A novel functional polymorphism in the fatty acid desaturase 2 gene (*Fads2*): possible role in basal metabolic rate

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As membrane components, polyunsaturated fatty acids (PUFAs) play an important role in cellular processes and have been shown to be associated with basal metabolic rate (BMR). While the link between BMR and membrane lipid composition is clear on an interspecific level, the underlying mechanism linking them on an intraspecific level is not well understood.

Here we describe a new polymorphism in the fatty acid desaturase (*Fads2*) gene for Δ-6 desaturase (D6D), a key enzyme for PUFA synthesis, in 78 mice from two outbred lines selected for low (L-BMR) and high (H-BMR) BMR as well as for 34 mice from unselected lines. The aim of this study was to verify a possible association between *Fads2* genotypes and BMR. We found a significant correlation between *Fads2* variants and BMR within unselected lines of mice. We also used a F_{ST} outlier test to asses the effect of selection on the variation between L-BMR and H-BMR lines of mice at the *Fads2* gene, using the *Fads2* gene, together with data from the 11 microsatellite loci. Taken together, these results suggest that *Fads2* is expected to become a major focus of membrane, metabolic rate and human metabolic syndrome research.