MS41-02 | Four for the Price of One: Cross-Seeding to Obtain Crystals of Ancestral Elongation Factor Tus

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Elongation factor Tu (EF-Tu) is an essential translation factor which brings aminoacyl tRNAs to the ribosome. The strong correlation between the thermal stability of EF-Tu and the optimal growth temperature of the host makes EF-Tu an attractive candidate for studying protein evolution. Gaucher et al. [1] have reconstructed several sequences of EF-Tu, which represent the ancient nodes of the bacterial evolutionary tree.

In this study we crystallised, and subsequently determined, high-resolution structures of four of these nodal EF-Tus—EF-Tu 170, 184, 262, and 317. They have high sequence identity with each other (84-92%), and Tm values ranging from 39.1 to 66.7°C. Crystals of EF-Tu 262 which were obtained first, diffracted to 2Å and were used to cross-seed the other three homologs by matrix microseeding [2]. Hits generated in this round of matrix microseeding were then used for further cross-seeding experiments of the proteins with each other in various permutations. Intriguingly, the best crystals were obtained by cross-seeding the nodes that had more similar biophysical characteristics, rather than the highest sequence identity.

Despite the many successes reported with cross-seeding [2], it is still unclear why it works for some homologs and not others. We suggest that the biophysical properties of the homologs may be a more important consideration than their sequence identity when selecting an appropriate cross-seed.

- [1] Gaucher EA, Govindarajan S & Ganesh OK (2003) Nature 451, 704–707.
- [2] D'Arcy A, Bergfors T, Cowan-Jacob SW & Marsh M (2014) Acta Crystallogr. F Struct. Biol. Commun. 70(Pt 9): 1117–1126.