



Prediction Model for Alcohol flushing Syndrome

PCR

Primers and Probe :

rs number	ASP1_SEQ	ASP2_SEQ	LSP_SEQ	STA_SEQ
rs10849915	GACTTACCAGTTTT CTGGCTCG	TGACTTACCAGTTTT CTGGCTCA	ATGCAGAGAGCTGTA CATTGTAGCT	ACAAAGTGAGGGTGA CTTACCA
rs2074356	AGCTGGTAAACAGTA TGACTTCAGATG	CAGCTGGTAAACAGT ATGACTTCAGATA	TCTGTGGTCTGGTGG TTAACA	AGTAATTTTCTCAAGT CCACACAGC
rs4646776	GGCTGGAGCCACAA CAG	GGCTGGAGCCACAA CAC	TGGCCTTGAAGGTAG CCCT	CCAACGCCATTGGGC AC
rs671	CCCACACTCACAGTT TTCAC TTT	CCCACACTCACAGTT TTCAC TTC	ACGGGCTGCAGGCA TACA	CCTCAAGCCCCAACA GG

Data Analysis

		rs671	rs4646776	rs2074356	rs10849915
	Major allele	A	G	C	C
	Minor allele	G	A	G	T
Positive	Freq. major	0.353	0.684	0.357	0.296
Negative	Freq. major	0.019	0.986	0.023	0.098
Control	Freq. major	0.19	0.828	0.185	0.177

*Supplemental data [1] ;

	Sensitivity	Specificity	Accuracy
rs671	0.6392157	0.9627907	0.787234
rs4646776	0.5568627	0.804651	0.670213
rs2074356	0.6431373	0.9534884	0.785106
rs10849915	0.572549	0.972093	0.755319



Prediction Model for hair shape characteristics

PCR

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rs2074356	AGCTGGTAAACAGTA TGACTTCAGATG	CAGCTGGTAAACAGT ATGACTTCAGATA	TCTGTGGTCTGGTGG TTAACA	AGTAATTTTCTCAAGT CCACACAGC
rs4646776	GGCTGGAGCCACAA CAG	GGCTGGAGCCACAA CAC	TGGCCTTGAAGGTAG CCCT	CCAACGCCATTGGGC AC
rs671	CCCACACTCACAGTT TTCAC TTT	CCCACACTCACAGTT TTCAC TTC	ACGGGCTGCAGGCA TACA	CCTCAAGCCCAACA GG

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Prediction Model for hair shape characteristics

TaqMan real-time PCR assay

Materials Required:

TaqMan® Universal PCR Master Mix (Thermo Fisher Scientific) *

TaqMan TAMRA probe *

Forward and Reverse primer*

Primers and Probe :

Target ID	Sequence (5'→3')	Reference
forward primer	TGCTGACACCTCTGGTTTTTGTA	[1]
reverse primer	GTGCCAGCTGCAGGGTTTAG	
probe	(FAM)-CACGGTGATGCATAGGCACCTGC-(TAMRA)	[2]

SBE Reaction Mixture:

Reaction Component	Vol. (ul)	Final
2X TaqMan Universal Master Mix II	5	1 X
Forward primer (50 µM)	0.16	250 nM
Reverse primer (50 µM)	0.16	250 nM
TaqMan probe (10 µM)	0.25	800 nM
template DNA	()*	50 ng
distilled water	up to 10	
Total	10	

*depends on concentration of DNA sample

Thermal Cycling:

50°C for 2 minutes
95°C for 10 minutes

95°C for 15 seconds
60°C for 1 minutes
for 45 cycles

[1] Gerste-Thompson JL et al. 2010. Clin Chem 56(9):1466-74.

[2] Zubakov D et al. 2010. Curr Biol 20(22):R970-1.



signal-joint TCR Receptor Excision Circles (sjTREC) quantification

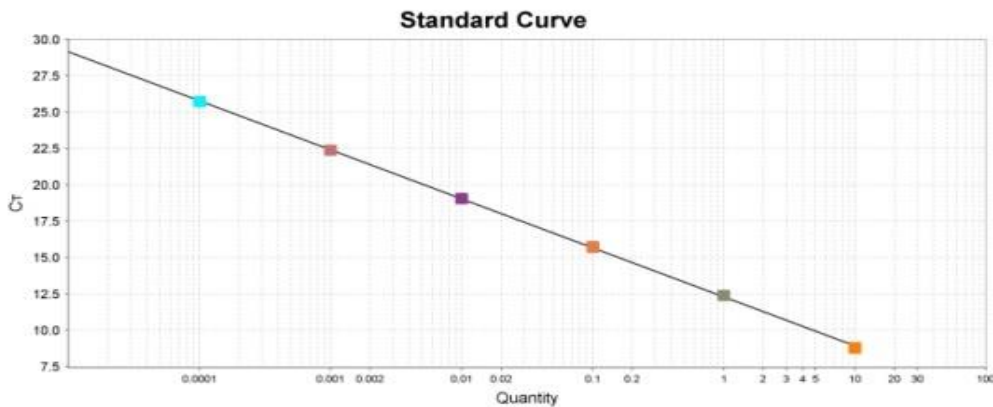
Data Analysis

Materials Required:

IBM SPSS Statistics

Microsoft Excel

1. Convert the obtained Ct value to copy number using the equation (Eq.)



2. Calculate $\text{Log}[\text{sjTREC content per } 1 \mu\text{g of DNA}]$ using the copy number calculated in 1.

3. Calculate the predicted age by applying the sjTREC content into the age estimation model [3]

