Genetic determinants of HSP70 gene expression following heat shock

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The regulation of heat shock protein expression is of significant physiological and pathophysiological significance. Here we show that genetic diversity is an important determinant of heat shock protein 70 expression involving local, likely cis-acting, polymorphisms. We define DNA sequence variation for the highly homologous HSPA1A and HSPA1B genes in the major histocompatibility complex on chromosome 6p21 and establish quantitative and specific assays for determining transcript abundance. We show for lymphoblastoid cell lines established from individuals of African ancestry that following heat shock, expression of HSPA1B is associated with rs400547 (P 3.88 × 10⁻⁸) and linked single nucleotide polymorphisms (SNPs) located 62–93 kb telomeric to HSPA1B. This association was found to explain 31 and 29% of the variance in HSPA1B expression following heat shock or in resting cells, respectively. The associated SNPs show marked variation in minor allele frequency among populations, being more common in individuals of African ancestry, and are located in a region showing population-specific haplotypic block structure. The work illustrates how analysis of a heritable induced expression phenotype can be highly informative in defining functionally important genetic variation.

INTRODUCTION

Induction of heat shock proteins is a critical and highly conserved cellular response protecting cells from a range of stresses including damage caused by normal physiological processes, extreme environmental stress or disease. Protection arises from a variety of mechanisms, notably the molecular chaperoning function of heat shock proteins acting to identify misfolded or partially denatured proteins, leading to their repair or transportation to sites of degradation (1). The heat shock protein 70 (Hsp70) family is the most highly conserved of the many heat shock protein families across a wide range of species from bacteria to plants and animals (2). A number of different genes encode human inducible Hsp70 proteins notably HSPA1A (HSP70-1) and HSPA1B (HSP70-2) located in the major histocompatibility complex (MHC) class III region on chromosome 6 (3–5). These highly homologous single exon genes are found in a tandem arrangement within a 14 kb region of chromosome 6p21.3, with an additional homologous heat shock gene HSPA1L located in the reverse orientation approximately 4 kb upstream of HSPA1A whose expression is constitutive and predominantly confined to the testis (6). This cluster of three heat shock genes is also found in the mouse and rat and is hypothesized to have arisen by gene conversion with homogenization of the whole coding region of HSPA1A and HSPA1B, together with parts of HSPA1L (7). The coding regions of HSPA1A and HSPA1B are highly homologous, differing at only six single base substitutions, while some sequence differences are noted in the promoter and 3′-untranslated regions (UTRs).

Expression of heat shock proteins has been shown to be highly heritable (8,9), suggesting a significant component in determining individual responsiveness at the level of gene expression. The occurrence of cis- or trans-acting modulators of heat shock protein gene expression would be of significant biological interest, notably in the context of susceptibility to disease. To date, however, no studies have been reported analysing heat shock-induced gene expression as a quantitative trait for human subjects, a powerful approach which has been applied almost exclusively to unstimulated cells (10). There is growing evidence, however, that the role of regulatory genetic variants is likely to be highly context specific (11). For HSPA1A and HSPA1B, the question is of particular relevance given that these genes are heat shock

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inducible, and that polymorphism involving these genes or extended haplotypes over the MHC has been implicated in susceptibility to a number of infectious, inflammatory and autoimmune diseases (12–16) as well as malignancy (17–19) and drug hypersensitivity (20,21).

Extensive linkage disequilibrium (LD) has made fine mapping of disease associations difficult, while the identification of specific functional variants involving HSPA1A and HSPA1B based on reporter gene assays or association of candidate single nucleotide polymorphisms (SNPs) with levels of gene expression has often been controversial (12–14,22). Moreover, the remarkable homology of these genes has caused some difficulties in the unambiguous assignment of SNP locations to specific sequences and in clearly distinguishing between HSPA1A and HSPA1B transcript when assaying gene expression (23–25). In this study, we sought to define the extent and nature of DNA sequence variation involving HSPA1A and HSPA1B among individuals of European and African ancestry, and to determine by quantitative trait mapping how genetic variation may modulate expression of these important stress response genes in a physiologically relevant context, namely response to heat shock.

