Corrigendum

Biochemical and genetic analysis of *Streptococcus mutans* α -galactosidase

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Two errors appeared in the published sequence of the *Streptococcus mutans* α -galactosidase (*aga*) gene (Fig. 3); a 'G' was omitted from position 961 and a 'T' was incorrectly inserted at position 1314. The correct nucleotide sequence and the corrected deduced amino acid sequence are shown overleaf, with the altered region underlined. Only Fig. 3 was wrong and other data and conclusions in the paper remain valid. Steps are being taken to ensure that the GenBank entry (accession no. M60777) is corrected. The authors are grateful to B. Henrissat for bringing their attention to the mistake.

M G I V I K D N L F Y I H T K D S S L I	20	D G W F G H R F D D N S S L G D W F V N	380
ATGGGCAATGTTATTAAGATAACCTTTTATATACACACCAAGACTCATCATTTGATT	60	GATGGTTGGTTGGTCATCGTTTGTATGACATAGCTCACTTGGTGTGTTGGTTGTCAAT	1140
I E R D G D L L K H L G K K I E A Y	40	E E K L G G S L D S F I K E I H D R G L	400
ATTGAAGAAAGAGATGGTATGCTTTTAAACATCTAGGTAAAAAATTGAAGCCTAT	120	GAAGAAAACCTGGGGTGGTCCCTGTAGACTTTATCAAGGAATTCATGATAGAGGATTA	1200
H F S N T V F E K D H A F S A N P V A D	60	Q F G L W F E P E M V S V D S K L Y R A	420
CATTTTCCAACTGTTTGAAGATCATGCTTTTTCAGCTAATCCAGTGGGGAC	180	CAGTTTGGCCTTGGTTTGAACCAAGATGTTATCAGTTGCAGACGACCAATTTATAGAGCT	1260
N R N A T S Y D T C Q R Q I F G V H G F G D	80	H P D W V I O A D O R E H T Y S R N Q L	440
AATAGAAATATAGTTATGATCAAAAGACAAATATTGGTTCCTGCTTGGTGTAT	240	CATCTGATGGGTCACTCAGGAGATCAGCGAGACACTATTCTCGCAATCATTTG	1320
F R V P S L I L Q H D N N D L T R F K F	100	V L N L A N L D V V A Y I K T V L D K L	460
TTTAGAGTGCCTCACTAATCCTTCAACATGATAATATGATTAAACCGTTTAAATTT	300	GTCTTGAATCTAGCTAATCTCGATGATGTTGCTTATATAAACTGTCTTGTATAAGCTG	1380
K K A K I I K G I K A R G L P N P H S	120	L T E N T I D V V K W D Y N R N I T N I	480
AAGAAGCTAAATATTAAAGGGGGGATCAAGCAAGAGTTTGGCTTAATCCACATAGC	360	CTGACAGAAAATACGATTGATTATGTTAAATGGGACTACATCGCAATATAACCAATATT	1380
S E S A Q S L A L I L E D D L A K S R I	140	G N G R T Y L E T Q M Q S H A Y I L G L	500
ACTGAGAGTGCCTCAAGCTTGGCTCTTATCTTAGAAGATGATTTGGCAAAATCGCGCAT	420	GGCAATGGCAGAACTTACTTGGAAACGCAATGCAGTCGCATGCTTATATACCTGGGGTTG	1500
V S D Y T A Y D D N A T I S T F V K F E	160	Y D M F S Y L T T K H D K V L F E S C S	520
GTCTCTGATTATACGGCTTATGATGATAATGCCACCAATTTCAACCTTTGTCAAATTTGAA	480	TATGATATGTTTCTTACTTAACAACAAACGATAGGTCTTGTGTGAATCCTGTCTCA	1560
