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Abstract

The Impact of Genetic Variability of *CYP1A2*, *ADORA2A*, and *AHR* on Caffeine Consumption and Response among Adult New Zealanders †

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Three single nucleotide polymorphisms (SNPs) have known links to caffeine consumption, metabolism, and post-consumption effects and responses: cytochrome P450 1A2 (*CYP1A2*; rs762551), adenosine A2A receptor (*ADORA2A*; rs5751876), and aryl-hydrocarbon receptor (*AHR*; rs4410790). This study aimed to describe the allele frequency of these SNPs in the New Zealand population and explore relationships between the genetic profile of individuals and their caffeine intake and responses.

Eligible participants (aged > 15 years) were invited to provide a saliva sample for genetic analysis of the three SNPs, and to complete a caffeine consumption and habits questionnaire (CaffCo). Genetic data for the SNPs were analysed using MassARRAY analysis on DNA extracted from the saliva samples. Caffeine intake was assessed as low (<80 mg/day), moderate (80–400 mg/day) or high (>400 mg/day) based on Food Standards NZ classifications for intake. Caffeine intake was examined according to genotype for the three SNPs.

Of 255 participants, half (49.4%) were "fast" metabolisers (*CYP1A2* AA), 40.4% were "slow" metabolisers (*CYP1A2* CA), and 10.2% were "ultra-slow" metabolisers (*CYP1A2* CC) of caffeine. Nearly half carried *ADORA2A* CT (46.3%), followed by CC (29.0%), and TT (24.7%). Half (51.8%) of the participants carried *AHR* CT, followed by CC (30.6%), and TT (17.6%) genotypes. Overall, 14.1% of participants reported a caffeine intake >400 mg/day and 52.9% an intake of 80–400 mg/day. Carriers of the genotype *ADORA2A* TT consumed 65 mg/day less caffeine than carriers of the heterozygote genotype (*ADORA2A* CT; $p = 0.034$). No association was found with the other analysed SNPs.

This is the first study in New Zealand to identify genetic variation in relation to caffeine intake. We observed a decreased caffeine consumption among individuals with the *ADORA2A* TT genotype. Further studies are needed to assess caffeine response in relation to these genes, to understand and develop appropriate strategies for informing genotype-based advice on caffeine use.