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Eccentric muscle challenge shows osteopontin polymorphism modulation of muscle damage

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A promoter polymorphism of the osteopontin (OPN) gene (rs28357094) has been associated with multiple inflammatory states, severity of Duchenne muscular dystrophy (DMD) and muscle size in healthy young adults. We sought to define the mechanism of action of the polymorphism, using allele-specific in vitro reporter assays in muscle cells, and a genotype-stratified intervention in healthy controls. In vitro reporter constructs showed the G allele to respond to estrogen treatment, whereas the T allele showed no transcriptional response. Young adult volunteers ($n = 187$) were enrolled into a baseline study, and subjects with specific rs28357094 genotypes enrolled into an eccentric muscle challenge intervention ($n = 3$ TT; $n = 3$ GG/GT (dominant inheritance model)). Female volunteers carrying the G allele showed significantly greater inflammation and increased muscle volume change as determined by magnetic resonance imaging T1- and T2-weighted images after eccentric challenge, as well as greater decrement in biceps muscle force. Our data suggest a model where the G allele enables enhanced activities of upstream enhancer elements due to loss of Sp1 binding at the polymorphic site. This results in significantly greater expression of the pro-inflammatory OPN cytokine during tissue remodeling in response to challenge in G allele carriers, promoting muscle hypertrophy in normal females, but increased damage in DMD patients.

INTRODUCTION

Genetic association studies are a powerful tool to identify regions of the human genome associated with specific traits, both in health and disease. A limitation of the approach is the challenges frequently associated with defining the biochemical and physiological consequences of the genetic variants. We hypothesized that targeted interventions in genotype-stratified healthy volunteer groups could provide a means of testing molecular models for specific polymorphisms.

A common polymorphism in the transcriptional promoter of the osteopontin (OPN) gene (rs28357094) has been found to be a strong genetic modifier of muscle size in young adult volunteers (1), and muscle weakness and disease progression in Duchenne muscular dystrophy (DMD) (2). Both studies showed a dominant inheritance model of the polymorphism effect on phenotypes (TT versus GG/GT genotype groups). The T-to-G single nucleotide polymorphism (SNP) is located 66 bp upstream of the OPN transcription initiation site overlapping a specificity protein-1 (SP1) transcription factor-binding site. The minor G allele has shown to significantly inhibit the binding of SP1, and this loss of binding results in an 80% reduction in transcriptional activity in multiple human immortalized cell lines (3). The same rs28357094 polymorphism has been associated with predisposition to autoimmune disorders including systemic lupus erythematosus and juvenile dermatomyositis (4,5).

Osteopontin is an acidic glycoprotein that is a member of the small integrin binding N-linked glycoprotein family that is involved in several biological pathways (6–8). OPN is viewed as an inflammatory cytokine that promotes cellular activation, migration and chemotaxis. The protein has an arginine–glycine–aspartate-
binding domain, an adjacent SVVYGLR motif showing potent angiogenic properties (9) and CD44 receptor-binding affinity that allows it to interact with a diverse range of cells (10). It has been extensively studied in a number of physiological processes including bone remodeling, tissue repair, wound healing, autoimmune disorders and numerous inflammatory conditions (11–13).

The OPN protein is at very low or undetectable levels in normal skeletal muscle. However, induction of muscle damage results in a 100-fold increase in OPN gene transcription (1,14). Muscles from Duchenne muscular dystrophy patients, as well as the dystrophin-deficient dog and mouse models also show very high levels of OPN mRNA and protein, consistent with chronic inflammation and myofiber degeneration/regeneration observed in these muscles (2,15). High OPN expression in pre-natal diaphragm of the dystrophin-deficient dogs has been seen in CD11b infiltrating cells prior to post-natal necrosis, and was considered an early biomarker of dystrophin deficiency (16). OPN is considered a pro-inflammatory cytokine in muscle, where it serves as a chemoattractant for macrophages (14), and possibly neutrophils (13), and studies of double knockouts of dystrophin and OPN suggest that OPN can be deleterious to muscle remodeling (17).

However, during normal muscle damage and repair, OPN is important for effective neutrophil and macrophage recruitment, clearing of necrotic cells and effective regeneration (18). Thus, increased OPN expression in muscle is seen in both normal and pathological muscle remodeling, and may serve both a normal physiological role and a pathological role (as is the case for many TGFbeta-associated proteins).

