



Genética Molecular e de Populações RCG01777 Ano 2015

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1. Identifique a posição da mutação C178X no gene F9 da coagulação e desenhe um par de *primers* para amplificar a região da posição da mutação (tamanho do produto de amplificação de aproximadamente 350pb) para validá-la por sequenciamento numa população de 100 hemofílicos. Para tanto responda as seguintes questões:
 - a) Para cada primer, informe a percentagem de [CG], temperatura de melting (T_m), temperatura de anelamento ($T_{an.}$);
 - b) Qual o tamanho exato do produto de PCR?;
 - c) Considerando as três temperaturas que são definidas para a reação de PCR, qual seria as temperaturas para o PCR em questão?;
 - d) Com relação a mutação descrita no enunciado, responda suas características em relação a substituição de nucleotídeos e aminoácidos. Use os quadros anexo para responder esta questão;
 - e) Tomando como base a resposta sobre a mutação, esta pode ser considerada patogênica? Por que?

Gene F9



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1 aaagacaagctacaggctggagacaatatatttaatccacctatctatgaaaggactcat
61 atctagaatatataaacaaccttaagaatctgacagtaaaaaaaaaaaatcagactaact
121 ggaccactcatacattgctgatggaaatgtaaagtggtagacgccattttggtaaacatca
181 ttgctcgcgtgacgaagatacggcgggtccgactgaggaaccgtgcggccacggtaaacgt
241 agcgactcggccgatctcgattcgggaagacgcgtcccttcccgtttccgacccaaatcgg
301 ccgcgggtggcagaagcccacgaaatcagaggtgaaatttaataatgaccactgcccattc
361 tcttcacttgcccaagaggccattggaaatagtccaaagaccattgagggagatggac
421 attatttcccagaagtaaatacagctcagcttgactttggtacaactaatccaccttac
1 M Q R V N M I M A E S P G L
481 cactttcacaatctgctagcATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCC
15 I T I C L L G Y L L S A E C T V
541 TCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGgtttgtttcctt
601 ttttaaaatacattgagtatgcttgccttttagatatagaaatatctgatgctgtcttct
661 tcactaaattttgattacatgatttgacagcaatattgaagagtctaacagccagcagcgc
// 721 aggttggttaagtactggttctttgtagctaggttttcttcttcttatttttaaaacta
// 6541 actaaaagtaaaattgaattttaattcctaaatctccatgtgtatacagtactgtggaa
6601 catcacagattttggctccatgccctaaagagaaaattggccttcagattatttgattaa
6661 aaacaaagacttttcttaagagatgtaaaattttcatgatgttttctttttgctaaaact
31 F L D H E N A N K I L
6721 aaagaattattcttttacatttcagTTTTCCTTGATCATGAAAACGCCAACAAAATTCG
42 N R P K R Y N S G K L E E F V Q G N L E
6781 AATCGGCCAAAGAGGTATAAATTCAGGTAAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAG
62 R E C M E E K C S F E E A R E V F E N T
6841 AGAGAATGTATGGAAGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTTTTGAAAACACT
82 E R T
6901 GAAAGAACAgtgagtatttccacataataaccttcagatgcagagcatagaatagaaaat
6961 ctttaaaaagacacttctctttaaaattttaaagcatccatataatttatgtatgtaa
7021 atgttataaaaagataggaaatcaataccaaaacactttagatattaccgttaatttgctc
85 T E F W K Q Y V D
7081 tcttttattctttatagACTGAATTTTGGAAGCAGTATGTTGGtaagcaattcattttat
7141 cctctagctaataatataaacaatatgagaattatgtgggttttttctctgcataaataga
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94 G D Q C E S N P C L N G G S C K
10801 ctatctcaaagATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA
110 D D I N S Y E C W C P F G F E G K N C E
10861 GGATGACATTAATTCCTATGAATGTTGGTGTCCTTTGGATTTGAAGGAAAGAACTGTGA
130 L D
10921 ATTAGGtaagtaactatttttgaatactcatggttcaaagtttccctctgaaacaagtt
