clinicians not only to plan treatments but also to inform patients about the options and potential consequences of therapies in better ways. This can help to involve patients in the decision-making process regarding management and can improve compliance.

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From the authors:

We thank P. Mohapatra and co-workers for their interest in our article. Their comments highlight some of the current challenges in predicting response to epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKIs) in lung cancer. We built our nomogram to predict the presence of *EGFR* activating mutations, as these alterations represent the best available predictive biomarker in this setting, at a time when data about tumour response to EGFR TKIs were not available from large cohorts of patients [1]. Once such data emerge, a predictive model of tumour response to EGFR TKIs, as well as other targeted therapies in other molecular subsets of lung tumours, may be developed.

As we stated, *EGFR* genotyping is now a standard, and should be obtained when possible. Physicians, as well as healthcare providers, need to work on offering each patient with lung cancer molecular diagnoses, including *EGFR* mutation genotyping, as well as testing for other oncogenic alterations if specific targeted therapies are available [2]. Despite undeniable progress in recent years, one must keep in mind that molecular diagnoses are not routinely available in numerous countries, including European countries. Mutation genotyping based on serum tumour DNA or circulating tumour cells is a promising concept, and may be useful when access to tumour tissue is limited [3, 4]. However, such techniques remain to be evaluated and implemented in routine practice, even in developed countries. Of note, the two papers cited by P. Mohapatra and co-workers included only 58 and 35 patients, respectively [3, 4]. Ultimately, the evaluation of such new predictive biomarkers is challenging, and beyond the small experience reported so far, dedicated prospective trials may be required to accurately assess their sensitivity, specificity and positive and negative predictive values.

In the end, nomograms are user-friendly graphical representations of predictive models. Nomograms have been evaluated in specific clinical situations, and subsequently integrated in clinical practice guidelines, especially in prostate cancer [5, 6]. As we discussed in our article, our nomogram, despite its strong accuracy in non-Asian patients, does have some limitations. Any prediction instrument incorporates a certain degree of uncertainty. Although we built our model using an international multicentre cohort of patients, our nomogram needs to be further validated in additional cohorts. Its potential role in individual decision making remains to be determined. Aiming at facilitating subsequent studies, we have developed a website (www.myEGFRscore.com) that, based on our predictive model, provides the individual probability of *EGFR* mutation in non-Asian patients with lung adenocarcinoma tumours, in an even more straightforward way in routine clinical care.

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