RESULTS

Sequence variation involving HSPA1A and HSPA1B

DNA sequence variants involving HSPA1A and HSPA1B genic sequences and a 2 kb interval 5′ or 3′ to each of these genes were identified by resequencing 48 unrelated individuals from the International HapMap Project (26), 24 individuals of European ancestry (CEU panel) and 24 of African ancestry [Yoruba from Ibadan Nigeria (YRI) panel]. In order to unambiguously assign variants for these highly homologous gene regions, genomic DNA was first PCR amplified using long range specific primers and high fidelity Taq polymerase, and then cloned into pCR4-TOPO before being subject to Sanger sequencing. We obtained overlapping gene-specific sequence amplicons spanning chr6: 31889526–31894556 (HSPA1A) and chr6: 31902517–31906207 (HSPA1B) with 2× coverage. This identified 20 SNPs in the HSPA1A gene region and 16 SNPs in the HSPA1B region (Fig. 1), including five novel SNPs involving HSPA1A and two for HSPA1B. We noted that of the SNPs identified in the HSPA1A region, five lie upstream of the transcriptional start site (TSS), five within the 5′-UTR, seven in the coding region and three downstream of the gene. In the HSPA1B region, five SNPs were identified upstream of the TSS, three in the 5′-UTR and eight in the coding region of the gene. No insertions or deletions were identified. Of the seven novel SNPs identified, three were missense mutations (Fig. 1). No SNPs were found in the 3′-UTR of either gene.

We proceeded to genotype 60 unrelated founder individuals in the CEU and YRI panels in order to establish allele frequencies for the variants identified and determine their relationship to underlying allelic structure. The location, nature and minor allele frequency (MAF) of SNPs in the two populations are summarized in Figure 1. Overall, there was greater SNP diversity among individuals of African ancestry (YRI panel). Allele frequencies were found to vary between populations such that of the 36 SNPs identified in the two populations, 12 were monomorphic in the CEU panel and 7 in the YRI panel. Among the SNPs polymorphic in both populations, MAF varied significantly. These included SNPs such as rs1043618, rs6457452 and rs1061581 previously implicated in disease susceptibility and longevity (12,13,27–29).

HSPA1A and HSPA1B are thought to have arisen by duplication and gene conversion. Our data showed that two pairs of SNPs were found in the same positions in the coding sequence of HSPA1A and HSPA1B. The first pair, rs562047 (HSPA1A) and rs17856061 (HSPA1B), is non-synonymous SNPs located 330 bp from the ATG of each gene which results in a missense mutation in the Hsp70 protein, p.Glu110Asp, as a result of a G to C nucleotide substitution. The second pair of SNPs, rs541340 (HSPA1A) and rs35682610 (HSPA1B), are synonymous and are located 1710 bp downstream of the coding start site.

HSPA1A and HSPA1B expression following heat shock

In order to determine how local or distant genetic variants may modulate expression of HSPA1A and HSPA1B, we established EBV-transformed lymphoblastoid cell lines (LCLs) as a model system in which we could reproducibly induce heat shock for a physiologically relevant cell type. This would allow expression quantitative trait (eQTL) mapping across a panel of LCLs established from unrelated individuals for whom dense genotyping data are available as part of the International HapMap Project (30). This approach has previously been highly informative for genome-wide mapping of expression-associated SNPs using resting HapMap LCLs (31–33), notably for individuals of African ancestry in whom high levels of haplotype diversity facilitates fine mapping of SNP associations (34). Inducible Hsp70 expression following heat shock has been reported in LCLs (35) as well as the B cell lymphoma cell line Raji (36) and primary peripheral blood lymphocytes (25,37).