The genetic association of the OPN gene promoter polymorphism, rs28357094, with 17% increase in muscle size in healthy young adult females (1), and muscle wasting and weakness in Duchenne muscular dystrophy patients (2) was consistent with an important role of the OPN protein in modulating muscle response to damage and remodeling. However, the effect of the polymorphism on gene expression was difficult to rationalize with the observed phenotype associations. Specifically, the G allele has been shown to cause a 80% reduction in OPN gene promoter activity, and the same G allele was associated with a more severe DMD phenotype in young boys, and larger muscle in female (and not male) adult volunteers. To develop a molecular model for the effect of the polymorphism on muscle, we carried out both in vitro studies of the OPN gene promoter using reporter assays and in vivo studies of an eccentric muscle challenge in adult female volunteers. The in vitro assays used site-directed mutagenesis to remove the possible effects of additional polymorphisms that may be in linkage disequilibrium with the rs28357094 locus and studied estrogen responsiveness of the different alleles. OPN has been previously reported to be estrogen responsive, and the gene promoter contains estrogen-response elements (EREs) (19,20), but the possible interactions of the ERE and the rs28357094 have not been previously studied. Our data show a strong effect of the polymorphism on the response of the OPN gene to estrogen, and the in vitro and in vivo data presented are consistent with a novel molecular model that explains the effects of OPN on muscle remodeling.

RESULTS

The −66 bp OPN polymorphism shows differential effects on baseline and estrogen-responsive transcriptional regulation in muscle cells

Allele-specific OPN promoter fragments (−899 to +109 bp) were cloned into pGL4.15 luciferase reporter vectors to examine the effects of the −66 bp T/G SNP on OPN promoter activity. The constructs were then transfected into human skeletal muscle myoblasts, and baseline luciferase activity was then determined. The minor G allele caused an 80% reduction in baseline luciferase expression in transfected cells compared with the ancestral T allele (Fig. 1A). These results correspond to established data that suggest that the G allele causes a significant reduction in OPN expression (3).

Cells transfected with the allele-specific constructs were then treated with 100 nM of estrogen in serum-free media and a luciferase assay was performed 24 h after the estrogen treatment (Fig. 1B). Myoblasts transfected with constructs containing the
The G allele and treated with estrogen showed a 3-fold increase in luciferase activity compared with untreated cells. Cells transfected with constructs containing the T allele did not show any significant differences in expression when treated with estrogen (Fig. 1B).

### Eccentric exercise challenge in AA adult females

Subjects were enrolled into the Assessing Inherited Metabolic Markers in the Young (AIMM Young) at Howard University (21). As part of the AIMMY IRB consent, subjects were asked if they could be re-contacted for future studies. Genomic DNAs of 187 African-American (AA) participants in the AIMM Young study were genotyped for the −66 T/G OPN variant (rs28357094). The G allele showed an allele frequency of 8.8% in the AA group, with 17% of subjects showing GT or GG genotype (dominant inheritance model). The allele frequency observed in the AA participants was about half that observed in Caucasian populations (1). We limited the current study to the analysis of the interaction between time and arm (P = 0.02). The G allele is associated with greater loss of strength after eccentric challenge

Measures of isometric strength test were done before the bout, and at each of 4 days after the bout on both the exercised non-dominant arm and non-exercised dominant arm. Volunteers with the common TT genotype showed a time-related drop in force of the exercised non-dominant arm, but also showed a drop in the non-exercised arm such that the difference in arms was not significant (Fig. 3A). The volunteers carrying the G allele showed a more substantial drop in force of the exercised non-dominant arm, whereas the non-exercised arm showed no decrease in strength (Fig. 3B). The difference in percentage drop in force between the exercised and non-exercised arms for the G allele carriers was highly statistically significant considering both d0-d2 (P < 0.001) and d0-d4 (P < 0.001) as was the interaction between time and arm (P = 0.02).

### The G allele is associated with greater muscle swelling and inflammation

T2 images were taken of both dominant and non-dominant arms before the eccentric challenge and 4 days after the challenge. All MRI assessments were done using a pre-formed cast set at 120° angle, and images obtained in a knee coil. All images were done on the same MRI unit by the same staff. Visits 3 and 4 consisted of assessments of baseline isometric strength test and baseline pain assessments.

