

Mutation of the PTC gene • "PTC gene" = gene TAS2R38 on chromosome 7

• t: "non-taster" allele = AVI allele

→ 3 amino acid substitutions

• SatI digest of TAS2R38 DNA PCR product: • PAC PCR product cleaved by SatI • AVI PCR product <u>not</u> cleaved by SatI

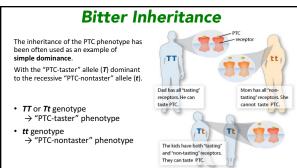
• 3 single nucleotide polymorphisms (SNP)

• SNP r same size PCR product for PAV & AVI alleles

• Proline...Alanine...Valine → Alanine...Valine...Isoleucine • Primers r bracket 303 bp PCR product within TAS2R38 gene DNA

But one of the SNP is within the PCR product → disrupts a SatI restriction site

• T: "taster allele" = PAV allele



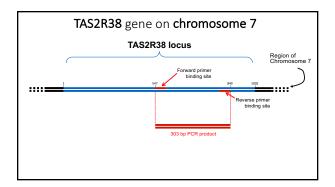
Reagent	Stock concentration	Reaction concentration	Volume per reaction	Volume per cocktail (n+1)
Water	-	-		
Buffer	5x	1x		
MgCl ₂	25 mM	1.5 mM		
Nucleotides	10 mM	200 μΜ		
PTC Forward Primer	10 μΜ	1 μΜ		
PTC Reverse Primer	10 μΜ	1 μΜ		
Taq polymerase	5 U/μl	1.25 U		
Total Cocktail			40 µl	
DNA template			10 μΙ	Ø
Reaction Volume			50 μl	

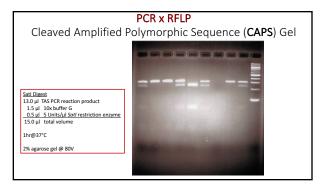
Step	Temperture (°C)	Time
Denature DNA Templates	95°	45 seconds
Anneal primers	55°	45 seconds
Product extension	72°	90 seconds
₹ Repeat for 40 cycles		
Final extension	72°	10 minutes
Final hold	4°	∞

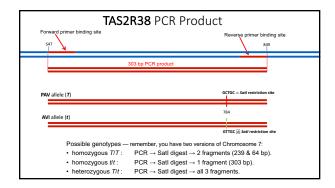
Figure 1. The Human PTC Gene. The gene that is primarily responsible for human PTC taste sensitivity is located on the long arm of chromosome 7. The sequence of the nontaster allele is shown below with attention drawn to common single nucleotide polymorphism sites (SNPs), Fnu4H1 restriction endonuclease sites, primer sites for gene amplification by PCR. The Figure also indicates the amino acid substitutions corresponding to the SNPs, the restriction digest fragment lengths obtained in RFLP analysis, and the amino acid sequence for the nontaster gene product. The amino acid sequence also indicates the initiation site for translation of the chimpanzee nontaster allele (light blue M). Note that the amino acid sequence given is still for the human nontaster allele, not the chimpanzee allele.

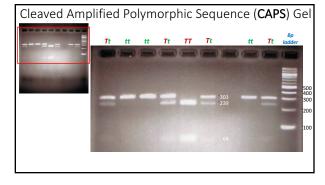
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The TAS2R38 or PTC Gene
                             (7q35-q36)
                                                Taster/nontaster PAV/AVI
ORIGIN
  1 atgttgactc taactcgcat ccgcactgtg tcctatgaag tcaggagtac atttctgttc
 61 atttcagtcc tggagtttgc agtggggttt ctgaccaatg ccttcgtttt cttggtgaat
121 ttttgggatg tagtgaagag gcaggcactg agcaacagtg attgtgtgct gctgtgtctc 145c/g 49pro/ala
181 agcatcagcc ggcttttcct gcatggactg ctgttcctga gtgctatcca gcttacccac
241 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg
301 attgcaaacc aagccaacct ctggcttgct gcctgcctca gcctgcttta ctgctccaag
361 ctcatccgtt tctctcacac cttcctgatc tgcttggcaa gctgggtctc caggaagatc
421 toccagatgo toctgggtat tattotttgo toctgoatot goactgtoot otgtgtttgg
481 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca
601 tggtctgtgc ctcctttcct attgtttctg gtttcttctg ggatgctgac tgtctccctg
661 ggaaggcaca tgaggacaat gaaggtctat accagaaact ctcgtgaccc cagcctggag
721 geccacatta aageeetcaa gtetettgte teetttttet gettetttgt gatateatee
781 tgtgttgcct tcatctctgt gcccctactg attctgtggc gcgacaaaat aggggtgatg 785c/t 262ala/val
841 gtttgtgttg ggataatggc agcttgtccc tctgggcatg cagccatcct gatctcaggc 886g/a 296val/ile
901 aatgccaagt tgaggagagc tgtgatgacc attctgctct gggctcagag cagcctgaag
961 gtaagagccg accacaaggc agattcccgg acactgtgct ga
red bold = SNPs
                    green = forward primer
                                              blue = reverse primer(complement)
dark red = Fnu4H1 restriction site 5'-GCNGC-3'
                                   3'-CGNCG-5'
RFLP: nontaster = PCR + digest yields 303bp fragment
      Taster homozygote = PCR + digest yields 238bp and 64bp fragments
      Taster heterozygote = all three fragments
              translation="MLTLTRIRTVSYEVRSTFLFISVLEFAVGFLTNAFVFLVNFWDV
              VKRQALSNSDCVLLCLSISRLFLHGLLFLSAIQLTHFQKLSEPLNHSYQAIIMLWMIA
              NQANLWLAACLSLLYCSKLIRFSHTFLICLASWVSRKISQMLLGIILCSCICTVLCVW
              CFFSRPHFTVTTVLFMNNNTRLNWQNKDLNLFYSFLFCYLWSVPPFLLFLVSSGMLTV
              SLGRHMRTMKVYTRNSRDPSLEAHIKALKSLVSFFCFFVISSCVAFISVPLLILWRDK
              IGVMVCVGIMAACPSGHAAILISGNAKLRRAVMTILLWAQSSLKVRADHKADSRTLC"
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Genetic Penetrance and Expressivity genotype phenotype • Single genes do not function in isolation! • One step in multi-step pathways • Expression subject to pleiotropic, epistatic, epigenetic, & environmental modification • Penetrance: what fraction of the population exhibits the phenotype related to that allele • Expressivity: what variation in the population is there in how

strongly the phenotype is demonstrated for that allele

