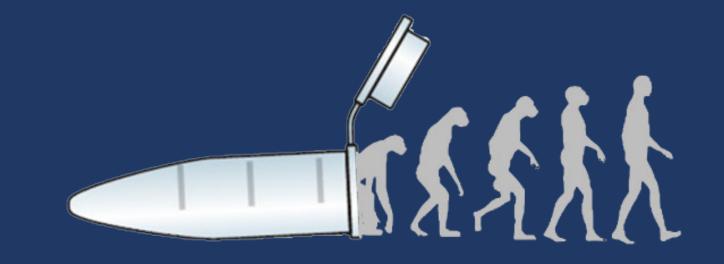


Did Early Functional Proteins Use Metal Ions to Bind ATP?

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Introduction

Origin of Life **Primordial** proteins

Proteins -> Chains of amino acids

- Proteins are building blocks of life
- 20 canonical amino acids
- Trifonov et al.¹ order of amino acids
- Four libraries of **random** proteins²
 - Only **5**, **9**, **16**, **or all 20** amino acids

Early

5 AA

9 AA

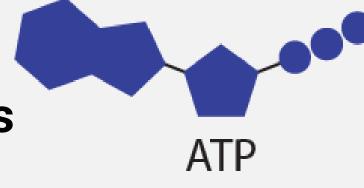
16 AA

20 AA

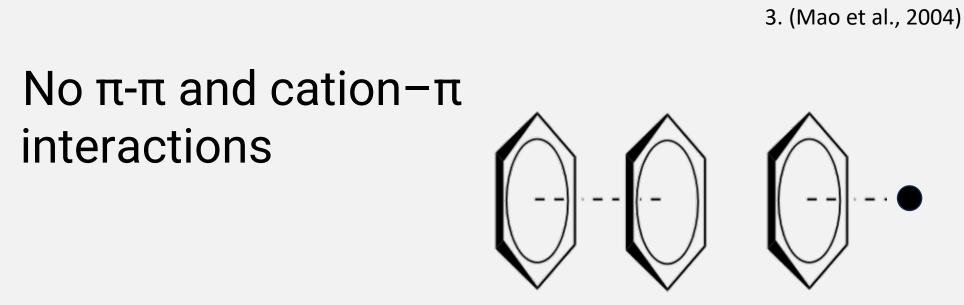
Modern

mRNA display selection:

Stick to ATP → ATP Binders

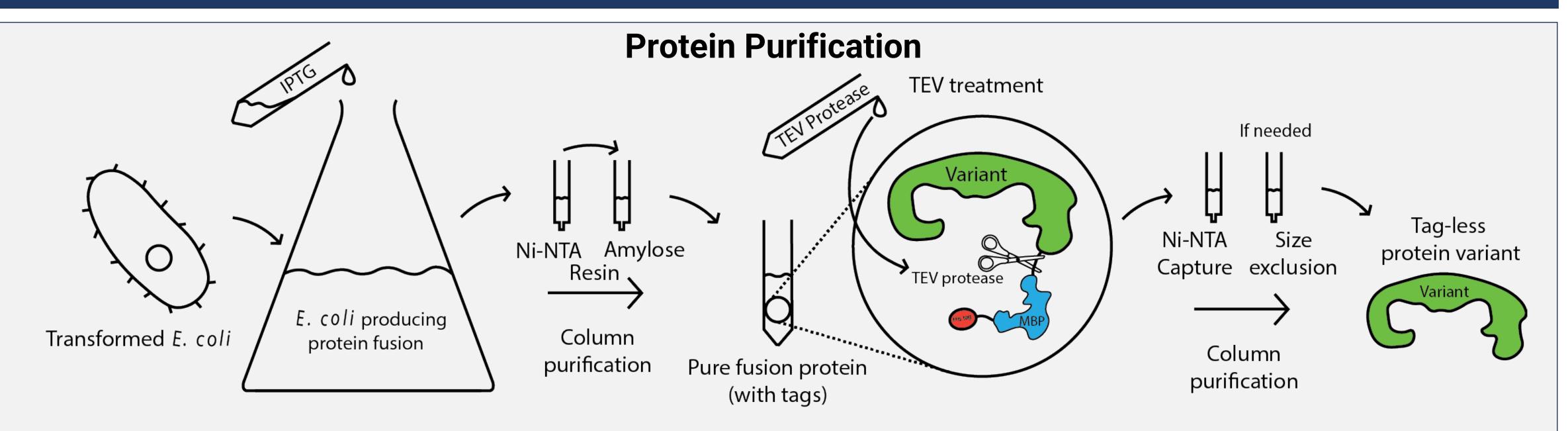


- How do they bind ATP?
- Effect of divalent metals?
- 5AA library lacks aromatic and (+) amino acids