The eccentric muscle challenge was done at visit 4 (Day 0 for post-challenge assessments; Fig. 2) as previously described (22). The subject was positioned with their non-dominant arm at 90° angle and then instructed to resist extension of the arm with maximal voluntary elbow (biceps) contraction, with the extension force generated by the evaluator with a bar and chain connected to the modified preacher’s bench. The arm was gradually lengthened from 90° to 180° over a 5 s time. Repeated bouts were done with a 15 s rest period between bouts, until exhaustion (fatigue; average 12 bouts) (Table 1). Measures of isometric strength test were done for both the non-dominant (eccentric) and dominant (non-exercised) arms for 4 consecutive days following the intervention. Assessments of pain were also done at each visit. The post-bout MRI was done subsequent to baseline strength and pain assessments, 4 days after the bout of eccentric contractions (visit 9) (Fig. 2). This time point was previously shown to exhibit the greatest degree of muscle swelling (22).

### Table 1 Participants in the eccentric muscle challenge intervention

<table>
<thead>
<tr>
<th>ID</th>
<th>OPN genotype</th>
<th>Age (years)</th>
<th>Height (cm)</th>
<th>Weight (lbs)</th>
<th>Neck circumference (cm)</th>
<th>Mid-waist circumference (cm)</th>
<th>Hip circumference (cm)</th>
<th>BMI (lbs/in²)</th>
<th>Eccentric exercise reps</th>
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<tbody>
<tr>
<td>101</td>
<td>GG</td>
<td>23</td>
<td>171.9</td>
<td>251.8</td>
<td>14.3</td>
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<td>50.1</td>
<td>38.6</td>
<td>11</td>
</tr>
<tr>
<td>102</td>
<td>TT</td>
<td>20</td>
<td>176.0</td>
<td>223.9</td>
<td>14.5</td>
<td>41.7</td>
<td>44.0</td>
<td>32.8</td>
<td>16</td>
</tr>
<tr>
<td>103</td>
<td>GG</td>
<td>19</td>
<td>168.9</td>
<td>186.9</td>
<td>13.8</td>
<td>32.9</td>
<td>45.8</td>
<td>29.7</td>
<td>10</td>
</tr>
<tr>
<td>104</td>
<td>TT</td>
<td>19</td>
<td>175.0</td>
<td>202.3</td>
<td>nd</td>
<td>nd</td>
<td>nd</td>
<td>30.0</td>
<td>10</td>
</tr>
<tr>
<td>105</td>
<td>GT</td>
<td>21</td>
<td>171.9</td>
<td>172.8</td>
<td>13.2</td>
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<td>45.9</td>
<td>26.5</td>
<td>12</td>
</tr>
<tr>
<td>106</td>
<td>TT</td>
<td>21</td>
<td>178.1</td>
<td>160.8</td>
<td>13.3</td>
<td>30.2</td>
<td>39.2</td>
<td>23.0</td>
<td>16</td>
</tr>
</tbody>
</table>

Phenotypic features of the six AA females participating in the eccentric challenge intervention are shown. One participant (104) declined some measurements (nd, not done).

Figure 2. Protocol design for eccentric contraction challenge of the biceps muscle in young adult female volunteers. Initial visits were for informed consent, anthropomorphic measures and assessments of baseline phenotypes including MRI of both the dominant and non-dominant upper arm. Eccentric challenge of the non-dominant arm was at visit 4 (Day 0) with exit MRI at Day 4. Eccentric challenge was done only once on visit 4 (Day 0), with all subsequent visits done to assess the delayed effects of this challenge on strength and MRI changes.

