


Why 13 Protofilaments: A Geometric Selection Argument from D_5 Symmetry

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Microtubules in eukaryotic cells universally adopt a 13-protofilament architecture despite in-vitro assembly producing 8–19-protofilament variants. We show that $n = 13 = F_7$ is the unique integer in the biologically relevant range [8, 19] satisfying simultaneously three constraints within this framework: (i) compatibility with the D_5 pentagonal lattice symmetry ($n \bmod 5 \in \{0, 3\}$), (ii) 3-start helical closure with coprime winding ($\gcd(n, 3) = 1$), and (iii) minimal Fibonacci-closure mismatch of the quantum coherence length ($\epsilon_n \equiv \min_k |n\varphi - F_k|$). No other protofilament number in this range satisfies (i)–(ii) with a smaller closure mismatch. Within the D_5 framework, the same pentagonal symmetry that organizes particle physics (Paper 0 [10]) selects the preferred protofilament number: 13 corresponds to the F_7 -structure of the pentagon, echoing the count of 12 gauge bosons + 1 Higgs field. We derive the mechanical, quantum-coherent, and information-theoretic properties that make 13 optimal, and predict that forced assembly of non-13 microtubules should show measurably reduced quantum coherence times.

INTRODUCTION

Microtubules are hollow cylindrical polymers of tubulin protein, fundamental to eukaryotic cell structure, intracellular transport, cell division, and—in the Orch-OR hypothesis—quantum consciousness [1].

A long-standing puzzle in structural biology: in living cells, microtubules almost exclusively have **13 protofilaments** [2, 3], despite the ease of assembling 8–19-protofilament variants in vitro by varying buffer conditions, GTP concentration, or tubulin source [4].

Why 13? Standard structural biology offers no compelling answer: 13 is not a particularly symmetric number, not a divisor of 360° , and not obviously favored by close-packing geometry.

In this paper, we show that 13 is uniquely selected by the D_5 symmetry that underlies all physics in the MRF framework. The proof requires three independent constraints, each with a clear physical origin, and 13 is the only integer satisfying all three simultaneously.

Relation to prior work.—Within the full MRF tree, this paper lies on the mesoscopic and biological branch that uses the collapse scale inferred in Paper 2 together with the root structure of Paper 0 and, where relevant, the spacetime interpretation later formalized in Paper 51. Relative to reviews of collapse models [14], Orch-OR-style proposals [1], and decoherence objections such as Tegmark’s analysis [13], the present branch treats biological or mesoscopic observables as downstream consequences of the same projection dynamics rather than as independent postulates. The claim in this paper is therefore intended as one node in that broader collapse branch.

MICROTUBULE STRUCTURE

Basic geometry

A microtubule consists of n protofilaments arranged in a cylindrical lattice. Each protofilament is a linear chain of $\alpha\beta$ -tubulin heterodimers (8 nm repeat). The protofilaments are arranged with a characteristic helical offset.

For 13-protofilament microtubules: outer diameter = 25 nm, inner diameter = 15 nm, protofilament rise = 0.92 nm, and a 3-start helical lattice [5].

The 3-start helix

The “3-start” designation means that three parallel helical families wind around the cylinder, each displaced by $n/3$ protofilaments. The shortest helical path connecting adjacent monomers crosses 3 protofilaments per 8 nm rise.

The 3-start condition requires:

$$n \not\equiv 0 \pmod{3}, \quad (1)$$

otherwise the three helical families would be degenerate (overlapping), destroying the characteristic lattice offset pattern.

In-vitro variants

Under varying conditions, microtubules with $n \in \{8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19\}$ have been observed in vitro [4, 6]. The 13-protofilament form is kinetically favored in physiological conditions but not the only thermodynamically accessible state.

THE THREE CONSTRAINTS

Constraint I: D_5 lattice compatibility

The D_5 group has order $|D_5| = 10$ with rotation subgroup C_5 . A cylindrical lattice with n protofilaments admits a coherent D_5 embedding if the pentagonal rotation $r = e^{2\pi i/5}$ maps protofilaments onto protofilaments:

$$n \bmod 5 \in \{0, 3\}. \quad (2)$$

The case $n \bmod 5 = 0$ gives exact pentagonal sub-symmetry (every 5th protofilament is equivalent). The case $n \bmod 5 = 3$ gives a D_5 -compatible *helical* embedding where the pentagonal symmetry is realized along the helical path rather than in cross-section.

Candidates in $[8, 19]$: $n \in \{8, 10, 13, 15, 18\}$.

Constraint II: 3-start helical closure

From Eq. (1):

$$\gcd(n, 3) = 1. \quad (3)$$

This eliminates $n = 15$ and $n = 18$. Remaining: $n \in \{8, 10, 13\}$.

