

The Influence of Glucagon-Like-Peptide-1 Receptor Single Nucleotide Polymorphisms on Gastric Emptying Rate in Caucasian Men- A Pilot

Adora Yau¹, John McLaughlin², Ronald J. Maughan³, William Gilmore¹, Jason J. Ashworth¹ and Gethin H. Evans¹.

¹*School of Healthcare Science, Manchester Metropolitan University, M1 5GD, UK,*

²*Institute of Inflammation and Repair, University of Manchester, M13 9PT, UK*

³*School of Sport, Exercise and Health Sciences, Loughborough University, LE11 3TU, UK.*

Gastric emptying is the rate-limiting step in the absorption of nutrients in the small intestine. The emptying rate of a glucose solution has been shown to be highly variable between individuals^[1]. The gastrointestinal hormone glucagon-like peptide-1 which is prominently secreted following carbohydrate ingestion, has been shown to exert inhibitory effects on gastric emptying rate^[2]. Previous work has shown an influence of glucagon-like peptide-1 receptor (GLP-1R) genetic variation on gastric emptying rate in mice^[3]. This pilot study investigated the effect of GLP-1R single nucleotide polymorphisms (SNPs) on the rate of gastric emptying in humans.

Forty-eight healthy non-smoking UK Caucasian males aged 18-35 yr (mean \pm SD age 23 \pm 5 yr, height 178.2 \pm 6.9 cm, weight 75.82 \pm 11.24 kg, BMI 23.9 \pm 3.3, body fat 19.0 \pm 6.2%) took part in this investigation. Following an overnight fast, participants completed a single experimental trial involving the ingestion of 595 ml of a 6% glucose solution containing 100 mg ¹³C sodium acetate. Gastric emptying rate of the solution was measured by ¹³C breath test whereby breath samples were collected at baseline and 10 min intervals for 60 min. A venous blood sample was obtained from each participant for genetic analysis. Twenty-eight haplotype-tagging (Tag) SNPs in the GLP-1R locus incorporating 10,000bp upstream and downstream of the major transcription initiation site and the last exon, respectively, were identified from the HapMap database. Twenty-seven SNPs were successfully genotyped using Sequenom MassARRAY iPLEX GOLD analysis. Gastric emptying results were analysed by genotype and phenotype using Kruskal-Wallis and Wilcoxon statistical tests, respectively. Values are median [quartiles].

A significant effect of genotype on time of maximum emptying rate (T_{lag}) was seen for neighbouring SNPs rs742764 and rs2254336. For SNP rs742764, T_{lag} was faster in genotype CC compared to genotype TT and TC (35 [30-36] vs. 41 [37-46] and 41 [39-45] min; $P < 0.01$). For SNP rs2254336, T_{lag} was slower in genotype AA compared to genotype TT and TA (43 [39-49] vs. 36 [34-41] and 39 [35-42] min; $P < 0.05$). An effect of phenotype was also seen for SNP rs2254336 where T_{lag} was slower in homozygotes of the major allele A compared to participants with the minor allele T (43 [39-49] vs. 39 [34-41] min; $P < 0.05$). Further effects of phenotype were seen for SNP rs2268657 where T_{lag} was faster in homozygotes of the major allele A compared to participants with the minor allele G (37 [34-39] vs. 41 [37-45] min; $P < 0.05$) and for SNP rs9283907 where half emptying time ($T_{1/2}$) was slower in homozygotes of the major allele G compared to participants with the minor allele A (67 [59-82] vs. 55 [53-61] min; $P < 0.05$).

The results of this study suggest that gastric emptying rate may be influenced by SNPs within the GLP-1R gene. Replication of this pilot study in larger cohorts is required to confirm the contribution of GLP-1R gene variation to gastric emptying rate.

[¹] Yau, *et al.* (2013). *Int J of Sport Nutr Exerc Metab*, 23, S13.

[²] Wettergreen *et al.* (1993). *Dig Dis Sci*, 38, 665-673.

[³] Kumar *et al.*, (2008). *Am J Physiol Regul Integr Comp Physiol*, 294, R362-371.