<table>
<thead>
<tr>
<th>Visit</th>
<th>Days</th>
<th>Baseline MRI</th>
<th>Eccentric challenge</th>
<th>Exit MRI</th>
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<tr>
<td>1</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td></td>
<td></td>
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<tr>
<td>3</td>
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<td>4</td>
<td>3</td>
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<td></td>
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<tr>
<td>8/9</td>
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</tbody>
</table>

Measures of pain were also done at each visit. The post-bout MRI was done subsequent to baseline strength and pain assessments, 4 days after the bout of eccentric contractions (visit 9) (Fig. 2). This time point was previously shown to exhibit the greatest degree of muscle swelling (22).
The non-exercised dominant arm showed similar features in all subjects, with no evidence of inflammation or muscle swelling (Figs 4 and 5). In the TT genotype volunteers, the post-exercise non-dominant arm showed hyper-intense regions of the biceps evident in OPN-102 and OPN-106 (Fig. 4, white arrows). Subject OPN-104 showed no obvious hyper-intense T2 regions.

In the G allele carriers, there was striking hyper-intense regions involving the majority of the biceps in all three subjects (Fig. 5, white solid arrows). In two of the subjects (OPN-103, OPN-105) there was markedly hyper-intense regions at the ventral region of the biceps extending into the underlying subcutaneous fat (Fig. 5, stippled arrows). The area of inflammation appeared centered on the brachial artery and included apparent increased T2 signal in the veins and arteries, but not the brachial plexus.

The cross-sectional area of each biceps muscle was determined and the percent change in area of the exercised non-dominant arm determined between the pre-challenge and post-challenge images (Fig. 6). The TT homozygote subjects showed an average of 3% increase in biceps cross-sectional area, whereas the G allele carriers showed an average of 15% increase in size. The difference in swelling between the TT and G genotype carriers was statistically significant ($P < 0.05$).

**DISCUSSION**

The goal of our study was to provide *in vitro* and *in vivo* data sufficient to build a unifying model for the action of the −66 bp T/G polymorphism in the Sp1 transcription factor-binding site of the OPN gene promoter in muscle. Our previous findings had presented somewhat of an enigma, where the G allele was associated with larger muscle volume in young adult volunteer females (1), yet weaker muscles in young DMD boys (2). Moreover, previous studies had shown the G allele to result in 80% loss of OPN gene expression in different human immortalized cell lines (3), suggesting that less OPN (an inflammatory cytokine) results in larger muscles in females, yet weaker muscles in DMD boys. Testing of allele-specific reporter constructs in human muscle cells confirmed previous findings in other cell types, with a loss of ~80% of promoter strength (Fig. 1A).
Our search of the \textit{OPN} gene promoter for enhancer elements found potential enhancer sequences for multiple steroid hormone-binding sites [estrogen receptor (−674 bp), glucocorticoid receptor (−926 bp), vitamin D receptor (−1877 bp)], as well as a potential Nuclear factor kappa beta (NFkB) binding site (−1162 bp) (Fig. 7). Given the female-specific effect of the promoter polymorphism on muscle size, we hypothesized that there may be an allele-specific interaction between the estrogen enhancer and the more proximal Sp1 transcription factor site. Indeed, treatment of muscle cells with allele-specific reporter constructs showed that estrogen induced a 3-fold increase over baseline for the G allele, but no change in expression for the T allele (Fig. 1B).

These data suggest a hypothetical model for the sex-specific effects of the polymorphism on muscle size in females. High estrogen levels in young adult females lead to increased damage-induced OPN levels in G allele carriers due to lack of residency of the more proximal Sp1 transcription factor binding. On the other hand, T allele homozygotes have the estrogen (and possibly NFkB) response blocked due to residency of the Sp1 transcription factor near the mediator complex (Fig. 7). This model predicted that young adult females carrying the G allele may show greater sensitivity to muscle damage, and the muscle damage may in turn cause more hypertrophy in these women.

Bouts of eccentric muscle activity (lengthening contractions) are known to induce mild muscle damage and stimulate muscle hypertrophy. We hypothesized that a bout of eccentric activity in young adult females stratified for OPN genotype would show a differential response to an eccentric bout, with the G allele carriers showing greater inflammation and swelling. To test this, female volunteers were recruited from the AIMM Young baseline genotype/phenotype study of young adults (21). Three females of each genotype undertook an eccentric exercise bout of the non-dominant upper arm (biceps), with longitudinal measures of strength and imaging by MRI. This study confirmed our hypothesis. The G allele carriers showed significantly greater muscle swelling at Day 4 after the bout and greater loss of strength (Figs 3–6). Surprising, there was striking inflammatory signal in the MRI in two of the three G allele carriers, centered on the brachial large blood vessels (Fig. 5). The inflammation extended into the biceps, and also into the subcutaneous fat tissue.

