

# GENETIC POLYMORPHISM OF BITTER TASTE PERCEPTION IN TEMPE, ARIZONA AND ITS ASSOCIATION WITH NUTRITIONAL STATUS

D.C. Woodley<sup>1,\*</sup>, B. Cabrera<sup>2,\*</sup>, L.J. Darwin<sup>3</sup>, R.V. Clarke<sup>1</sup>, L. Bucklin<sup>1</sup>, K. McClendon<sup>1</sup>, and S.A. Holechek<sup>1,4</sup>.

<sup>1</sup> School of Life Sciences, Arizona State University, Tempe, Arizona, USA

<sup>2</sup> School of Mathematical and Statistical Sciences, Arizona State University, Tempe, Arizona, USA

<sup>3</sup> School of Human Evolution and Social Change, Arizona State University, Tempe, Arizona, USA

<sup>4</sup> Simon A. Levin Mathematical, Computational and Modeling Sciences Center, Arizona State University, Tempe, Arizona, USA

dcwoodle@asu.edu

bcabrer4@asu.edu

The ability to perceive phenylthiocarbamide (PTC) bitterness varies in the population and influences food preferences, eating behavior and thus nutritional status. Polymorphisms in the human bitter receptor gene (hTAS2R38) correlate with differences in bitterness recognition of PTC with five main different haplotypes present in the American population. These haplotypes have been defined by three single nucleotide polymorphisms (SNPs) which encode for non-synonymous amino acid substitutions at position 49 (alanine/proline, A49P), 262 (valine/alanine, V262A), and 296 (isoleucine/valine, I296V). Genetic polymorphism and food preferences in a sample of the ASU student population were evaluated. For our model, the most common haplotypes PAV and AVI will represent the supertaster and nontaster groups respectively. The other three haplotypes, AAV, PVI and AAI are grouped into the taster category. We proposed a system of ordinary differential equations to describe how the distribution of these haplotypes along with the infectious social influence of eating habits plays a role in an individual's nutritional status and impacts the obesity epidemic. We used a compartmental model to show how each taster group contributes to the healthy or unhealthy population. Using numerical simulations, it was shown that the taster and supertaster classes were the greatest contributors to the obese population as this class was more likely to favor unhealthy food choices. This suggests that both genetics and social environment contribute synergistically to nutritional status with our model highlighting the potential risk in a population for obesity in the future.