We proceeded to design a quantitative real-time PCR assay that would discriminate between transcript arising from HSPA1A or HSPA1B. The high degree of sequence homology between the genes has led to difficulties in previous studies with the specificity of transcript quantification (23–25). A minor groove binder (MGB) TaqMan probe with a 5′ reporter dye and 3′ non-fluorescent quencher was used to minimize background while stabilizing probe hybridization and allowing use of shorter primers (38). Assays were designed to the 3′-UTR of HSPA1A and HSPA1B as some sequence variation is seen here between the two genes (Supplementary Material, Fig. S1). In order to investigate the specificity of the resulting primer-probe sets, the full-length cDNA sequence for either HSPA1A or HSPA1B was cloned into pCR4-TOPO and used as template for the gene-specific TaqMan assays. No signal above background was detected when the plasmid not matching the primer-probe set was used as template for the TaqMan probe assay. To quantify expression of HSPA1A and HSPA1B in the biological samples, a standard curve was included on all plates with assays performed in technical duplicates for each of the three biological replicate experiments. This demonstrated that, for LCL GM15817, both transcripts were highly inducible within 30 min of heat shock, rising to a maximum following heat shock for 1 h plus 1 h recovery (Fig. 2). We also observed marked upregulation of Hsp70 protein.
production following 1 h of heat shock at 42°C, which was maximal after 6 h of recovery at 37°C when a 77-fold induction in Hsp70 levels was found (Fig. 2).

**eQTL mapping for HSPA1A and HSPA1B**

We proceeded to map expression of the two inducible Hsp70 genes as a quantitative trait using LCLs established from 60 unrelated individuals from the YRI HapMap panel. We assayed gene expression at the transcript level for HSPA1A and HSPA1B using gene-specific quantitative real-time PCR for resting cells, and for cells after heat shock at 42°C for 1 h. Growth rates were determined to ensure uniform cell densities. Two independent biological replicate experiments were performed for each LCL. HSPA1A and HSPA1B gene-specific expression was normalized against the housekeeping gene GAPDH based on the difference in the threshold cycles (ΔCt).

**Figure 1.** Sequence diversity in HSPA1A and HSPA1B gene regions. (A) Sanger-based sequencing amplicons shown (grey arrows) together with the location of SNPs. (B) SNPs were identified by resequencing and then genotyped in all 60 founder individuals for each HapMap population panel. *SNPs for which MAF data were available from resequencing only (24 individuals each panel).
eQTL mapping was performed using SNP genotyping data for the HSPA1A and HSPA1B gene regions we had determined for these individuals together with genome-wide genotyping data for 2 268 955 SNPs with an MAF greater than 5% available through the International HapMap Project (26). We first considered the ΔCt values following heat shock for Hsp70 gene expression using the mean of two biological replicate experiments carried out for each LCL. The most striking result was seen for HSPA1B expression with evidence of a major local, likely cis-acting, eQTL located 62–93 kb telomeric to HSPA1B (Fig. 3, Supplementary Material, Table S1). This was the strongest genome-wide association observed and showed four SNPs in complete LD associated with HSPA1B expression after heat shock (P = 3.88 × 10⁻⁸): rs400547, an intronic SNP located in C6orf27 (c.2499+10C>G, respectively) and rs707936, an intronic SNP in C6orf27 (c.2499+10C>T). We then investigated whether this result was reproducible. Strikingly, the same SNP markers are robustly associated with expression of HSPA1B after heat shock in both biological replicate experiments (Supplementary Material, Fig. S2). Possession of a copy of the A allele of rs400547 is associated with 60% lower expression of HSPA1B following heat shock compared with those individuals who do not have a copy (Fig. 4). A clear allelic dose effect was seen with mean levels of HSPA1B expression (relative to GAPDH): 0.69 (95% confidence intervals 0.49–0.89) for those homozygous GG, 0.34 (0.23–0.44) for individuals heterozygous GA and 0.08 (0.04–0.12) for those homozygous AA.

When we analysed basal HSPA1B expression, the same SNPs showed the strongest association with mean HSPA1B expression (Fig. 4, Supplementary Material, Fig. S3). Basal expression of HSPA1B is considerably lower than that seen following heat shock (mean levels 0.010 versus 0.453) but is detectable in LCLs. We found that the same four linked SNPs were associated with basal HSPA1B expression (P = 6.45 × 10⁻⁸) (Supplementary Material, Table S1). Possession of rs400547 was associated with 85% lower basal expression of HSPA1B. The same association was also demonstrated when we considered each biological replicate experiment separately and found that the strongest association for each replicate was with rs400547 and linked SNP markers (Supplementary Material, Fig. S2).

