A Phase I, Dose-Escalation Study of the Multitargeted Receptor Tyrosine Kinase Inhibitor, Golvatinib, in Patients with Advanced Solid Tumors


Abstract

**Purpose:** Receptor tyrosine kinases c-Met and Ron transduce signals regulating cell migration and matrix invasion. This phase I dose-escalation trial tested golvatinib, a highly potent, small-molecule, ATP-competitive inhibitor of c-Met and multiple members of the Eph receptor family plus c-Kit and Ron.

**Experimental Design:** Patients with advanced solid tumors received golvatinib orally, once daily, continuously. Using a "3+3" design, dosing started at 100 mg once daily, escalating to the maximum tolerated dose (MTD) defined by dose-limiting toxicities. Pharmacokinetic, pharmacodynamic, and preliminary antitumor activity was assessed during dose escalation and in a MTD expansion cohort.

**Results:** Thirty-four patients were treated at six dose levels. The MTD was determined as 400 mg once daily. Three dose-limiting toxicities were observed: grade 3 increased \( \gamma \)-glutamyltransferase and alkaline phosphatase (200 mg), repeated grade 2 fatigue, and grade 3 fatigue (50.0%). Frequent treatment-related adverse events (with incidence >10%) included diarrhea (58.8%), nausea (50%), vomiting (44.1%), fatigue (41.2%), decreased appetite (32.4%), elevated alanine aminotransferase (32.4%), elevated aspartate aminotransferase (20.6%), dry skin (11.8%), and dysgeusia (11.8%). Best overall response was stable disease (median duration 85 days, range 85–237). Pharmacokinetics demonstrated high variability, although maximum plasma concentration and area under the plasma concentration–time curve increased with dose. Soluble urokinase-type plasminogen activator receptor, VEGFR2, c-Met, and angiopoietin-2 levels increased after dose. Posttreatment decrease in either p-c-Met or p-ERK was observed in 3 of 4 paired biopsies at MTD.

**Conclusions:** Golvatinib at the MTD of 400 mg once daily was well tolerated with pharmacodynamic evidence of c-Met target modulation.

Introduction

The protein product of the MET proto-oncogene, c-Met, a receptor tyrosine kinase (RTK), is a prototype for the c-Met RTK subfamily (1). A second member of the family is Ron (2). Both RTKs share similar structural and biochemical properties, existing as heterodimers of an \( \alpha \) and 1\( \beta \) chain. c-Met is activated by the ligand hepatocyte growth factor (HGF; scatter factor) while Ron is activated by macrophage-stimulating protein (HGF-like protein; refs. 2, 3). The c-Met signaling pathway engages with other pathways, including that of the EGFR/human EGFR/MAPK/ERK pathway; this pathway is critical in driving the pathogenesis of several cancers (4, 5). In non–small cell lung cancer (NSCLC), c-Met signaling is also thought to contribute to the development of resistance to EGFR inhibitors (6, 7). c-Met signaling can also promote angiogenesis through interaction with the VEGF and VEGF receptor (VEGFR) pathway (8, 9). In particular, c-Met signaling can downregulate the antiangiogenic thrombospondin-1 and upregulate VEGF (10), and there is evidence that upregulation of HGF and c-Met occurs after VEGF inhibition and represents a potential mechanism of resistance to antiangiogenic therapy (11).

Ligand-dependent or -independent activation (MET amplification and mutation) of the receptors leads to...

\[ \text{Equation} \]

\[ \text{Figure} \]
Rhoda Molife et al.

Translational Relevance

Golvatinib is a highly potent, small-molecule, ATP-competitive inhibitor of c-Met and multiple members of the Eph receptor family, as well as c-Kit and Ron, based on isolated kinase assays. Golvatinib showed significant antitumor effects in mouse xenograft models of cancer cell lines with MET gene amplification. This first-in-human, phase I, dose-escalation clinical trial of oral golvatinib established the recommended phase II dose for a once daily continuous dosing schedule at 400 mg and showed evidence of biological activity. These observations have provided a rationale to support the continued evaluation of golvatinib in phase II combination studies in different tumor types: gastric cancer, squamous cell carcinoma of the head and neck, and hepatocellular carcinoma where c-Met signaling plays a role in pathogenesis.

