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RESPONSE TO COMMENT ON VASSY ET AL.

Polygenic Type 2 Diabetes Prediction at the Limit of Common Variant Detection. Diabetes 2014;63:2172–2182

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Abbasi et al. (1) raise excellent points about the current and future states of type 2 diabetes risk prediction. Two issues in particular are worth consideration.

First, our clinical and polygenic prediction models do not include time-varying assessments of known risk factors such as BMI and fasting glucose (2). Abbasi et al. are correct that doing so would likely improve the models' predictive accuracy. Instead, we patterned our models on what is more common in clinical practice. In many ways, the Framingham Heart Study cardiovascular disease risk score defines the paradigm of using a "snapshot in time" approach to risk assessment. That is, what can the characteristics of a patient sitting in front of the clinician tell him or her about that patient's risk of an outcome 10 years from now? The dynamic risk factors Abbasi et al. propose will be especially salient if clinicians increasingly incorporate risk factor trajectories into their clinical decision making.

Second, their tiered approach to risk stratification (i.e., obtaining more resource-intensive information only among those individuals whose history suggests higher risk) places an appropriate emphasis on the risks, benefits, and costs of screening. We agree with their call for an evaluation of such screening strategies, although we would argue that anthropometry and basic laboratory analyses are already routinely measured in the many clinical settings. An interesting question, then, is whether collection of genome-wide data will be increasingly routine in the clinical setting or even brought by the patients themselves after consulting genotyping services outside of the standard clinical setting. We think our analyses show that even if each individual had his or her genotype for common genetic variation stored in the electronic medical record, its marginal value in diabetes risk prediction would be small. Whether more sophisticated genetic information available soon from high-throughput whole-genome sequencing with detailed functional annotation will improve type 2 diabetes risk prediction, drug targeting, or patient care overall remains an important question for the future.

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

References

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