In order to fine map this association further, we augmented the HapMap 2 SNP data set with data recently released from the 1000 Genomes Project (www.1000genomes.org) for the YRI cohort. For a 220 kb window which included the most strongly associated HapMap SNPs and the Hsp70 gene cluster, a total of 1 538 SNPs were tested for the association (Supplementary Material, Fig. S4). This confirmed the strong peak of association but did not resolve the association further. The analysis revealed that one additional SNP was associated with HSPA1B expression (rs378538) in complete LD with rs400547. rs378538 is a C to T SNP located in the CLIC1 promoter region, 683 bp upstream of the transcriptional start site.

The association with HSPA1B expression falls within a 158 kb region flanked by peaks of recombination (chr6: 31784000–31942000) with the strongest association involving five SNPs in complete LD (rs400547, rs1150793, rs707936, rs707915, rs378538) located in CLIC1, MSH5 and C6orf27. The extent of LD across the region of association and flanking regions was defined for the YRI HapMap population of European ancestry and contrasted with that seen among individuals of African ancestry (Supplementary Material, Fig. S5). There was no evidence of block structure involving the Hsp70 genes. However, there was some evidence of haplotype block structure elsewhere which was more extensive among African individuals.

This was notable for expression-associated SNPs in the LY6G gene cluster, DDAH2, CLIC1 and MSH5 where a 31.2 kb haploptic block (chr6: 31794476–31825675) was defined using Haploview and the confidence intervals method (39). This resolved nine common haplotypes with a frequency greater than 0.01 based on 21 SNPs with a MAF >0.05 (Supplementary Material, Fig. S6). We then tested for evidence of haploptic association using a linear regression model and found significant association. Haploptic 4, which includes the minor allele of rs400547, was significantly associated with HSPA1B expression following heat shock or in resting cells (P = 4.6 × 10⁻⁶ and 9.0 × 10⁻⁶), explaining 31 and 29% of the variance in gene expression, respectively (Supplementary Material, Fig. S6). The other haploptic bearing the minor allele of rs400547, haploptic 5, also shows association but with lower statistical significance as it is rare. A further haploptic, denoted haploptic 8, showed an apparent independent haploptic association with increased HSPA1B expression (Supplementary Material, Fig. S6).

The functional variant responsible for the observed association remains unresolved but a cis-acting effect is likely given the proximity of the region to HSPA1B. Four of the linked SNP markers are intronic (rs400547, rs1150793, rs707936, rs707915) and one is located in the promoter region of CLIC1 (rs378538), but none correspond to known regulatory elements. No association was found for the haploptic tagged by rs400547 with CLIC1 expression using publicly available data sets of gene expression for the YRI panel (31, 40). In silico analysis of transcription factor
Figure 3. Quantitative trait mapping for HSPA1B expression following heat shock. Expression-associated SNPs based on mean ΔCt values for HSPA1B expression for two biological replicate experiments in YRI HapMap founder LCLs following heat shock at 42°C for 1 h. (A) Manhattan plot showing strength of association from PLINK analysis plotted as –log10(P) values by chromosome for HSPA1B expression following heat shock. For rs400547 and linked SNPs, the observed association at $P \approx 3.88 \times 10^{-8}$ was significant at a conservative genome-wide significance threshold of $<5 \times 10^{-8}$ (59) and on permutation analysis (empirical $P$-value $= 2 \times 10^{-8}$). Other signals with moderate evidence of association which are candidates for further study are highlighted between $10^{-5}$ and $10^{-7}$ by the blue and red lines, respectively (60). (B) Association data shown at higher resolution for chromosome 6. (C) Single marker allelic association results for a 400 kb region spanning HSPA1B (chr6: 3165000–3205000) plotted as –log10(P) values (left y-axis) by genomic coordinate (x-axis). With reference to rs400547, SNPs with MAF greater than 5% and $r^2 < 0.2$ are shown as white squares, 0.2–0.5 (yellow), 0.5–0.8 (brown) and >0.8 (red). Recombination rate is also plotted (right y-axis). Gene structure for the region is shown below.
binding was performed using the JASPAR (http://jaspar.genereg.net) open-access database of transcription factor binding profiles (41). This showed evidence of allele-specific binding for only one SNP, predicting that BRCA1 binds with greater affinity to the associated G allele of rs1150793 (ACAAGAC) (score 6.4) (relative profile score 90.4%). The five SNP markers are in complete LD and show marked differences in allele frequency between populations based on data from the HapMap Project (30), being common in populations of African ancestry (MAF for rs1150793 is 0.344 in YRI panel of European ancestry) (pairwise FST YRI versus CEU 0.18). Within Africa, the observed MAF is lower in East Africa, being 0.177 in the Luhya people in Webuye, Kenya and 0.094 in the Maasai people in Kinyawa, Kenya.

