Letter to the Editor

Cancer Prevention Research

Lung Cancer Risk Prediction to Select Smokers for Screening CT—Response

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We read with interest the letter by Young and Hopkins, which emphasizes the need for optimizing existing lung cancer risk prediction models. On the basis of data from a case–control study conducted in current and former smokers, they estimated that the eligibility criteria of the COSMOS trial would identify only 57% of the cases in their series. We realized that exclusion of long-term former smokers in our trial would have represented a limitation for the development of a generalizable risk prediction model; another limitation being the small number of participants exposed to asbestos. For these reasons, we decided to recalibrate an existing model which was developed in a wider population rather than to build a new model based on our study-specific risk estimates. Our revised risk prediction model (1) has the same limits as the original model proposed by Bach and colleagues (2), that is, applicable to current smokers, and former smokers who quit 20 years ago or less, with a smoking history of 10 to 60 cigarettes a day for 25 to 55 years (3) and is therefore applicable to a broader population than that originally enrolled in the COSMOS study (current smokers, and former smokers who quit 10 years ago or less, who smoked at least 20 pack-years).

We fully agree that addition of clinical variables such as chronic obstructive pulmonary disease (COPD), or genetic risk variables including genetic markers could in theory further increase the sensitivity of our model. However, models such as the one proposed by Young and colleagues (4) have limited clinical applicability as they require the whole population to have lung function assessed and genetic tests conducted, whereas our risk prediction model relies only on individuals' past history and could be applied at large in the general population to select individuals amenable to low-dose computed tomographic (LDCT) screening.

Disclosure of Potential Conflicts of Interest

All authors confirm that the information reported above is accurate and understand that this information will be disclosed publicly. No potential conflicts of interests were disclosed.

Authors' Contributions

Conception and design: P. Maisonneuve, V. Bagnardi, G. Veronesi
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Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): P. Maisonneuve, V. Bagnardi
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Received January 26, 2012; accepted January 26, 2012; published online April 4, 2012.

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doi: 10.1158/1940-6207.CAPR-12-0044

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Cancer Prev Res 2012;5:699.