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##### Distribution of a Human RFLP in the ACTG2 (ACTA3) Gene Among African-American and Caucasian populations

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### Abstract.

Restriction fragment length polymorphisms (RFLPs) are variations in DNA sequences that can be detected by digestion with restriction enzymes. RFLPs are used to study variation and evolution within populations. This study focused on a specific RFLP occurring within the human ACTG2 (formerly ACTA3) gene. ACTG2 encodes a γ-actin specifically expressed in mammalian enteric muscle. The RFLP occurs within the first intron and, while not a linkage marker for any genetic condition, has implications as a marker in human evolution. Humans normally have two copies of each chromosome. Each chromosome contributes one allele towards the pair examined using Mendelian genetics. An earlier study of the RFLP, conducted among Japanese and Caucasian populations, published the finding that the RFLP allele occurred twenty-one times more frequently in Caucasian populations. This study expanded analysis on this RFLP by surveying allelic frequencies in African Americans. Two hypotheses to explain earlier allelic results were tested: (1) the RFLP occurred after human migration from Africa, and some unknown selection pressure existed that maintained the RFLP among Caucasians, or (2) the original, small Caucasian sample size accounted for the observed result. In the African Americans sample, as well as an expanded Caucasian sample, both forms of the RFLP were distributed evenly after random sampling analysis. The results suggest a sampling error as the most likely explanation for earlier studies conducted on Caucasians.

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**Based on the abstract above, please answer the following questions:**

1. What is the hypothesis tested in this paper?
   1. The RFLP occurred before people migrated to Asia and them some selection pressure maintained among Asians
   2. The RFLP is used to study variation and evolution of populations
   3. The RFLP occurred after humans migrated from Africa and selection pressure maintained the RFLP among Caucasians
   4. The original study had too few samples from African Americans and that explains the observed result
2. Can you predict what type of data would support the above hypothesis?
   1. Based on this hypothesis we can predict that the scientists will observe higher RFLP frequencies in Caucasians than in African Americans
   2. Based on this hypothesis we can predict that African Americans will have about 20 times higher frequencies of RFLP than Caucasians
   3. Based on this hypothesis we can predict that by adding more samples from African Americans we will see no difference in RFLP
   4. Based on this hypothesis if the RFLP are not different among populations then ACTG2 is not a relevant in human evolution
3. What is the model used in this study?
   1. They used actin protein analysis
   2. They used RFLP in a mouse gene
   3. They used yeast actin gene
   4. They used RFLP in human gene
4. What major analytical approaches were used in this study?
   1. Comparing frequencies of disease using genetic analysis among different populations
   2. Comparing frequencies of polymorphisms in one specific genes among different populations
   3. Comparing frequencies of acting gene to in African Americans and Caucasians
   4. Analysis of the effect of Mendelian genetics on chromosome distribution
5. What is one of the key research findings described in this paper?
   1. After random sampling African Americans have significantly higher frequencies of RFLP than Caucasians
   2. After random sampling Caucasians had significantly higher distribution of RFLP than African Americans
   3. There was a sampling error in the study populations and data cannot be interpreted
   4. There was a sampling error in the original study examining the RFLP in Caucasians and Japanese populations