Response to Genomic Association Analysis Identifies Multiple Loci Influencing Antihypertensive Response to an Angiotensin II Receptor Blocker

We appreciate the interest of Dr Frau et al1 in our genome-wide association analysis of blood pressure response to the angiotensin II receptor antagonist, candesartan, in which single nucleotide polymorphism associations were validated by demonstrating opposite direction associations with blood pressure response to the thiazide diuretic, hydrochlorothiazide.2 In lieu of multiple, independent same-race candesartan-treated samples available for replication analyses, this approach to single nucleotide polymorphism validation was motivated by the observation that all known predictors of blood pressure response to inhibitors of the renin–angiotensin system (eg, plasma renin activity, race, and age) have opposite direction associations with blood pressure response to diuretics.3 Although some methodological differences could conceivably account for nonreplication of the opposite direction associations for 6 lead single nucleotide polymorphisms tested by Dr Frau et al, our statistical analysis was based on a superset of 273 single nucleotide polymorphisms across all 6 gene regions. A comparable multigene-based approach may be reconsidered by the HYPERGENES Study4 investigators as their complete data set is analyzed.

Disclosures

None.

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