

Published on *Meeting Library* (https://meetinglibrary.asco.org)

<u>Home</u> > 89528-116

89528-116

Correlation of germline *MET* mutation with response to the dual Met/VEGFR-2 inhibitor foretinib in patients with sporadic and hereditary papillary renal cell carcinoma: Results from a multicenter phase II study (MET111644).

Subcategory: Renal Cell Cancer

Session Type and Session Title:

General Poster Session E: Renal Cancer

Abstract Number:

372

Citation:

J Clin Oncol 30, 2012 (suppl 5; abstr 372)

Author(s):

Ramaprasad Srinivasan, Donald P. Bottaro, Toni K. Choueiri, Ulka N. Vaishampayan, Jonathan E. Rosenberg, Theodore Logan, Andrea Lynne Harzstark, Brian I. Rini, Sandy Srinivas, Laurel M. Adams, Kevin Laubscher, Lone Harild Ottesen, David F. McDermott, W. Marston Linehan; Urologic Oncology Branch, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD; National Cancer Institute/National Institutes of Health, Bethesda, MD; National Cancer Institute/National Institutes of Health, Bethesda, MD; Lank Center for Genitourinary Oncology, Dana-Farber Cancer Institute/Brigham and Women's Hospital, Harvard Medical School, Boston, MA; Karmanos Cancer Institute, Wayne State University, Detroit, MI; Indiana University Melvin and Bren Simon Cancer Center, Indianapolis, IN; University of California, San Francisco, San Francisco, CA; Cleveland Clinic Taussig Cancer Institute, Cleveland, OH; Stanford Medical Center, Stanford, CA; GlaxoSmithKline, Research Triangle Park, NC; GlaxoSmithKline Oncology R&D, Middlesex, United Kingdom; Beth Israel Deaconess Medical Center, Boston, MA

Background: Activating mutations and/or amplifications in *MET* have been described in patients (pts) with papillary renal cell carcinoma (PRC). Foretinib, an oral multi-kinase inhibitor targeting

MET, VEGF, RON, AXL, and TIE-2 receptors, was evaluated in a phase 2 study in pts with PRC. An important objective of this study was to evaluate whether activation of the MET receptor pathway by mutation, amplification, or gain of chromosome 7 was predictive for or correlated with clinical outcomes. Methods: Pts were stratified based on status of MET pathway activation. Blood samples were collected at screening for determination of germline *MET* mutational status. Archival tumor tissue samples were obtained for the analysis of somatic *MET* mutation, amplification of the MET locus (7q31), and gain of chromosome 7 using standardized assays. Results: A total of 74 pts were enrolled on the trial (37 each in intermittent and daily dosing arms); overall efficacy and safety data are reported separately at this meeting. Sixty-seven pts were evaluable for both mutation status and response. 5/10 pts (50%) with a germline MET mutation experienced a PR, while 5 pts (50%) had SD as their best response, including 4 pts who demonstrated tumor SLD reductions of > 10%, but did not achieve PR by RECIST 1.0. Responses were also seen in pts without germline MET mutation. However, the presence of a germline MET mutation was highly predictive of a response as only 5/57 pts (9%) without a mutation experienced a PR. Other measures of MET pathway activation did not appear to correlate with activity with only 1/5 pts (20%) with somatic MET mutation having a PR; furthermore, in the absence of a concomitant *MET* mutation, no responses were seen in patients with MET amplification (n=2) and only 1/18 (5%) pts with a gain of chromosome 7 experienced a PR. **Conclusions:** The presence of germline *MET* mutations correlated strongly with activity of the MET inhibitor foretinib in pts with PRC. These data provide early proof of principle that MET may be a valid therapeutic target in a subset of patients with PRC.

Source URL: https://meetinglibrary.asco.org/content/89528-116