Proceedings of the Nutrition Society (2011), **70 (OCE4)**, E212 doi:10.1017/S0029665111002631

Summer Meeting, 4–6 July 2011, 70th Anniversary: From plough through practice to policy

Influence of SNP rs3811647 on Fe metabolism and response to an Fe supplemented food in menstruating women

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Fe deficiency anaemia is a worldwide multifactorial disease, in which genetic factors play an important although mostly unknown role. Recent studies demonstrated that variants in the transferrin gene (*TF*) explained ~40% of genetic variation of transferrin levels[(1)]. The aim of the project is to study the association between SNP rs3811647 located in *TF* and Fe status biomarkers in menstruating women, and to study the influence of this SNP on changes in these biomarkers in response to an Fe supplemented food, previously reported to be efficacious at improving Fe status[(2)].

Women (*n* 122) were selected according to the following criteria: caucasian menstruating women, ferritin < 40 ng/ml, Hb ≥ 11 g/dl, 18–45 years, non-smoker, non-pregnant and non-breastfeeding. Volunteers participated in a randomised double-blind placebo-controlled study of 16 weeks of duration. P group (*n* 58) or F group (*n* 64) consumed a placebo or an Fe-enriched food, respectively. Hb, serum ferritin and serum transferrin (Tf) were determined at baseline and monthly. Genotyping of SNP rs3811647 was carried out by minisequencing[(3)]. Baseline data were analysed by one-way ANOVA. Two-ways repeated measures ANOVAs were performed with group (P or F) and genotype (AA, AG, GG) as between-subjects factors.

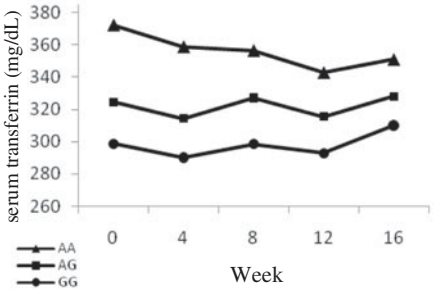

Fig. 1. Changes in P group by genotype.

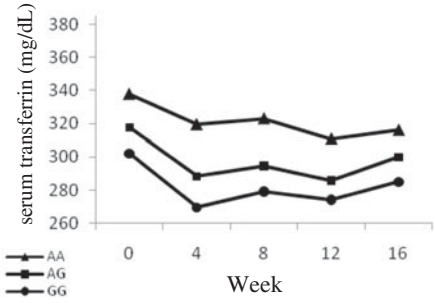

Fig. 2. Changes in F group by genotype.

The SNP rs3811647 was related to serum transferrin levels, but not Hb or ferritin levels, in Fe deficient women. At baseline, serum transferrin was significantly higher ($P<0.001$) in AA women (342.2, SD 67.3, mg/dl) than AG heterozygous (314.6, SD 51.6, mg/dl) and GG homozygous (292.2, SD 48.6, mg/dl). This suggests that AA carriers have higher risk of Fe deficiency anaemia.

Fig. 1 and 2 show the changes in serum transferrin during the intervention. Within-subjects time effect was significant ($F(2.7, 308.6) = 6.8$; $P<0.001$), and there were no time × group, time × genotype or time × group × genotype interactions. The between-subjects effects were group ($F(1, 114) = 3.6$; $P = 0.05$) and genotype ($F(2, 114) = 4.1$; $P<0.05$) but no group × genotype interaction was found.

It is concluded that transferrin decreases for all genotypes in response to the functional food, but SNP rs3811647 appears to determine transferrin levels more than the consumption of the Fe supplemented food.

Supported by Project Ref. AGL2009 11437/ALI. R Blanco-Rojo was supported by a JAE-predoc grant from European Social Fund (ESF).

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