Nucleotide sequence of bovine copper/zinc superoxide dismutase cDNA generated by the polymerase chain reaction

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Superoxide dismutase (SOD; EC 1.15.1.1) is a metalloenzyme, classified as an antioxidant due to its capacity to catalyze the dismutation of superoxide anion to hydrogen peroxide. SOD isozymes can be distinguished by the metal atoms bound at their active sites and by their cellular or subcellular localization: the cytoplasmic form of SOD incorporates copper and zinc atoms (Cu/Zn SOD) (1). The nucleotide sequence of bovine Cu/Zn SOD cDNA, synthesized by the polymerase chain reaction (PCR) (2), is reported here. Template cDNA for PCRs was synthesized from bovine lung microvessel total cellular RNA. Oligonucleotide primer sequences for PCR syntheses were based on several regions of the human Cu/Zn SOD nucleotide sequence (3). Nucleotide sequence determinations were performed on both uncloned and cloned PCR-generated Cu/Zn SOD cDNAs using the dideoxynucleotide chain termination method (4).

These results demonstrate approximately 88% nucleotide sequence similarity within the coding regions of bovine and human Cu/Zn SOD cDNA. A six nucleotide deletion in the bovine sequence relative to human confirms the previous observation that bovine Cu/Zn SOD has two less amino acids

than the human form (5). The cDNA sequence reported here is the first demonstration that this deletion is present in the bovine Cu/Zn SOD mRNA.

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1 gcg acg aag gcc gtc tgc gtg ctg aag ggc gac ggc ccg gtg caa ggc acc atc cac ttc
1 Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly Thr Ile His Phe

61 gag gca aag gga gat aca gtc gtg gta act gga tcc att aca gga ttg act gaa ggt gat
20 Glu Ala Lys Gly Asp Thr Val Val Val Thr Gly Ser Ile Thr Gly Leu Thr Glu Gly Asp

121 cat gga ttc cac gtc cat cag ttt gga gac aat aca caa ggc tgt acc agt gca ggt cct
40 His Gly Phe His Val His Gln Phe Gly Asp Asn Thr Gln Gly Cys Thr Ser Ala Gly Pro

181 cac ttt aat cct ctg tcc aaa aaa cac ggt ggg cca aaa gat gaa gag agg cat gtt gga
60 His Phe Asn Pro Leu Ser Lys Lys His Gly Gly Pro Lys Asp Glu Glu Arg His Val Gly

241 gac ctg ggc aat gtg aca gct gac aaa aac ggt gtt gcc atc gtg gat att gta gat cct
80 Asp Leu Gly Asn Val Thr Ala Asp Lys Asn Gly Val Ala Ile Val Asp Ile Val Asp Pro

301 ctg att tca ctc tca gga gaa tat tcc atc att ggc cgc acg atg gtg gtc cat gaa aaa
100 Leu Ile Ser Leu Ser Gly Glu Tyr Ser Ile Ile Gly Arg Thr Met Val Val His Glu Lys

361 cca gat gac ttg ggc aga ggt gga aat gaa gaa agt aca aag act gga aac gct gga agt
120 Pro Asp Asp Leu Gly Arg Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser

421 cgt ttg gcc tgt ggt gta att gga att gcc aag
140 Arg Leu Ala Cys Gly Val Ile Gly Ile Ala Lys

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