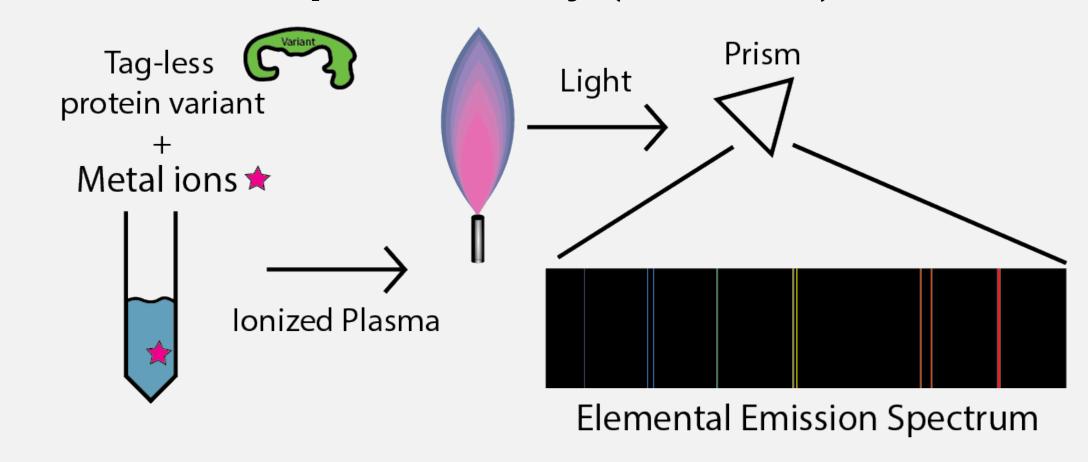


We hypothesized that magnesium ions, commonly used in nature to coordinate the phosphate groups of ATP, may also be utilized by our primordial-like model proteins.

Methods



Inductively Coupled Plasma Optical Emission Spectrometry (ICP-0ES)

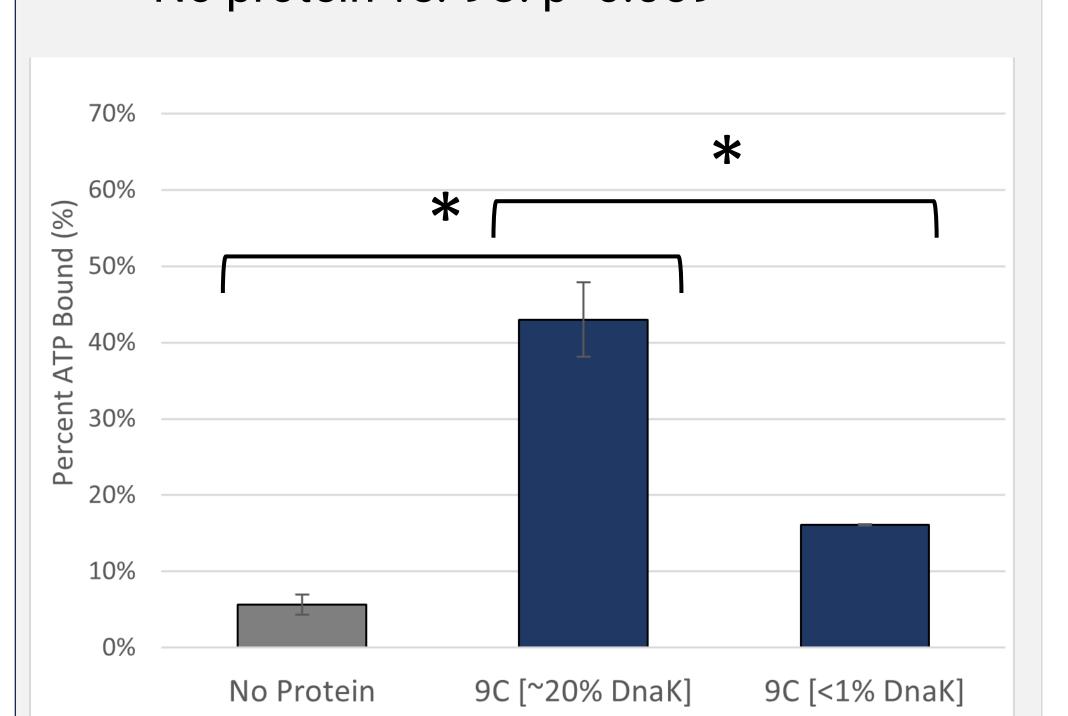


- 8 divalent metal ions (Ni²⁺, Ca²⁺, Cu²⁺, Mn²⁺, Zn²⁺, Co²⁺, Mo⁶⁺, and Mg²⁺) tested
- Triplicate samples with +/- SEM
- Metals at 50 uM except Mg2+ at 400uM
- 7.5uM protein and 1 nM 32P-ATP