N L S D K P V I L H R A L S T M F D L P	180	G G G G R N D L G M M C Y P Q V W S S	540
AATTTATCTGAAGCCTGTTATCTTCATCGTGTCTTATCAACAATTTGATTGATTACCT	540	GGAGTGGCGTCCGCAACATTTGGGGATGATGTTATTTCTCAAGTGGTGGTCAAGT	1620
A S H V D V I T F Q G A Y A R E K S L R	200	D N T D A I A R L P I Q Y G S S Y L Y P	560
GCAGCCATTTATGATGATCACTTTTCAGGAGCTTATGCTCGGAGAAGAGCTTCGG	600	GATAATACAGATCTATTGCAAGACTGCTATACAGTATGTTCTCTTATCTTTACCCA	1680
R H Q I E Q G L F K I G S N R G A S G H	220	T I S M G A H V S A V P N H Q M N R H T	580
CGCCACCAAGTTGAACAGGTCTGTTTAAATAGGCTTAATCGAGGAGCTTCAGACAT	660	ACTATTTCTATGGGAGCCATGTTTACGGCTTCCTAACCATCAAAATGAACCGTCTATACC	1740
A Q T P S L I L T E H D S N E F Y G E A	240	P L T T R A H V A M M G N L G Y E L D L	600
GCTCAACCCCTTCCTTAATTTTAAACAGAGCATGATGCAATGAGTTTATGGGGAGGCT	720	CCTCTTACAACAGAGCTCATGTTGCTATGATGGGAAATTTAGGTTATGAATGGGACTTA	1800
L A L Q L I Y S G N F Q A F V Q K N Q L	260	A V L T K N E K K A V A N Q I K H Y K K	620
TTGGCTTTACAATTAATCTATAGCGGAATTTTCAAGCTTTTGTTCAAAAAATCAATTA	780	GCAGTCTTAACCAAAAATGA AAAAGGCTGTGGCAATCAGATTAAACATTATAAAAAG	1860
N V V R L G I G I N D D N F S W E L Q A	280	I R S V V V Q F G K L Y R L I N P E V G I	640
AAGTGGTTCGCTTAGGCATCGGAATAATGATGATAATTTTTCATGGGAAGTGGAGCT	840	ATAAGTCTGTTGTACAATTTGGCAAGCTTTACCGCTTAATTAATCCGAACTGGAAAT	1920
N Q S F E T P V A L I T Y T D K G L T D	300	N E V A V Q Y T Y D N Q V L V T Y V R I	660
AATCAGAGTTTGAACACCTGAGCTTTGATAACCTACATGATGATAAGGGATTAACGGAT	900	AATGAGTAGCAGTCAATATACCTATGACAACTCAGTACTGTTTACCTATGTCCTGAT	1980
L T Q E S H N F I K R H I I P K N F A N	320	Q S T I E M M E T T V K L R G L D A D A	680
CTGACACAAGAAAGTCATAATTTTATTAAGCTCATATTATTCCTAAGAAATTTTGCTAAT	960	CAATCAACCTATAGAGATGATGGAGCAACTGTAAAGTTGAGAGGACTAGATGCAGATGCC	2040
K E R P I L I N N W E A T Y F D F N R S	340	I V V L I E T G Q A F S G A E L M Y A G	700
AAGGAACGCTCTATCTAATAATTTGGAGGCAACATATTTTGATTTTAAATCGGAGT	1020	ATTTATGTTCTTATAGAAACTGGACAGCCCTTTTCAGGTGGGAGTTAATGATGCGGGA	2100
Q L L G L A D E A R K L G I E L F V L D	360	L T I D M P Q G D Y L S K Q Y V F I K K	720
CAATGCTGGGCTGGCAGATGAAGCCAGAAAACCTGGGCAATGCACTTTTGTGCTTGAC	1080	TTGACCATGATATGCCGCAAGGTGATTTATGAGTAAACAATACTATTTTATTAATAAAG	2160

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TAG

Fig. 3. Corrected nucleotide sequence of the *aga* gene of *S. mutans* strain Ingbritt and the deduced amino acid sequence and nucleotides are numbered on the right of the sequence. The region affected by the error is underlined.