For HSPA1A expression, we found a number of distant expression-associated SNP markers (Supplementary Material, Fig. S7 and Table S1) which are candidates for further investigation. However, the observed expression-associated SNPs did not include the major local association on chromosome 6 seen for HSPA1B.

Previous studies looking to define SNP association with Hsp70 gene expression have been restricted to specific candidate SNPs. Association was reported for rs6457452 and rs10615181 (also known as ‘HSPA1B–179’ and ‘HSPA1B+1267’, respectively) with lower expression associated with the C allele of rs6457452 and no apparent effect of rs10615181, although these data have been controversial (12–14,22). In our data set, we find a weak association with rs6457452, but this is not consistent across data sets (Supplementary Material, Fig. S8). This is unlikely to have arisen due to LD with rs400547 ($r^2 = 0.148$).

**DISCUSSION**

Heat shock proteins play a critical role in normal physiological processes and disease pathogenesis. The role of genetic variation in modulating expression of the different members of heat shock protein families remains unresolved but is of significant interest given evidence of heritability and disease association. Here we define a major local eQTL locus for HSPA1B, mapping to a region between 60 and 90 kb telomeric to the gene. The relatively large magnitude of the effect observed combined with the use of a carefully defined and robust phenotype, heat shock and a quantitative and specific assay of transcript abundance has allowed resolution of this eQTL using a relatively modest sample size. The association was seen to be reproducible between biological replicate experiments and also be present in the basal levels of gene expression observed in this cell type. The study was designed to detect local, likely cis-acting associations and is not adequately powered to establish distant, likely trans-acting associations unless these were of large magnitude.

The association with HSPA1B expression is located in a region involving CLIC1/MSH5 previously proposed to have been subject to selection (42). The five SNP markers tagging the associated allele show marked variation in allele frequency between populations, being high among those of African ancestry but rare in other populations. Allele frequencies were highest in Yoruban individuals from West Africa compared with the Luhya or Maasai populations in East Africa. We note the haplotypic block structure present in Yoruban individuals for the expression-associated region and that haplotypic association suggests there may, in addition, be a high producer allele. However, the defined block does not include rs707936 (in complete LD with rs400547), which is located in C6orf27. Sequencing and genotyping of additional individuals, including individuals from different African populations, would allow the haplotypic structure to be resolved with greater precision and enable fine mapping of the observed association with gene expression. Additional alleles are likely to be identified which will direct efforts to establish the functional basis of the observed association. The very low allele frequency in Caucasians means that currently available QTL data sets are not informative for this haplotype and that further analysis in populations of European ancestry is unlikely to be productive unless adequately powered. For the Hsp70 gene locus itself, our analysis showed no evidence of
haplotype block structure in either the African or Caucasian populations studied, with relatively few coding variants and no variants in the 3'UTR of either HSPA1A or HSPA1B.

The local nature of the association and the fact it is not seen with HSPA1A suggest that spatial conflation or promoter sequence differences between HSPA1A and HSPA1B may be important in determining specificity for a cis-acting event, perhaps involving recruitment of a transcriptional complex to a promoter or enhancer element involving CLIC1/MSHS which comes into proximity with HSPA1B through DNA looping. One of the five SNPs, rs378538, is located in the CLIC1 promoter region, but the regulatory significance of this region has not been characterized. The biological role of CLIC1 as a sensor and effector during cell stress (43) may be relevant in terms of co-regulation with a heat shock response; however, the eQTL analysis suggests that the associated SNPs do not modulate CLIC1 expression in resting cells. A further linked SNP, rs150793, in silico has the potential to recruit BRCA1 which is known to be rapidly responsive to heat shock at the protein level and participate in heat shock pathways (44), including modulation of heat shock gene expression using reporter gene systems. The functional basis of the observed association will require further detailed analysis.

