two is the error this note exists to refuse.

6 References

[1] Companion communication: *Translation is a merger, not an invention* (this author). Establishes the generator / memory / frozen-contract framework assumed throughout.

[2] Blackmond D.G. (2019). The origin of biological homochirality. *Cold Spring Harb. Perspect. Biol.* 11:a032540. (Review of the nucleotide-world chirality problem treated here as upstream.)

[3] Tamura K., Schimmel P. (2004). Chiral-selective aminoacylation of an RNA minihelix. *Science* 305:1253. (Bare D-ribose stem prefers L; mirror L-ribose prefers D.)

[4] Tamura K., Schimmel P.R. (2006). Chiral-selective aminoacylation of an RNA minihelix: mechanistic features and chiral suppression. *Proc. Natl. Acad. Sci. USA* 103:13750–13752. See also the geometric analysis of the sub-kcal/mol preference: Aida M. *et al.* (2018), *Nucleic Acids Res.* 46:11144.

[5] Tjhung K.F., *et al.* (2024). Prebiotic chiral transfer from self-aminoacylating ribozymes may favor either handedness. *Nat. Commun.* 15:7980. (D-ribose ribozymes reach either handedness; no intrinsic L-bias.)

[6] Powner M.W., *et al.* (2025). Thioester-mediated RNA aminoacylation and peptidyl-RNA synthesis in water. *Nature* 644:933–944. (Recent prebiotic bridge from thioester chemistry to charged RNA.)

7 Claim--source verification table

Each row pairs a claim with its supporting reference(s) and states whether the reference establishes the claim or supports a step that is the author's own. The two empirical anchors ([3], [5]) are the load-bearing pair; the thesis is the reconciliation between them.

Claim (as stated)	Ref.	Standing
A bare D-ribose acceptor-stem mimic aminoacylates L-amino acids over D (∼4-fold), with no enzyme or ribozyme; mirror L-ribose flips the preference.	[3]	**Established.** Direct experimental result.
The bias is a sub-kcal/mol ground state — small enough to be overridden by an active site.	[4]	**Established (magnitude).** Mechanistic / geometric analysis of the preference.
D-ribose self-aminoacylating ribozymes reach *either* handedness, with direction conserved within sequence families; no intrinsic L-commitment.	[5]	**Established.** Exhaustive ribozyme search; the paper's own stated conclusion.
The two results above are not rivals but measurements of two layers (ground-state bias vs heritable override).	[3], [5]	**Author's reconciliation.** The synthesis is the contribution; the inputs are established.
The realised handedness was *frozen* at the merger, not determined by the sugar — and the D-preferring machinery is the evidence that a freeze was needed.	[1], [5]	**Author's claim.** Depends on the companion merger framework [1]; [5] supplies the warrant for demoting determination.
The bare-minihelix bias is demoted from cause to ground state; its measurement is retained, its interpretation revised.	[3]	**Author's reinterpretation** of an established result (originally read as determinative in [3]).
The operational code is a chirality transducer: sugar homochirality → amino-acid homochirality, made heritable by the merger.	[3], [1]	**Author's thesis.** Mechanism grounded in [3]; heritability/freezing from [1].

Claim (as stated)	Ref.	Standing
The opposite handedness of the two biopolymers is one transduced break, not two independent ones.	—	**Author's claim.** A consequence of the transduction direction; no single source, falsifiable via §5.
Falsifier: D-amino-acid rejection should be acceptor-stem-derived and co-located with the operational code, not the anticodon layer.	[4]	**Open prediction.** Geometry work [4] makes the derivation plausible; the phylogenetic test is unrun.

Note on priority. The transfer of handedness through aminoacylation is not claimed as novel — it is the established Tamura–Schimmel result [3] and its descendants. What is staked here is the *three-layer reconciliation*: that the bare bias and the either-handedness result are the ground state and the override of a single system, and that the realised sign was fixed not by the sugar but by the merger that froze the code. The demotion of "determination" to "ground-state bias," and the identification of the merger as the chirality-fixer, are the parts worth timestamping before circulation.