Letter to the Editor

Comment on: Lin et al. (2007) *SUMO4* M55V Variant Is Associated With Diabetic Nephropathy in Type 2 Diabetes: *Diabetes* 56:1177–1180

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Lin et al. (1) have recently reported a positive association of the *SUMO4* M55V variant with diabetic nephropathy in an Asian cohort of 430 patients with type 2 diabetes. The authors found a strong association of the G allele with an increased risk for diabetic nephropathy.

Thus far, little is known about the physiologic role of the recently discovered posttranslational modifier *SUMO4*. One of the putative substrates of *SUMO4* is the inhibitor κBα (IκBα), which negatively regulates transcriptional activity of the proinflammatory transcription factor nuclearfactor-κB (NF-κB) (2). SUMOylation seems to stabilize Iκ-Bα resulting in a reduced activation of NF-κB. Since excessive NF-κB activation is supposed to promote micro- and macrovascular disease (2,3) SUMOylation of IκBα might modulate the development of late diabetes complications.

In contrast to Lin et al., we report no association of the *SUMO4* M55V variant with diabetic nephropathy in 752 Caucasian patients with type 1 and type 2 diabetes (n = 237 and 515, respectively). The characterization of the study population was previously described in detail (4). To increase power, subjects with homozygous and heterozygous genotypes were combined for statistical analysis. No association was detected, either when all 752 diabetic patients were analyzed together (GG and GA, 32.6%; AA, 36.6%; P = 0.36) or when a separate analysis of patients with type 1 (GG and GA, 22.2%; AA, 19.2%; P = 0.70) and type 2 (GG and GA, 37.2%; AA, 43.9%; P = 0.20) diabetes was performed.

These differences might be explained by the ethnical background of the studied cohorts, e.g., Asian and Caucasian population, and thus demand further studies in different ethnic groups to clarify the effect of the *SUMO4* M55V variant in diabetic nephropathy.

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