ERRATUM

Erratum to: Pharmacokinetic–pharmacodynamic relationship of bosutinib in patients with chronic-phase chronic myeloid leukemia

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The author would like to correct the errors in the publication of the original article. The corrected details are given below for your reading.

The first paragraph under heading "Safety Parameters" should read as

"Data from the pooled safety analysis (Appendix Table A2) demonstrated that although gastrointestinal toxicities (e.g., diarrhea [77 %], nausea [40 %], and vomiting [35 %]) were frequently reported across the two studies, most events were of low severity grade. Other toxicities of clinical interest included thrombocytopenia (29 %), rash (31 %), ALT elevation (21 %), AST elevation (17 %), and neutropenia (16 %)."

Secondly, the last sentence in the page 216 beneath the heading "Discussion" should read as

"These data compare favorably with the findings from previous studies of patients with CP CML treated with dasatinib or nilotinib in the second- or third-line settings."

Finally, Fig. 2g has a wrong indication inside the figure label. It should correctly read as

"E_{max}" model

The revised figure is placed in the following page.
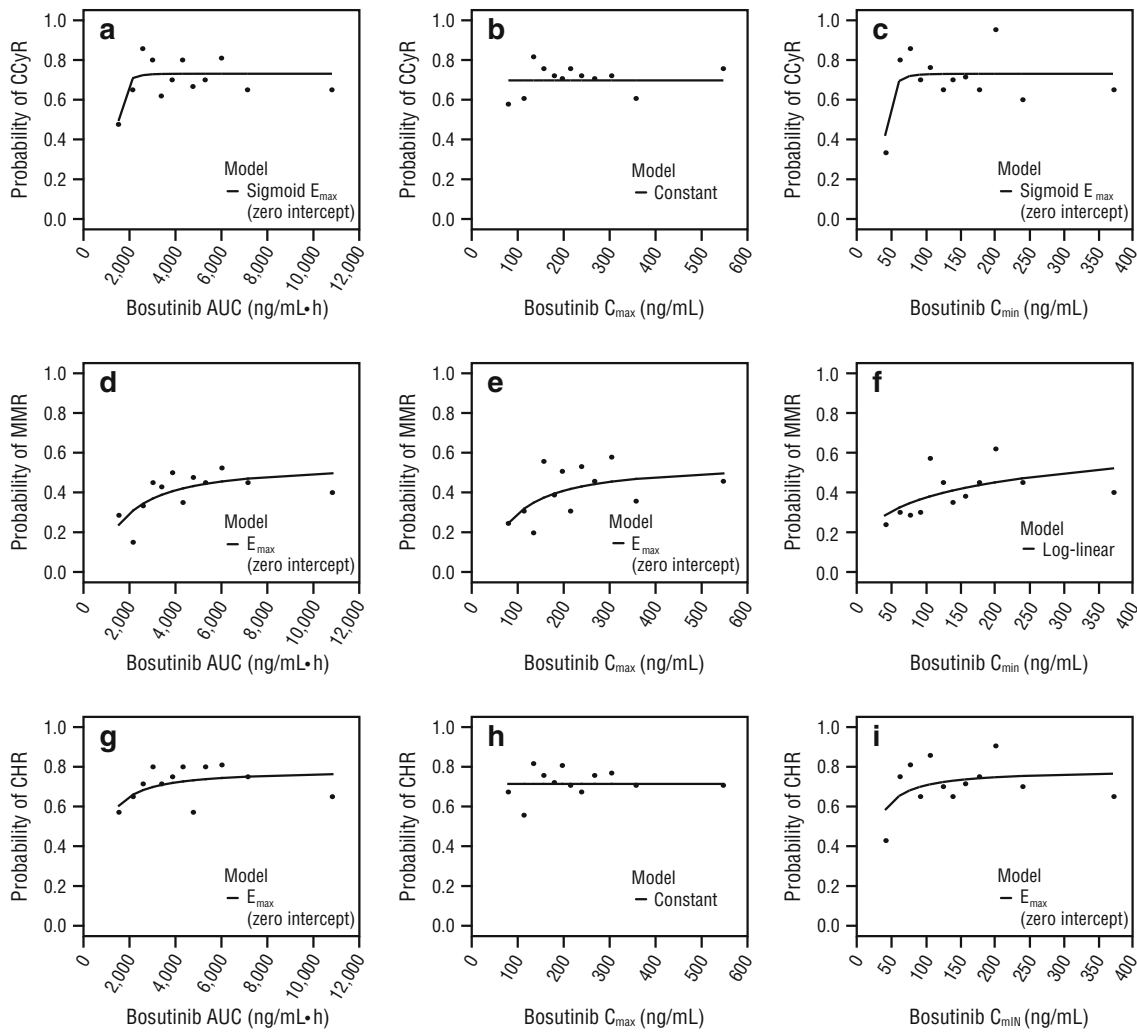
Fig. 2 Probability of response at 1 year versus bosutinib exposure in patients with newly diagnosed CP CML. **a**, **b**, and **c** are the probability of achieving a CCyR at 1 year versus AUC, C_{max}, and C_{min}, respectively. **d**, **e**, and **f** are the probability of achieving a MMR versus AUC, C_{max}, and C_{min}, respectively. **g**, **h**, and **i** are the probability of achieving/maintaining a CHR versus AUC, C_{max}, and C_{min}, respectively. Response data were coded as binary variables, where 0 corresponded to no response and 1 corresponded to response; exposure metrics were derived from a previously developed bosutinib population pharmacokinetic model. Solid lines are predictions of the best models. Solid lines are predictions of the best models. *CP CML* chronic-phase chronic myeloid leukemia, *CCyR* complete cytogenetic response, *AUC* area under the curve, C_{max} maximal plasma concentration, C_{min} minimum plasma concentration, *MMR* major molecular response, *CHR* complete hematologic response