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ERRATUM

RNase H2 of *Saccharomyces cerevisiae* is a complex of three proteins

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The publishers would like to apologize for not including the text shown in bold in the Abstract and last paragraph of the Introduction, both given in full below.

The composition of RNase H2 has been a long-standing problem. Whereas bacterial and archaeal RNases H2 are active as single polypeptides, the *Saccharomyces cerevisiae* homolog, Rnh2Ap, when expressed in *Escherichia coli*, fails to produce an active RNase H2. By affinity chromatography purification and identification of polypeptides associated with a tagged *S.cerevisiae* Rnh2Ap, we obtained a complex of three proteins **[Rnh2Ap (Rnh201p), Ydr279p (Rnh202p) and Ylr154p (Rnh203p)]** that together are necessary and sufficient for RNase H2 activity. Deletion of the gene encoding any one of the proteins or mutations in the catalytic site in Rnh2Ap led to loss of RNase H2 activity. Even when *S.cerevisiae* RNase H2 is catalytically compromised, it still exhibits a preference for cleavage of the phosphodiester bond on the 5′-side of a ribonucleotide–deoxyribonucleotide sequence in substrates mimicking RNA-primed Okazaki fragments or a single ribonucleotide embedded in a duplex DNA. Interestingly, Ydr279p and Ylr154p have homologous proteins only in closely related species. The multisubunit nature of *S.cerevisiae* RNase H2 may be important both for structural purposes and to provide a means of interacting with other proteins involved in DNA replication/repair and transcription.

Highly purified RNases H2 from human tissue culture cells (12,16) and calf thymus (17) exhibit biochemical properties distinct from RNase H1 but shares many common properties with archaeal and bacterial RNase HII. Genes encoding clear homologs of bacterial RNases HII are found in eukaryotes, and when the gene is deleted in *Saccharomyces cerevisiae*, a 70% reduction in RNase H activity in crude extracts is observed (7,18). Overproduction of this polypeptide results in only a modest increase in RNase H activity and expression of this polypeptide in *E.coli* yields an RNase H with little (11) or no enzymatic activity (19). In contrast, RNases HII from bacteria and archaea are active when expressed in *E.coli* (3,4,6,20,21). Therefore, it seems likely that eukaryotic RNases H2 may require posttranslational modification or an additional subunit(s). Many reports using highly purified RNases H2 derived from mammalian sources suggest the possibility of at least one additional component (15). To determine the composition and enzymatic properties of eukaryotic RNases H2, we employed the well-studied eukaryotic organism, *S.cerevisiae*, **and discovered three genes (*RNH201*, *RNH202*, and *RNH203*) are necessary and sufficient to form an active enzyme**.