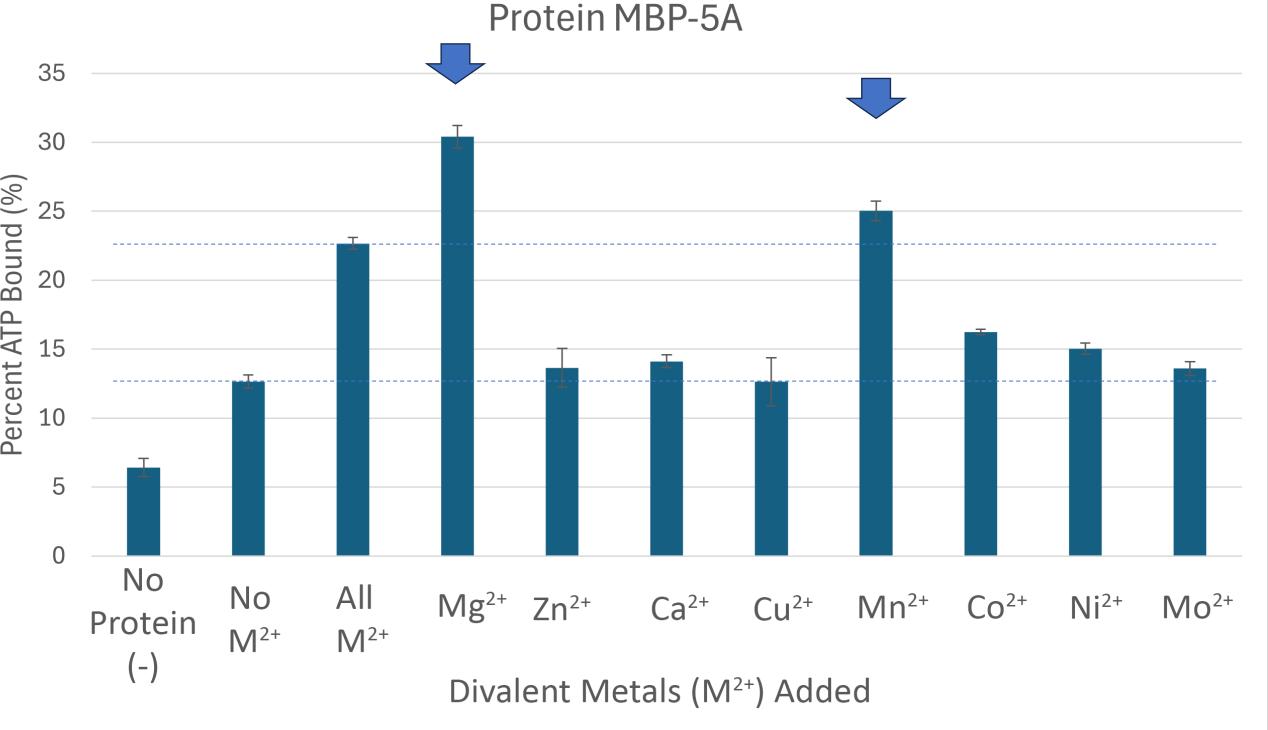
³²P ATP-Binding Assay · Metal ion MI tag ³²P Rad Centrifugation Spin Filter Metal ion ³²P Rad

Results

- 9C's ATP-binding was 27% higher with ~20% DnaK
- Pairwise student's t-tests:
- 9C [~20% DnaK] vs no protein: **p=0.007**
- 9C [~20% DnaK] vs 9C: p=0.002
- No protein vs. 9C: p=0.059



- Magnesium and manganese both recovered ATP-binding in 5A and 5D
- Minimal effect from other divalent metals
- Intermediate ATP-binding of no M²⁺ control



Conclusions

- Magnesium and manganese both recovered or improved ATP-binding in 5A and 5D
 - Also utilized by DnaK, could be the result of contamination
- ATP-binding of **no M²⁺** condition could be due to trace metals in sample
- Preliminary ICP-OES results were inconclusive
 - Dialysis was incomplete
- Strange proteins had strange behavior
 - Highly negatively charged peptides may have had an early evolutionary role in coacervates

Future Directions

- Validate metal dependent ³²P ATP-binding affinity with a **DnaK KO** strain (EN2)
- Measure ³²P ATP-binding affinity of dialyzed protein control
- Repeat ICP-OES trace metal testing with new metals stock solutions, multiple sample replicates, and multiple rounds of dialysis for more stringent removal of metal ions
- Measure ³²P ATP-binding affinity of protein fragments to determine minimal binding domains

Acknowledgements

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References:

¹Trifonov, E. N. (2004). The Triplet Code From First Principles. Journal of Biomolecular Structure and Dynamics, 22(1), 1-11. https://doi.org/10.1080/07391102.2004.10506975 ²Newton, M. S., Morrone, D. J., Lee, K., & Seelig, B. (2019). Genetic Code Evolution Investigated through the Synthesis and Characterisation of Proteins from Reduced-Alphabet Libraries.

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⁴Mao, L., Wang, Y., Liu, Y., & Hu, X. (2004). Molecular Determinants fo ATP-binding in Proteins: A Data Mining and Quantum Chemical Analy Journal of Molecular Biology, 336(3), 787-807. https://doi.org/10.1016/j.jmb.2003.12.056

