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RESPONSE TO COMMENT ON SPROUSE ET AL.

SLC30A8 Nonsynonymous Variant Is Associated With Recovery Following Exercise and Skeletal Muscle Size and Strength. Diabetes 2014;63:363–368

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The authors wish to thank Dr. Weijers (1) for his insightful comments on our article (2). Dr. Weijers is correct that most genetic variants identified using genome-wide association studies (GWAS) are not yet currently used in clinical practice to predict disease risk. Manolio et al. (3) addressed this lack of clinical use in an exquisite review in *Nature Reviews Genetics*. Their review discusses not only criticisms and limitations of the GWAS method and how they affect the potential impact of GWAS findings in clinical care, but also how GWAS findings have been or probably will be leveraged to improve disease prediction, biomarker identification, treatment selection, and drug dosing.

It was not the goal of our article to analyze whether a single nucleotide polymorphism (SNP) predicts the likelihood of developing type 2 diabetes (T2D). Rather our goal was to explore whether rs13266634, located within the *SLC30A8* gene and previously identified (by GWAS) as an influencing risk for T2D, also influences exercise phenotypes—specifically the response of skeletal muscle to resistance exercise.

We are not the first group to examine a GWAS SNP for a relationship with a new phenotype. For example, a SNP in the *FTO* gene, known to be associated with BMI and T2D, has been shown to be associated with brain volume (4). This relationship is not surprising as there is a known interaction between elevated BMI, brain atrophy, and increased expression of the *FTO* gene in the brain. Careful exploration of the many complex relationships between GWAS SNPs and novel phenotypes may eventually allow GWAS analysis to move into the clinical setting.

Again, we thank Dr. Weijers for his comment.

Duality of Interest. No potential conflicts of interest relevant to this article were reported.

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