#flo #ref #ret #disorganized #incomplete

0.1 | General

0.1.1 | SNiPs

- rs4680
  - pain tolerance, worrier/warrior
  - https://www.snpedia.com/index.php/Rs4680
- CYP1A2 gene
  - specifically, rs2069514
    - encodes for the 1C variant,
    - which encodes for slow caffeine metabolism
- rs6902875
  - episodic memory
  - https://pubmed.ncbi.nlm.nih.gov/25317765/

0.2 | Write-up

0.2.1 | A : : rs4680

Also known as Val158Me, rs4680 is an extensively studied SNP located in the COMT gene. The COMT enzyme, encoded by the COMT gene, is responsible for breaking down dopamine in the brain's prefrontal cortex (cite). rs4680 causes the enzyme to function roughly 25% as efficiently as the wild type. The result of wild-type versus rs4680 is commonly referred to as the warrior versus worrier hypothesis (cite). A worrier, one with the rs4680 SNP, has higher dopamine levels. Thus, supposedly, they should have lower pain tolerance, be more prone to stress as well as more exploratory, and more efficient at information processing. Conversely, the wild-type warriors should have higher pain tolerance, be less prone to stress, less exploratory, and less efficient at cognition in most conditions (cite).

0.2.2 | B : : rs2069514

rs2069514 is a 1C type allele of the CYP1A2 gene (cite). CYP1A2 encodes one of the cytochrome P450 mixed function oxidase enzymes, all of which are vital in the metabolism of xenobiotics (cite). One such xenobiotic is caffeine, the processing of which is affected by 1C and 1F type mutations on the CYP1A2 gene. Humans with 1F type mutations are known as 'fast' caffeine metabolizers, whereas 1C type mutations lead to 'slow' caffeine metabolism. Those who carry at least one 1C type mutation will be slower at processing caffeine, and thus, will be more affected by it. rs2069514 is one such 1C mutation, leading to decreased activity by the CYP1A2 enzyme (cite a, b).

0.2.3 | C : : rs6902875

Much less is known about rs6902875, except that it is related to much significantly better episodic memory. This was tested specifically in seniors (cite). After genome-wide linkage analysis on 467 LLFS (Long Life Family Study) participants, a significant link between the 6q24 region