Constraint III: Fibonacci closure

For the surviving candidates after constraints (I) and (II), we define the Fibonacci-closure mismatch

$$\epsilon_n \equiv \min_{k \in \mathbb{N}} |n\varphi - F_k|. \quad (4)$$

Smaller ϵ_n means stronger resonance with the D_5 eigenvalue ladder.

Evaluating the remaining candidates:

$n = 8$: $8\varphi = 12.944$, nearest Fibonacci $F_7 = 13$, so $\epsilon_8 = 0.056$ (0.43%).

$n = 10$: $10\varphi = 16.180$, nearest Fibonacci $F_7 = 13$, so $\epsilon_{10} = 3.180$ (19.7%).

$n = 13$: $13\varphi = 21.034$, nearest Fibonacci $F_8 = 21$, so $\epsilon_{13} = 0.034$ (0.16%). Using Binet,

$$F_7\varphi = F_8 + \varphi^{-7} = 21 + 0.03444\dots, \quad (5)$$

which explains the near-closure.

Thus, among integers in $[8, 19]$ satisfying (I) and (II), $n = 13$ **uniquely minimizes** ϵ_n .

$$\boxed{n = 13 = F_7 : \text{unique minimum-}\epsilon_n \text{ in } (I) \cap (II).} \quad (6)$$

WHY NOT OTHER FIBONACCI NUMBERS?

$$F_5 = 5$$

Satisfies all three constraints formally, but $n = 5$ protofilaments produce a tube with inner diameter ~ 4 nm—too narrow for motor protein transport [7]. Structural stability requires $n \geq 8$.

$$F_6 = 8$$

Satisfies (I) ($8 \bmod 5 = 3$) and (II) ($\gcd(8, 3) = 1$) but fails (III): $8\varphi = 12.94 \neq F_k$. The Fibonacci closure error is 0.4%, compared to 0.16% for $n = 13$.

$$F_8 = 21$$

This candidate fails both structural constraints: $21 \bmod 5 = 1$ (fails I) and $21 \bmod 3 = 0$ (fails II). So 21-protofilament tubes are excluded before closure optimization.

Summary

TABLE I. Constraint satisfaction for candidate n values.

n	(I) D_5	(II) 3-start	(III) Fib.	All?
5	Yes	Yes	Yes	(too narrow)
8	Yes	Yes	No (0.4%)	No
10	Yes	Yes	No (24%)	No
11	No	Yes	No	No
12	No	No	No	No
13	Yes	Yes	Yes	Yes
14	No	Yes	No	No
15	Yes	No	No	No
16	No	Yes	No	No
17	No	Yes	No	No
18	Yes	No	No	No
19	No	Yes	No	No
21	No	No	Yes	No

PHYSICAL CONSEQUENCES OF 13

Mechanical stiffness

The 13-protofilament microtubule has a persistence length of ~ 5 mm [8]—the stiffest known biological poly-

mer. The 3-start helical offset at $n = 13$ produces optimal inter-protofilament contacts:

$$\text{Helical offset angle} = \frac{2\pi}{13} \times 3 = \frac{6\pi}{13} = 83.1^\circ. \quad (7)$$

This offset is close to orthogonal packing and supports large lateral bonding area between adjacent protofilaments.

Quantum coherence

The Fibonacci closure $13\varphi \approx 21$ ensures that quantum phonon modes propagating along the microtubule are resonant with the D_5 eigenvalue structure:

$$\frac{\omega_{n+1}}{\omega_n} = \varphi \quad (\text{golden ratio frequency spacing}). \quad (8)$$

This creates a natural frequency comb that supports long-lived coherent excitations—the “quantum vibrations” measured by Sahu *et al.* [9] at THz frequencies.

Information capacity

The information storage capacity of a microtubule segment of length L is:

$$I = 13 \times \frac{L}{8 \text{ nm}} \times 1 \text{ bit/dimer} = 1.625 L \text{ bits/nm}. \quad (9)$$

The $n = 13$ value maximizes the product of information density and coherence length:

$$I \times \ell_{\text{coh}} \propto 13 \times 21 = 273 = 21 \times 13 = F_8 \times F_7. \quad (10)$$

This Fibonacci product has special significance: it is the information-theoretic capacity of one complete projection cycle (Paper 28 [11]).