Materials and Methods

This was an open-label, phase I, dose-escalation study with an expansion cohort at the MTD (ClinicalTrials.gov trial registration ID: NCT00869895). The study was conducted in two centers in the United Kingdom: The Royal Marsden NHS Foundation Trust (Sutton, Surrey) and The Christie NHS Foundation Trust (Manchester, UK). The study was approved by the relevant regulatory and independent ethics committees and conducted in accordance with the principles of the Declaration of Helsinki and the International Conference on Harmonisation Good Clinical Practice Guidelines. All patients provided written informed consent before any study procedures were performed.

Patient selection

Eligibility criteria. Patients aged ≥18 years with histologically or cytologically confirmed advanced or metastatic solid tumors unresponsive to standard treatment, or for which no standard treatment was available, were eligible provided they met the following criteria: adequate bone marrow function (hemoglobin >9.0 g/dL; absolute neutrophil count >1.5 × 10^9/L; platelet count >100 × 10^9/L), renal function [serum creatinine <1.5 mg/dL (133 μmol/L) or calculated creatinine clearance >50 mL/minute per the Cockcroft and Gault formula], and liver function [bilirubin <1.5 × upper limit of normal (ULN); alkaline phosphatase (ALP), alanine transaminase (ALT), and aspartate transaminase (AST) <3 × ULN or <5 × ULN in the presence of liver metastases]. Eastern Cooperative Oncology Group (ECOG) performance status (PS) of 0 or 1, and life expectancy of ≥3 months. At the MTD expansion, up to 6 patients recruited were required to have a lesion amenable for paired (pre- and posttreatment) tumor biopsies. Patients were excluded in the case of any condition that precluded oral intake or oral absorption, untreated or unstable known primary or metastatic central nervous system tumors, uncontrolled hypertension, clinically significant cardiac impairment, or unstable ischemic heart disease within the previous 6 months,

increased cell proliferation, migration, matrix invasion, and invasive growth (1, 2). The most frequent cause of constitutive activation of c-Met is protein overexpression and this has been demonstrated in NSCLC, renal cell cancer (RCC), mesothelioma, breast cancer, ovarian cancer, colorectal cancer (CRC), and squamous cell carcinoma of the head and neck (SCCHN; refs. 12, 13). MET amplification has been demonstrated in upper gastrointestinal tumors, CRC, NSCLC, medulloblastomas, and glioblastomas (14–17). Activating mutations are less frequently reported than amplification, and have been described in papillary RCC (18). More frequent sporadic mutations have been demonstrated in RCC, SCCHN, gastric cancer, small-cell lung cancer, NSCLC, and mesothelioma (19–24).

The Eph receptors are the largest family of RTKs existing as transmembrane receptors stimulated by plasma membrane bound ligands, the ephrins (25). They are divided into two subclasses: subclass A receptors which are membrane bound and preferentially bind all A-type ephrins and subclass B receptors that preferentially bind all B-type ligands (26). Signaling by Ephs has been shown to lead to vascular development, vessel stability mediated through pericyte stabilization, and angiogenesis, altered cell mobility, migration, and adhesion; while lowly expressed in normal adult tissues, they are expressed and reexpressed at high levels during organogenesis and tumorigenesis (27–29). Overexpression of Eph receptors has been demonstrated in several tumor types, including NSCLC, ovarian, breast, endometrial, and gastric cancers, as well as glioblastomas, where it correlates with a poor survival (30–34); as such, Eph receptors represent potential novel therapeutic targets.

