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Origins of Biological Protein Synthesis. C.W. Carter, Jr., A. Kim, J.M. Roach, Dept. of Biochem. Biophys., UNC Chapel Hill, Chapel Hill, NC.

Rodin and Ohno proposed that antisense homology between aminoacyl-tRNA synthetase (aaRS) class I and II-defining peptides arose from their origin in sense/antisense coding on opposite strands of one primordial gene. Tertiary homology between class I and II aaRSs, respectively, and two contemporary sense/antisense proteins[1], showed that tertiary scaffolds organizing class I and II catalytic peptides also can be coded sense/antisense. We focus on two implications of this hypothesis for early protein evolution:

1. Two aaRS sufficed to initiate the protein evolutionary "big bang" using error-prone, binary patterns drawn from the two major subclasses of amino acids, Ia and IIa, which now include, respectively, (LIVMRC) and (AGSTHP).

2. The contemporary proteome may have evolved largely from the two aaRS progenitors. Class I aaRS share a Rossmann fold and so belong to the largest known superfamily, which contributed ~50 distinct enzymes to the Last Universal Common Ancestor (LUCA)[2], and were plausibly progenitors of this superfamily. There is less evidence, so far, for a corresponding superfamily including class II aaRS, which should be apparent if the two classes arose simultaneously from sense/antisense coding by the same gene.
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[1] Carter CW, Jr., Duax WL. *Mol. Cell* 2002;10:705-708.
[2] Aravind L, et al., *Curr. Op. Str. Biol.* 2002;12:392-399.