This work has defined expression-associated SNPs for HSPA1B which will be important as candidate SNPs for disease association studies and to facilitate the fine mapping of reported associations involving this gene region. This may be particularly relevant for infectious diseases including severe sepsis that has been associated with genetic diversity involving the Hsp70 locus (12,13,28) and may have exerted significant selective pressures. Particular variants conferring a selective advantage would be consistent with reported associations with longevity and survival (25,27,29), and our findings of population differences in MAFF may be a product of selective pressures. It is noteworthy that one of these SNPs, rs707915, which is in complete LD with rs400547, has been reported to be associated with type 1 diabetes after accounting for MHC class II alleles (45). A further linked SNP rs707936 found on the expression-associated haplotype showed some evidence of disease association with multiple sclerosis in African Americans, but further work is required to define this (46).

**MATERIALS AND METHODS**

**Cell culture and heat shock**

LCLs were maintained in RPMI 1640 supplemented with 10% fetal calf serum (FCS) and 2 mM l-glutamine at 37°C in a humidified 5% CO2 environment. Growth rates were determined for each cell line to ensure uniformity in cell numbers on harvesting and Trypan blue staining used to define cell viability. Two biological replicate heat shock experiments were performed for each cell line. Cells were subjected to heat shock by incubation in a water bath at 42°C followed by recovery at 37°C for the times indicated. 2 × 10^7 cells were harvested for RNA quantification.

**Quantitative TaqMan PCR and RNA analysis**

Total RNA was purified using Qiagen RNeasy mini kit including on-column DNase digestion (Qiagen). cDNA was synthesized using oligo dT primers and Superscript III reverse transcriptase (Invitrogen). Real-time PCR assays were performed using the ABI7900 (Applied Biosystems) using TaqMan minor groove binder (MGB) probes. Primer and probe sequences are given in Supplementary Material, Table S2. Three technical replicates were run for each sample. PCRs comprised 1×TaqMan Universal PCR Master-Mix (without UNG), 250 nM probe, 400 nM forward primer, 400 nM reverse primer and 10–100 ng of template. PCR conditions were 50°C for 2 min, then 40 cycles of 95°C for 10 min, 95°C for 15 s and 60°C for 1 min. A standard curve comprising dilutions of homologous standards from a known starting concentration of mRNA were included on each plate. In order to confirm the specificity of the primer probe sets, plasmids containing HSPA1A or HSPA1B were prepared. To do this, a 2.5 kb fragment spanning HSPA1A (chr6: 31891253–31893749) was cloned into pCR4-TOPO (Invitrogen) using the primer pair 5′-GGTCTCGTGACGACTTTATAA-3′ and 5′-CAACCTATGCGACCTACTGA-3′. Similarly, a 2.6 kb fragment spanning HSPA1B (chr6: 31903457–31906065) was cloned into pCR4-TOPO (Invitrogen) using the primer pair 5′-CCACCGACGACTTATAAAGCAGCA-3′ and 5′-TCAGACACTATCCCTCCGCAGAA-3′.