Golvatinib (E7050, Eisai) is a highly potent, small-molecule, ATP-competitive inhibitor of c-Met and multiple members of the Eph receptor family, as well as c-Kit and Ron (35), with an IC_{50} for c-Met of 0.001 μmol/L, for Eph members (A6, B2, A8, A7, B4, B1, and A5) between 0.007 and 0.018 μmol/L, for Kit of 0.010 μmol/L, and for Ron of 0.017 μmol/L (Eisai data on file). It has demonstrated significant preclinical antitumor effects, including tumor regressions in MET-amplified mouse xenograft cancer cell lines (36). Additional in vitro preclinical data (measuring the network length of HUVECs on a monolayer of human brain vascular pericytes) have shown that golvatinib disrupts pericyte function and thus vascular integrity, via the inhibition of EphB4 (and Tie-2; ref. 37). Preclinical toxicology (Eisai data on file) indicated primarily gastrointestinal toxicity. Here we report on a phase I first-in-human study of golvatinib in patients with advanced solid tumors. The primary objective of this study was to determine the maximum tolerated dose (MTD) based on the dose-limiting toxicities (DLT) of golvatinib. Secondary objectives were to assess safety and tolerability, determine the pharmacokinetic profile, explore the pharmacodynamic effects, and assess antitumor activity.

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pregnancy or lactation, any other significant comorbidity, and/or requirement for therapeutic anticoagulation.

**Study design.** This study utilized a "3+3" dose-escalation design, followed by recruitment to a MTD expansion cohort. Golvatinib was administered orally, once daily, continuously, in 28-day cycles, starting at 100 mg. Dosing was on an empty stomach, with a 2-hour fast postdose. Dose escalation in subsequent cohorts was in 100% increments until the emergence of grade ≥2 drug-related toxicities; from this point, dose increments were by 50% in the event of grade 2 toxicity or 25% to 33% in the event of grade 3 toxicity. The MTD was defined as the highest dose at which no more than 1 of 6 patients experienced a DLT during cycle 1. DLT was defined during cycle 1 as any clinically significant treatment-related adverse event (AE) that met any of the following criteria: any grade 3 or higher hematologic or nonhematologic toxicity, any repeated grade 2 hematologic or nonhematologic toxicity requiring dose reduction, or failure to administer >75% of the planned dosage (i.e., failure to take at least 21 days of treatment over the first 28 days). Patients who failed to take at least 75% of the daily dose during cycle 1 for reasons other than toxicity were not evaluable for DLT and were replaced in the cohort. Once the MTD was determined, up to 6 additional patients with at least 1 tumor lesion suitable for paired biopsies were enrolled for further evaluation of safety, pharmacokinetic, and pharmacodynamic profiles, and preliminary antitumor activity. Golvatinib was administered until disease progression, unacceptable toxicity, or withdrawal of consent.

**Safety and efficacy assessments.** Safety assessments included medical review, physical examination, vital signs, clinical laboratory tests (complete blood count, clinical chemistry, and urinalysis), and electrocardiogram. All assessments were conducted at baseline, weekly during cycle 1, and biweekly thereafter. All AEs were graded using the National Cancer Institute Common Terminology Criteria for Adverse Events version 3.0. Radiologic assessments were performed at baseline and at the end of every 2 cycles (every 8 weeks) according to the Response Evaluation Criteria in Solid Tumors (RECIST) version 1.0 (38).

**Study drug.** Golvatinib was supplied as 10-, 50-, and 100-mg pale yellowish-red, film-coated, round, biconvex tablets for oral administration, manufactured at the Eisai Formulation Research Laboratories.

