The agouti related protein (AgRP) exerts its anabolic effects on food intake by antagonising the alpha-melanocyte stimulating hormone (α-MSH) at its receptors, melanocortin receptors 3 and 4 (MC3R and MC4R). A single nucleotide polymorphism (SNP) in the promoter of the human AgRP (hAgRP), −38C>T, was associated with low body fatness. The −387 allele that was associated with low body fatness also resulted in lower promoter activity. Here we report a novel SNP, −3019G>A, again in the promoter of hAgRP, which is in complete linkage disequilibrium (LD) with the −38C>T SNP (linked alleles: −3019A/−38T and −3019G/−38C). Functional analyses in a human adrenal and two mouse hypothalamus cell lines showed that the −3019A allele had significantly higher promoter activity. Hence, the two linked alleles (−3019A and −38T) had opposite effects on promoter function and yet they were both associated with low body fatness. The region encompassing the −38C>T SNP had approximately 1000-fold higher activity than the region encompassing the −3019G>A SNP, potentially determining the net functional effect between these two SNPs.

Methods

Subjects

The HERITAGE Family Study cohort included 259 black subjects (88 men and 171 women) from 114 family units. The study design and inclusion criteria have been previously described. Although the HERITAGE cohort includes both Caucasian and black subjects, the −38C>T SNP was found in the blacks subjects only. Therefore no Caucasian data were used in the statistical analyses. The study protocols were approved by each of the Institutional Review Boards of the HERITAGE Family Study research consortium. Written informed consent was obtained from each participant.

Genotyping

Initial screening for polymorphisms in the promoter region of AgRP was carried out using a representative cohort of 40 individuals consisting of diabetic, obese, and lean white and black subjects. Several combinations of primers were used for amplification of genomic DNA by polymerase chain reaction (PCR) and bidirectional sequencing of the amplicons on an ABI 3700 DNA Analyzer (Applied Biosystems, Foster City, CA). Once the −3019G>A SNP was identified, genotyping was performed by amplification of genomic DNA and direct sequencing using a probe on the LI-COR DNA Analyzer 4200 (Lincoln, NE). The following primers were used: forward primer: 5'-ATT TAA CGC GTC CAT CTT CTC CTC TCC CTG-3'; reverse primer: 5'-CTT GGG CTA GTC AGC TGA GAT CGT -3'. PCR was performed as previously described. Since its identification in our laboratory, SNP −3019G>A has appeared in dbSNP with the rs# : 8047574. The nomenclature adopted for referencing gene names, symbols, and polymorphism descriptions was according to den Dunnen and Antonarakis.

Abbreviations: AgRP, agouti related protein; α-MSH, alpha-melanocyte stimulating hormone; LD, linkage disequilibrium; MC3R and MC4R, melanocortin receptors 3 and 4; SNP, single nucleotide polymorphism; UCP1, uncoupling protein 1
Transfection constructs and cell culture

Constructs to examine the impact of the −3019G>A SNP on promoter activity were made by amplification of genomic DNA from a heterozygous individual and directional cloning of the PCR products into the pGL3-basic vector (Promega, Madison, WI). The amplified region containing the SNP was 203 nucleotides (nt) long. The forward and reverse primers contained recognition sites for the MluI and NheI restriction endonucleases for digestion of the PCR products to facilitate directional cloning into the vector. The sequence of the primers (inclusive of the restriction sites for the enzymes) was as follows: forward primer: 5′-TTT GAA CGC GTC ACA GGA AAC ACA TGG CTG-3′; reverse primer: 5′-CTT GGG CTA GCG TCT CCC TCT TTC-3′. Constructs to examine promoter activity for the −38C>T SNP were prepared as previously described. Cell culture was carried out under standard conditions in a humidified incubator at 37 °C and 5% CO2. The GT1-7 cells were the kind gift of Dr Mellon and were grown in DMEM medium (Cellgro, cat. no 10-017-cv), 10% FBS, penicillin-streptomycin (Gibco, cat. no 15140-122) to 1%. The human adrenal NCI-h295R cells were purchased from the American Type Culture Collection (Manassas, VA) and were grown in the following media: DMEM/F12 50/50 MIX medium 500 ml (Cellgro, cat. no 13-090-cv) by adding BD ITS+culture supplement 5 ml (BD Biosciences, cat. no 354352) and Nu-serum I culture supplement 13 ml (BD Biosciences, cat. no 35-5100) and 0.75 M HEPES 10.5 ml penicillin-streptomycin (GIBCO, cat. no 15140–122) to 1%. The N-38 is a newly developed cell line that was generated through immortalisation of mouse primary hypothalamic cells at embryonic day 17 with SV40 T-antigen introduced through retroviral infection. The N-38 cell line, a clonal population of hypothalamic neurons, has been propagated to P-44 and maintains SV40 T-antigen expression after 2 years of continuous growth. All cell culture conditions for the N-38 cells were identical to those for the GT1-7 cells given above.