**DNA sequencing and genotyping for HSPA1A and HSPA1B**

The SequlalPrep Long PCR Kit (Invitrogen) was used to generate specific amplicons spanning HSPA1A (chr6: 31889526–31894556) and HSPA1B (chr6: 31902517–31906207) from 200 ng genomic DNA according to the manufacturer’s instructions. PCR amplification was performed using Tetrat thermo cyclers (MJ Scientific) cycling at 94°C for 2 min, then 94°C for 10 s, 62–54°C for 30 s, 68°C for 5 min for 9 cycles decreasing by 1°C per cycle, then 94°C for 10 s, 54°C for 30 s, 68°C for 5 min for 26 cycles (adding 20 s per cycle to extension time), and a final extension of 68°C for 5 min. PCR amplification was confirmed by the agarose gel electrophoresis and purified using PCR Cleanup Filter Plates (Millipore) before sequencing using BigDye terminator V3.1 cycle sequencing kit (Applied Biosystems) following the manufacturer’s instructions. Primer sequences are given in Supplementary Material, Table S2. Sequences were aligned using PhredPhrap (47,48) and visualized using Consed (49,50) to identify sequence variants. Genotyping was performed using the Sequenom iPLEX Mass-Array assay system in a 384-well format according to the manufacturer’s instructions. Primer sequences are shown in Supplementary Material, Table S2.

**HSP70 ELISA**

A sandwich ELISA was designed and optimized for cell lysates based on previously published methods (51–55). After heat shock, the cells were lysed in 200 μl lysis solution [PBS with 1 mM EDTA, 0.5% Triton X-100, and 1X Protease Inhibitors (Roche)] for 10^7 cells by incubating on ice for 30 min, then
three rounds of freeze–thaw cycles in a dry-ice ethanol bath. Cells were then centrifuged at 16,000g in a microcentrifuge at 4°C for 10 min, and total protein concentration of the supernatant estimated using the Bio-Rad Protein Assay solution (BioRad). Certified High Bind 96-well plates (Corning) were coated with 0.1 μg/ml of mouse anti-HSP70 monoclonal antibody (Stressgen) diluted in 0.1 M carbonate buffer, pH 9.6, and plates were incubated at 4°C overnight. They were then washed three times with PBS/0.05% Tween 20, blocked for 1 h at RT with blocking solution (1% BSA in PBS) and washed three times. One hundred microlitres of lysed cell solutions diluted to 1 μg/ml total protein in PBS and a range of HSP70 protein standards (Stressgen, NSP-555) ranging from 400 to 6.25 ng/ml (in duplicate) were used to create a standard curve. Plates were then incubated for 2 h at 37°C and then washed three times with PBST. Rabbit Anti-Hsp70 (bsp72) polyclonal antibody (Stressgen, SPA-812) was then added at a dilution of 1:500 [diluted in PBST and 2% mouse serum (Sigma)] and incubated for 1 h at RT. The plates were then washed three times with PBST. Goat Anti-Rabbit IgG:HRP [Horseradish Peroxidase Conjugate Absorbed with Human IgG (Stressgen, SAB-300)] was diluted 1:10,000 in a PBST/1% BSA solution and incubated for 1 h. The plates were then washed three times with PBST. One hundred microlitres of TMB (3,3′,5,5′-TetramethylBenzidine; Invitrogen) were added to each well and incubated approximately 10 min before addition of a stopping solution of 1 M HCl. Optical density was read at 450 nm using SoftMax microplate reader and SoftMax Pro 4 software.

Statistical genetic analysis

For the YRI panel, HapMap release 24 was used which included ~2.46 million autosomal and 72 mitochondrial SNPs of >0.05 MAF. These represent ~1.6 million independent SNPs genome-wide, after the exclusion of SNPs in complete LD ($r^2 = 1.0$). Quantitative trait analysis to define SNP association with gene expression was performed using PLINK (56). Samples and SNPs with genotyping failure rates of 0.1% were excluded from the analysis. Phenotypic means were compared across the genotypic states using the Wald test, to generate an asymptotic P-value with no normality assumptions. Empirical P-values controlling for family-wise error rates were calculated using a permutation procedure ($n = 5000$) involving phenotype label swapping to randomly allocate sample identifiers and break the phenotype–genotype relationship but retain the same patterns of LD between SNPs in the observed and permuted samples. For fine mapping a 900 kb region including the HSPA1A and HSPA1B genes, 1000 genome data (www.1000genomes.org) available for 38 founder YRI individuals were used with genotypes for the remaining YRI individuals used with impute version 2.0 (57). Haplotypic association was performed using HaploView version 4.1 (58), and the inferred haplotypes were analysed for the association with gene expression.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG online.

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Conflicts of Interest statement. None declared.

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