Our model suggests that G allele carriers show heightened sensitivity to mild muscle damage, with both exaggerated muscle swelling and inflammatory response, and this leads to greater susceptibility to muscle hypertrophy. In Duchenne muscular dystrophy, patient muscle shows a high degree of activation of NFkB pro-inflammatory pathways soon after birth, many years prior to clinical onset (23). Given the promoter structure of the \textit{OPN} gene, with multiple predicted steroid hormone enhancers and NFkB promoter element (Fig. 7), our model can be extended to the observed genotype/phenotype relationship in DMD. DMD patients carrying the G allele may show greater NFkB- and/or glucocorticoid-induced transcription of the \textit{OPN} gene during chronic inflammation, leading to exacerbation of the
pro-inflammatory state of muscle and worsening of phenotype, as we have previously reported. Thus, the integration of gene structure, in vitro reporter assays and intervention study in young adult volunteers provides a hypothetical unifying model for the interaction of the OPN promoter SNP and muscle remodeling. However, the complex regulation of the OPN gene in response to multiple inflammatory and steroid hormone promoter elements makes it challenging to predict the precise responses of the gene in vivo.

Limitations to the study presented here include the low number of volunteers enrolled into the eccentric intervention (n = 3 per genotype group), and the lack of muscle biopsies from the volunteers to correlate OPN protein and mRNA levels with respective genotypes and degree of inflammation. Extensive correlations of OPN genotype with OPN protein levels have been previously reported for DMD patient muscle, and there was no association of genotype with OPN levels (24). The argument presented in this previous publication is that the variable degree of inflammation in each biopsy and complex regulation of OPN protein in the extracellular space, both likely obscures the in vivo correlations of OPN genotype and OPN gene expression seen in vitro. Finally, we have not directly addressed the molecular basis of the association of the G allele with muscle weakness in DMD. Our results suggest that this association may be related to glucocorticoid treatment of DMD, but further genetic associations studies of DMD patient populations treated and un-treated with glucocorticoids must be done to test this hypothesis.

**MATERIALS AND METHODS**

**Human subjects**

One hundred and eighty-seven AA females previously recruited into the NIH P20 AIMM Young Study from Howard University were genotyped for the rs2857094 polymorphism. AIMM Young is an ongoing project that concentrates on the genetics of metabolic syndrome in young adults (21). It functions as a collaborative between the Georgetown-Howard Universities Center for Clinical and Translational Science and Children’s National Medical Center. AIMM Young subjects were re-contacted based on genotype and asked to complete an eccentric muscle challenge with MRI as the final outcome. A total of six females (3GG/GT and 3 TT) were subsequently enrolled into the eccentric exercise intervention. All females were 19–23 years of age, healthy and either sedentary or only recreationally active. Participants were screened prior to study entry to determine if they had any orthopedic, muscular or other medical conditions that would prohibit them from completing the study.
**Genotyping**

To determine the specific OPN genotype of rs28357094 (−66 T/G variant), DNA was extracted from the peripheral blood of all 187 individuals within the Howard University AIMM Young Study using standard manufacturer’s procedures (Qiagen, Valencia, CA, USA). DNA was then amplified on an ABI 2720 Thermal Cycler using TaqMan rs28357094 primers/probe: forward 5′-AAGTGTCTCTCCGTGGATGCTG-3′, reverse 5′-CTCCTGC TGCTGCTGACAAC-3′ and sickle cell probe rs334: forward 5′-AGTCAAGGGCAGACGACATCA-3′, reverse 5′-CTCACCA CCACTTCATCCA-3′.

**Biceps isometric strength test**

Participants performed isometric strength test of the biceps muscles using a modified arm curl bench (CSN Stores, MA, USA). To assess biceps flexion isometric strength, the arm was positioned at a 90° position with the curl bar attached to a load cell (Transducer Technologies, Inc., Whittier, CA, USA). During the test the subject was instructed to exert a maximal biceps muscle contraction at the 90° angle with the tension generated was recorded as maximal strength expressed in kilograms. Muscle strength was assessed in both the right and left arms with the subjects performing three maximal contractions on each arm. All statistical analyses utilized the average value for these three strength measurements.