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18001 ccaatgtatatttgaccatacatgagtcagtagttccatgtacttttagaaatgcatg
132 V T C N I K N
18061 ttaaatgatgctgttactgtctattttgcttcttttagATGTAACATGTAACATTAAGAA
139 G R C E Q F C K N S A D N K V V C S C T
18121 TGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTTGCTCCTGTAC
159 E G Y R L A E N Q K S C E P A V
18181 TGAGGGATATCGACTTGCAGAAAACCAGAAGTCTGTGAACCAGCAGgtcataatctgaa
18241 taagattttttaagaaaatctgtatctgaaacttcagcattttaacaaacctacataat
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20701 aagtgacaaggatgggcctcaatctcaatttttgtaatacatgttccatttgccaatgag
175 P F P C G R V
20761 aaatatacaggttactaatttttcttctatttttctagTGCCATTTCCATGTGGAAGAGTT
182 S V S Q T S K L T R A E T V F P D V D Y
20821 TCTGTTTCACAACTTCTAAGCTCACCCGTGCTGAGACTGTTTTTCCCTGATGTGGACTAT
202 V N S T E A E T I L D N I T Q S T Q S F
20881 GTAAATTCTACTGAAGCTGAAACCATTTTGATAACATCACTCAAAGCACCCAATCATT
222 N D F T R V V G G E D A K P G Q F P W Q
20941 AATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAATTCCCTTGGCAG
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242 V V
30421 attttttctagatcaaatgtattatgcagtaagagtccttaattttgttttcacagGTTG
244 L N G K V D A F C G G S I V N E K W I V
30481 TTTTGAATGGTAAAGTTGATCTTCTGTGGAGGCTCTATCGTTAATGAAAAATGGATTG
264 T A A H C V E T G V K I T V V A A G
30541 TAACTGCTGCCCCTGTGTTGAAACTGGTGTAAATTTACAGTTGTGCGCAGgtaaataca
30601 cagaaagaataataatctgcagcaccactagctctttaatatgattggtacacatattt
30661 tactaagggtctaataaaaattggtggtgaataaaattgggctaaaggcagaagggtcataat
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281
31201 agaaaatctgtgtatgtgaaatactgtttgtgacttaaaatgaaatttatttttaatagG
281 E H N I E E T E H T E Q K R N V I R I I
31261 TGAACATAATATTGAGGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTGCAATTAT
301 P H H N Y N A A I N K Y N H D I A L L E
31321 TCCTCACCACTACAATGCAGCTATTAATAAGTACAACCATGACATTGCCCTTCTGGA
321 L D E P L V L N S Y V T P I C I A D K E
31381 ACTGGACGAACCCTTAGTGCTAAACAGCTACGTTACACCTATTTGCATTGCTGACAAGGA
341 Y T N I F L K F G S G Y V S G W G R V F
31441 ATACACGAACATCTTCCTCAAATTTGGATCTGGCTATGTAAGTGGCTGGGGAAGAGTCTT
361 H K G R S A L V L Q Y L R V P L V D R A
31501 CCACAAAGGGAGATCAGCTTTAGTCTTCAGTACCTTAGAGTTCCACTGTTGACCAGC
381 T C L R S T K F T I Y N N M F C A G F H
31561 CACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACATGTTCTGTGCTGGCTTCCA
401 E G G R D S C Q G D S G G P H V T E V E
31621 TGAAGGAGGTAGAGATTCATGTCAAGGAGATAGTGGGGGACCCCATGTTACTGAAGTGGA
421 G T S F L T G I I S W G E E C A M K G K
31681 AGGGACCAGTTTCTTAACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAA
441 Y G I Y T K V S R Y V N W I K E K T K L
31741 ATATGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAAAACAAAGCT
461 T *
31801 CACTTAAaccttggctttttgtggattccattgatgtgaatcagtcaccctgtatttgat
31861 gatgcatgggactactgacaaaatcactctgacccccccaagctgctgccttctcctgcc
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	T			C		A		G	
T	TTT	Phe	F	TCT	Ser	S	TAT	Tyr	Y
	TTC			TCC			TAC		
	TTA	Leu	L	TCA			TAA	STOP	
	TTG			TCG			TAG		
C	CTT	Leu	L	CCT	Pro	P	CAT	His	H
	CTC			CCC			CAC		
	CTA			CCA			CAA	Gln	Q
	CTG			CCG			CAG		
A	ATT	Ile	I	ACT	Thr	T	AAT	Asn	N
	ATC			ACC			AAC		
	ATA			ACA			AAA	Lys	K
	ATG	Met	M	ACG			AAG		
G	GTT	Val	V	GCT	Ala	A	GAT	Asp	D
	GTC			GCC			GAC		
	GTA			GCA			GAA	Glu	E
	GTG			GCG			GAG		