All cells were serum starved for 24 h prior to transfection. Transient cotransfections with the AgRP promoter constructs and β-galactosidase plasmids were carried out for 24 h in the absence of serum using the Geneporter2 transfection reagent as prescribed by the manufacturer (Gene Therapy Systems, San Diego, CA). Subsequently, the media were supplemented with 20% FCS for 24 h. Cells were harvested using 1× Geneporter2 lysis buffer and the lysates were assayed for luciferase and β-galactosidase activities, as prescribed by the assay manufacturer (Promega, Madison, WI) in a luminometer (Zyixus, Pforzheim, Germany). All luciferase activity measurements were normalised to β-galactosidase values. Measurements were averaged from a series of a minimum of nine independent experiments per cell line.

Statistical analyses

AgRP −38C>T and −3019G>A haplotype frequencies were assessed using the EH program. Linkage disequilibrium (LD) was calculated as D′ = x_{ij}−p_ip_j, where x_{ij} is the A_1B_1 frequency, and p_1 and p_2 are the frequencies of alleles A_1 and B_1 at loci A and B, respectively. A standardised LD coefficient D′ was defined as D′ = D/D_{max}, where D_{max} = \min(p_{12}, q_{12}), when D = 0, or D_{max} = \min(q_{12}, p_{12}), when D > 0, and q_{12} and p_{12} are the frequencies of alleles A_2 and B_2 at loci A and B, respectively.

**RESULTS AND DISCUSSION**

An SNP was identified at position −3019 upstream of the putative transcription start site of the promoter of hAgRP (−3019G>A). The functional impact of the SNP was assessed by examining the promoter activity of the region (−3165/−2962) containing the SNP. Two constructs were made in the pGL3-basic luciferase reporter vector representing the two genotypes. The A/A construct had significantly higher promoter activity than the G/G construct in the mouse hypothalamus GT1-7 and the human adrenal NCI-h295R cell lines (fig 1A,B). This result was repeated in another mouse hypothalamic neuronal cell line, N-38 (fig 1C). The three cell lines endogenously express AgRP as assessed by real-time quantitative RT-PCR (data not shown).

<table>
<thead>
<tr>
<th>Genotype frequencies</th>
<th>AA</th>
<th>GA</th>
<th>GG</th>
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<tbody>
<tr>
<td>−3019G&gt;A</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>−38C&gt;T</td>
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<tr>
<td>Linkage disequilibrium test: 0 = 434.33, p = 0.0000001, D′ = 1.0</td>
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**Figure 1** Mean relative luciferase activities for the two genotypes of the −3019G>A SNP, in three cell lines: GT1-7 (A), NCI-h295R (B), and N-38 (C). Luciferase activities were normalised by β-galactosidase measurements for transfection efficiencies and the values shown are the means of a minimum of nine independent experiments for each genotype in each cell line. The standard deviations are represented by the vertical bars on the columns. Comparisons between genotypes in each cell line were performed by Student’s t-test and the p-values are shown above the bars.
The promoter activities of the two −3019G>A constructs were considerably lower than the promoter activities we have measured for other regions of the hAgRP promoter. Moreover, studies in our laboratory have shown that SNP −3019G>A lies in a region that might have suppressor effects on gene expression.

We subsequently genotyped the HERITAGE Family study population to evaluate the possible association of the −3019G>A SNP with obesity-related phenotypes. The SNP was found in black subjects only which was also the case for the −38C>T SNP. Subsequently we compared the allele frequencies of the two SNPs and found them to be identical between the “A−T” and the “G−C” pairs (table 1). This pattern indicates strong linkage disequilibrium (LD), which was confirmed by a formal LD test (table 1).

Since the −3019G>A and −38C>T SNPs are in complete LD and the functional data (fig 2) suggest the opposite. The results are therefore in disagreement in terms of LD and the functional effects of the two SNPs. However, the region that contains the −38C>T SNP had considerably (~1000-fold) higher promoter activity than the region containing the −3019G>A SNP (fig 2). Therefore, the net effect of the −3019A/−38T haplotype could be determined mostly by the −38T allele at basal conditions. One way to test this hypothesis would be by using longer promoter constructs that contain both SNPs, in all possible haplogroup combinations, and evaluating the impact of each nearby locus. Here we present a case of two SNPs that are in complete LD and yet the linked genotypes have opposite functional effects. This puts emphasis on the need to functionally characterise all SNPs in LD in the promoter, as LD may not necessarily predict the functional properties of the linked SNPs.

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Conflicts of interest: none declared.

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**REFERENCES**


Functional dimorphism of two hAgRP promoter SNPs in linkage disequilibrium

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