

placed in a boiling water bath for 15 minutes. After 15 minutes, the tubes were removed from the boiling water cooled and used for the PCR procedure.

PCR Procedure

For each trial, 0.2 mL Ready-to-Go PCR tubes from GE Healthcare were prepared with 22 μ L of dH₂O, 2 μ L of primer mix, and 1 μ L of DNA.

The tubes for the PAH and BRCA1 trials were thermocycled according to the following settings: 95°C for 10 minutes; 35 cycles of: 96°C for 45 seconds, 55°C for 45 seconds, and 72°C for 45 seconds; 72°C for 10 minutes; hold at 4°C.

The tubes used for the NF trials were thermocycled according to the following settings: 95°C for 10 minutes; 35 cycles of: 96°C for 45 seconds, 57°C for 45 seconds, 72°C for 1.5 minutes; 72°C for 10 minutes; hold at 4°C.

T1/P

Digestion (for PAH trials only): ordi(7(l7 8997(:20 Td (°)Tj -0.004 Tc 0.004 Tw5uTc 0Tw5uTc 0Tw5u /P <m60Ct9.271.157 Td [(T

pairs that were supposedly present in the mutated genome. After careful research, it was determined that the information cited by both Coriell and the article itself were outdated since the article was published over a decade before the human genome was even fully sequenced. It was then discovered that this article was referenced in a much more recent article, published *Clinical Chemistry* in 2010. In this article, it was stated that the insertion was located 44 base pairs upstream of the 4th exon, not the 6th (Chouet al., 2010). With this newfound information, the predicted location of the mutation was then found using Genbank, which then provided a sequence that I then entered into PrimerBlast.

The primer sequences generated by PrimerBlast (listed in Table 2) were predicted to amplify a segment of DNA that was 275 base pairs long without the mutation. With the mutation, the DNA segment that would be amplified would be approximately 575 base pairs long. These results were clearly seen upon electrophoresis of the four amplified samples of DNA. The "normal" DNA only produced a prominent band in the 275 base pair range, while the DNA containing the insertion showed two bands; one in the 275 base pair range, and the other in the 575 base pair range. The two DNA samples extracted from Angelica and Jessica showed only one band each in the 275 base pair range (Figure 2). These acted as controls for the experiment, since it was known that neither individual suffered from Neurofibromatosis Type 1.

1 3 5 7 9

Figure 2. Photograph taken of the electrophoresed gel from the final successful NF1 trial. Lane 1: Contained mutant NF-1 DNA, 2 bands seen, one was around 275 base pairs long, and the other was around 575 base pairs long; Lane 3: Contained normal DNA, one band around 275 base pairs long was seen.

canj(1)ra(w)z(a)8(Nt(N)72))Bto54((155(m)6(PTd||i)7f)1329)8)Ti)7h2yaH5(c)-3(e)-3(t)7hTm [(D 6 >>BD(t)7((
T2riIsF
(Nt)I7C Nt Ntny NtbTb(c)st)PcS(k)4(25)4(n)(e)3(98))T3D(n)322)430e295(5643L)1.1c(5p)

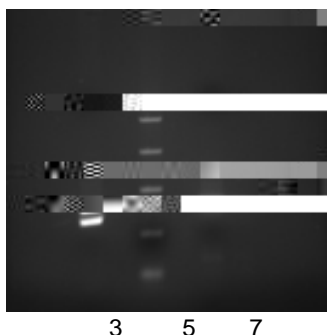


Figure 3. Photograph taken of the electrophoresed gel from the final successful BRCA1 trial. Lane 3 contained mutant BRCA1 DNA, one band that was 205 base pairs long, and one band that was 245 base pairs long were seen; Lane 5: PCR marker; Lane 7: Contained normal DNA, only one band that was 245 base pairs in length was seen.

Gene	Primer Sequences
PAH	Forward: 5' GTGATTCCCGAAAGTGAGAGC 3'
	Reverse: 5' ACTTTCTGCAGGGCCATTGA 3'
NF-1	Forward: 5' ATCACTTTTCTTTTGCCTGT 3'
	Reverse: 5' CAGCATCAGCATGTAGCGTG 3'
BRCA1	Forward: 5'AGAAACTGCCATGCTCAGAGAATC3'
	Reverse: 5'ATGAGGATCACTGGCCAGTAAGTC3'

Table 2. Primers that successfully identified mutations in the PAH, NF1 and BRCA1 genes.

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Biography

Jessica Imperato is currently a junior, and will graduate in May 2015 with dual B.S. degrees in Forensic Science and Biology. Originally from Thiells, New York, she hopes to pursue PhD in cellular and molecular biology, and eventually enter the clinical research field.

