Correction of the nucleotide and amino acid sequence of *Xenopus laevis* 42Sp50

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In previtellogenic (stage 1) *Xenopus* oocytes there is maximal synthesis and accumulation of 5S RNA and tRNA (1, 2). The 5S RNA and tRNA molecules synthesized during stage 1 are stabilized through their association with three very abundant proteins to form the 42S and 7S ribonucleoprotein particles (RNP). The 42S RNP is composed of the proteins p50 and p43 which are associated with tRNA and 5S RNA, respectively (3). The function of p50 in early oocytes is presumed to be primarily for storage of tRNA; however, purified p50 has been shown to transfer charged amino acids to ribosomes (4, 5).

We have discovered that the *Xenopus laevis* 42Sp50 cDNA clone reported by Dje *et al.* (5) does not encode a full length 42Sp50 protein. The reported sequence contains a mistake at nucleotide position 1050. We found a run of 5 C's at this location instead of the reported 6 C's. The corrected sequence shifts the reading frame and results in translation termination at nucleotide position 1067 producing a 258 amino acid protein. This has been confirmed by *in vitro* translation of X142Sp50 using wheat germ extract. The conceptual translation of the 42Sp50 cDNA reported by Dje *et al.* (5) contained 463 amino acids.

We have recloned the 42Sp50 cDNA. A lambda Uni-Zap cDNA library was constructed using stage 1-2 oocyte mRNA (6) and library reagents from Stratagene. One million plaques were screened (6) with X142Sp50 (5) and 53 new 42Sp50 clones were obtained. The 42Sp50 cDNA clone pMC1 was sequenced in both directions using deaza-dGTP and dTTP kits from United States Biochemical. The largest cDNA clone (pMC1) begins at nucleotide position 269 of X142Sp50 and ends with a poly A tail at position 1827. We mapped the transcription start site of 42Sp50 by primer extension using an oligonucleotide which was selected from the 5' end of the 42Sp50 cDNA of pMC1 and *Xenopus laevis* stage 1 oocyte mRNA (6). We found that the p50 transcription start site is located approximately 30 bases pairs upstream of the 5' end of pMC1. A comparison between pMC1 and the X142Sp50 sequence reported by Dje *et al.* (5) shows that the nucleotide sequences are 99.6% identical and the amino acid sequences are 99.1% identical.

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REFERENCES


![Figure 1. Schematic diagram of the 42Sp50 cDNA clones. The 42Sp50 cDNA clone reported by Dje *et al.* (5) is shown on top and our clone (pMC1) is shown below. The coding region is depicted as a thick bar and the untranslated regions as thin bars. The error in the published sequence is shown above the diagram.](image-url)