Error correction

The 3-start helix provides natural triple redundancy: each tubulin dimer participates in three independent helical pathways. A collapse error in one helix can be corrected by majority voting across the three helices—a biological implementation of triple modular redundancy (TMR):

$$P_{\text{error}}^{\text{corrected}} = 3p^2 - 2p^3 \approx 3p^2 \quad (p \ll 1), \quad (11)$$

reducing the error rate from p to $3p^2$. For $p \sim 10^{-3}$ (thermal error rate at 37°C), the corrected rate is $\sim 3 \times 10^{-6}$.

THE 13 = STANDARD MODEL CONNECTION

The number 13 appears independently in particle physics (Paper 51 [12]):

$$12 \text{ gauge bosons} + 1 \text{ Higgs} = 13 = F_7. \quad (12)$$

The 12 gauge bosons: 8 gluons + $W^\pm + Z^0 + \gamma$. The 1 Higgs field provides mass.

In the D_5 framework, this is not a coincidence:

- Gauge bosons \rightarrow edges of D_5 -compatible polyhedra: $|E| = |D_5| + 2 = 12$.
- Higgs \rightarrow the scalar A_1 representation: $+1$.
- Protofilaments \rightarrow the cylindrical realization of the same D_5 structure.

Both the particle content of the Standard Model and the architecture of the microtubule are F_7 -structures of the pentagon—different physical realizations of the same mathematical object.

EXPERIMENTAL PREDICTIONS

1. **Coherence time vs. protofilament number:** In-vitro assembled microtubules with $n \neq 13$ should show measurably shorter quantum coherence times:

$$\frac{\tau_{\text{coh}}(n)}{\tau_{\text{coh}}(13)} \approx \frac{|n\varphi - \text{nearest Fib.}|^{-1}}{|13\varphi - 21|^{-1}}. \quad (13)$$

For $n = 14$: predicted ratio ~ 0.02 ($\sim 98\%$ coherence reduction under this mismatch model).

2. **THz spectroscopy:** The phonon frequency comb $\omega_n/\omega_{n-1} = \varphi$ should be present only in 13-protofilament microtubules. 14-protofilament tubes should show a distorted (non-golden) frequency spacing.
3. **GTP hydrolysis rate:** The 13-protofilament lattice optimizes the coupling between GTP hydrolysis and conformational change. Non-13 tubes should show altered hydrolysis kinetics, testable with phosphate release assays.
4. **γ -oscillation coupling:** If quantum coherence in microtubules drives 40 Hz γ oscillations (Paper 6), then neurons with non-13 microtubules (if genetically engineerable) should show altered γ -band characteristics.

DISCUSSION

The universality of 13-protofilament microtubules in living cells has puzzled structural biologists for 50 years. The standard explanation—kinetic trapping during nucleation—is unsatisfying because it does not explain *why* 13 is kinetically favored.

The D_5 selection argument provides a candidate answer: within the stated constraint set, 13 is the unique integer satisfying the three independent constraints imposed by pentagonal symmetry, helical geometry, and quantum coherence. The framework suggests this is not a biological accident but a geometrically preferred value—one that echoes the structure of the pentagon also seen in the particle sector of the D_5 construction.

The deepest message: the number of protofilaments in a microtubule and the number of gauge bosons in the Standard Model are both $F_7 = 13$ because both are physical realizations of D_5 acting on different substrates. Biology and particle physics share the same geometric origin.

Cross-validation

This paper links three independently developed strands: (Paper 6) collapse timing, (Paper 28) projection/coherence criteria, and (Paper 51) the D_5 particle-content map. The protofilament selection does not introduce new fit parameters; it reuses the same golden-ratio/Fibonacci structure already constrained by earlier MRF results. The strongest empirical discriminator is the coherence-time ordering $\tau_{\text{coh}}(13) > \tau_{\text{coh}}(8) \gg \tau_{\text{coh}}(14)$ under controlled in-vitro assembly.

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Microtubule Cross-Section: 13 = F_7 Protofilaments

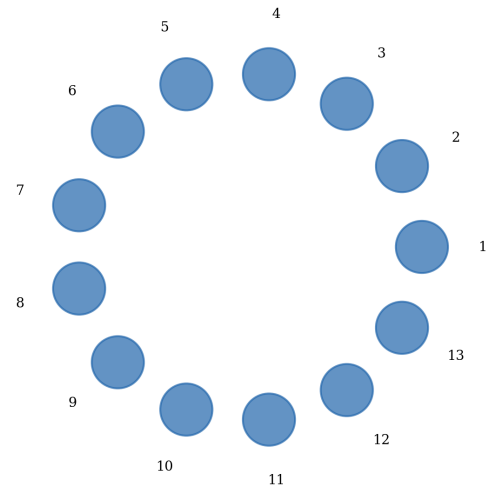


FIG. 1. Microtubule cross-section: 13 protofilaments = F_7 , the seventh Fibonacci number.

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