**Exercise protocol**

Each participant performed one set of maximal lengthening contractions (eccentric) on a modified preacher’s arm curl machine. The eccentric exercise protocol has been detailed previously (22). To perform this exercise, the active arm of the participant was placed on the padded support in a flexed position, while the passive arm rested on the participant’s side. The participant’s arm was then guided by the investigator from a completely flexed position to a fully extended position. The modifications in the arm were performed with 20% fetal calf serum and penicillin–streptomycin growth medium kit (Promocell, Heidelberg, Germany) supplemented with 20% fetal calf serum and penicillin–streptomycin (1% (v/v); all supplied by Life Technology, Carlsbad, CA, USA). Cultures were maintained in this complete growth medium in a humidified atmosphere under 5% CO₂ at 37°C.

**Cell culture and transfection**

Human skeletal myoblast cell line (obtained from Vincent Moully, Institut de Myologie, Paris, France) was maintained in skeletal muscle cell growth medium using skeletal muscle cell growth medium kit (Promocell, Heidelberg, Germany) supplemented with 20% fetal calf serum and penicillin–streptomycin (1% (v/v); all supplied by Life Technology, Carlsbad, CA, USA). Cultures were maintained in this complete growth medium with transfection reagent was removed; cells were washed and replaced with serum-free medium containing 100 nM estrogen for further 24 h. Cell lysates were prepared using lysis buffer consisting of 25 mM Gly (pH 7.8), 1% Triton X-100 (v/v), 15 mM MgSO₄ (heptahydrate), 4 mM EGTA and 1% (v/v); all supplied by Life Technology, Carlsbad, CA, USA). Cultures were maintained in this complete growth medium with transfection reagent was pre pared. Transfection was performed over a 48 h period in complete growth medium without antibiotic. The amount of DNA used for transfection was 2.5 μg. In the experiments where estrogen (Sigma-Aldrich, St. Louis, MO, USA) was added, the complete growth medium with transfection reagent was removed; cells were washed and replaced with serum-free medium containing 100 nM estrogen for further 24 h. Cell lysates were prepared using lysis buffer consisting of 25 mM Gly (pH 7.8), 1% Triton X-100 (v/v), 15 mM MgSO₄ (heptahydrate), 4 mM EGTA and 1% (v/v); all supplied by Life Technology, Carlsbad, CA, USA). Cultures were maintained in this complete growth medium with transfection reagent was removed; cells were washed and replaced with serum-free medium containing 100 nM estrogen for further 24 h. Cell lysates were prepared using lysis buffer consisting of 25 mM Gly (pH 7.8), 1% Triton X-100 (v/v), 15 mM MgSO₄ (heptahydrate), 4 mM EGTA and 1% (v/v); all supplied by Life Technology, Carlsbad, CA, USA). Cultures were maintained in this complete growth medium with transfection reagent was removed; cells were washed and replaced with serum-free medium containing 100 nM estrogen for further 24 h. Cell lysates were prepared using lysis buffer consisting of 25 mM Gly (pH 7.8), 1% Triton X-100 (v/v), 15 mM MgSO₄ (heptahydrate), 4 mM EGTA and
1 mM DTT in 10 ml water. Luciferase activity was measured using Luciferase Assay system (Promega) with Centro LB 960 microplate luminometer (Berthold Technologies, Oak Ridge, TN, USA). The data obtained were normalized to the protein concentration from each well.

**Statistical analysis**

Several phenotypes were compared with tests appropriate for the distribution of the dependent variable. A P-value of $\leq 0.05$ was considered statistically significant. As shown in Figure 1, the comparison of % decrease in luciferase activity between TT and G allele cells were performed using a student’s t-test and the comparison of fold change between baseline and post-estrogen treatment was performed in TT and G allele cells separately using a paired t-test. Analyses comparing changes in isometric strength between arms (Fig. 3) were performed using a repeated-measure ANOVA including main effects of arm and time and an arm $\times$ time interaction. Lastly, the comparison between median % change in muscle volume between TT and G allele individuals was performed using a Wilcoxon rank sum test.

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**Conflict of Interest statement.** None declared.

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