MOBILITY AND THE HUMAN DOPAMINE RECEPTOR DRD4

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There is considerable variance between individual propensities to travel, and there are reasons to think there is a genetic basis underlying that difference. Our project aims to ascertain whether there is a relationship between individual mobility and variation at one candidate gene, the gene that codes for the dopamine-receptor D4 (DRD4). The long (7R) version of the gene is more likely to be found in populations that have migrated long distances from their homeland. Moreover, populations that currently lead sedentary lifestyles have lower 7R frequencies than current nomadic populations. There is some proof that the 7R allele does indeed confer a selective advantage to nomads, as DRD4 7R positive genotypes have been associated with better nutritional intakes among nomadic groups. DRD4 7R has also been associated with personality traits, such as novelty-seeking and risk-taking, that might favor migration. However, no one has yet researched whether individual variation in mobility within a population is associated with the same gene variants. We hypothesize that there will be a correlation between the 7R allele of the DRD4 gene and range size in humans. Individuals with 7R will likely navigate further on a day to day basis, thus establishing a wider home range than individuals without the 7R allele. To test this hypothesis, we document the mobility of subjects based upon GPS tracking and identify the individual DRD4 alleles through DNA sequencing.

Each participant is given a small portable GPS, and is asked to pocket it each time they leave their home. The GPS logs the participant's movement, and the data is collected after a week's time. The participant also fills out a brief online questionnaire each evening to clarify the purpose of each displacement. Additionally, they complete a lifetime mobility questionnaire. We gather DNA samples by collecting cells from the inside of the subject's cheek, and use routine genetic analysis methods. We have yet to test our samples. We will first extract the DNA from the sample, then conduct a Polymerase chain Reaction (PCR) of the DRD4 genomic region. The PCR products will be visualized by gel electrophoresis. We will also use DNA sequencing in order to determine which allele is present.

Our project is still in progress, and we impatiently await results.