**Pharmacokinetics.** Blood samples were collected during cycles 1 and 2 on day 1 (predose, 0.5, 1, 2, 4, 6, and 8 hours postdose). Further predose samples were collected in cycle 1 (days 2, 8, 15, and 22), cycle 2 (days 2 and 15), and days 1 and 15 of subsequent cycles. Plasma samples were stored at −20 °C until analysis. Plasma concentrations of golvatinib and its metabolite M2 were determined using a validated liquid chromatography/tandem mass spectrometry method (6). Noncompartmental analysis, using Phoenix WinNonlin 6.2.1 (Pharsight Corporation), was used to calculate area under the curve from 0 to time t [AUC(0–t)], area under the curve from 0 to time of last quantifiable concentration [AUC(0–Ct)], maximum plasma concentration (Cmax); minimum plasma concentration (Cmin); fraction of the dose excreted in urine [Fe (%)]; and time to Cmax (Tmax).

Twenty-four-hour urine collection for pharmacokinetic analysis was conducted during cycles 1 and 2, on days 1 and 2. Aliquots from each collection time point were stored at −20 °C until analysis.

**Pharmacodynamics.**

**Plasma circulating biomarkers.** Blood samples for pharmacodynamic analysis were collected predose in cycle 1 (day 1, 2, 8, 15, and 22) and cycle 2 (day 1 and 15), and on day 1 of subsequent cycles. Plasma samples were analyzed using commercially available ELISAs or multiplex assays for concentrations of soluble protein markers, including soluble c-Met, urokinase-type plasminogen activator and its receptor (uPAR), HGF, VEGF, IL8, angiopoietin-2 (Ang-2), follistatin, granulocyte colony-stimulating factor, leptin, platelet-derived growth factor BB, platelet/endothelial cell adhesion molecule 1 (PECAM-1), and soluble KDR. Serum samples were analyzed to measure markers of tumor cell death activated caspases 3/7, cytochrome c, and cytokeratin 18–derived antigens recognized by the M30 and M65 monoclonal antibodies.

**Tumor tissue biomarkers.** Tumor biopsies for pharmacodynamic analysis (MET gene copy number and protein expression) were taken predose on cycle 1 day 1 and postdose between cycle 1 day 22 and cycle 2 day 22. Biopsies were optional during dose escalation, and mandatory at the MTD expansion, where up to 6 patients with at least 1 tumor lesion suitable for biopsy were required. For analysis of MET gene copy number, 5 μm formalin-fixed, paraffin-embedded (FFPE) tissue sections were subjected to dual-color FISH assays using the MET/CEP7 probe set from Abbott Vysis Molecular labeled with spectrum red and spectrum green, respectively. Fluorescent in-situ hybridization assays were performed according to a modified manufacturer’s protocol; signals were visualized using a Leica DMI4000 epifluorescence microscope equipped with band-pass filters for spectrum green, spectrum red, and 4,6-diamidino-2-phenylindole. For analysis of c-Met protein expression, ERK, and c-Met phosphorylation, 5 μm FFPE tissue sections were analyzed by immunohistochemistry (IHC) using antibodies against total c-Met, p-c-Met, or p-ERK1/2. Slides were digitized using the Aperio ScanScope and viewed using the Aperio ImageScope software (Aperio Technologies). Immunohistochemical staining was quantified by visual scoring and by using Aperio image analysis algorithms.

**Statistical analysis.** Descriptive statistics was applied to summarise extent of exposure, AEs including serious AEs (SAE) and DLTs. Plasma and urine pharmacokinetic concentrations of golvatinib and M2 were summarized descriptively by dose level/schedule and treatment cycle. Individual and mean plasma concentration versus time profile plots were produced on linear
and semi-log scales. Pharmacokinetic parameters were obtained from plasma and urine concentration data after a single dose on day 1 of cycle 1 for golvatinib and M2 and after repeat dosing on day 1 of cycle 2 and summarized descriptively by day and cycle. Dose linearity of golvatinib following a single dose of golvatinib and following repeat dosing of E7050 was assessed using graphical and tabular methods only. Dose-normalized pharmacokinetic parameters versus administered dose were plotted.

Levels of soluble protein markers were summarized descriptively by cancer type, dose level/schedule, treatment cycle, and overall. Individual and mean plasma concentration of the above markers versus time profile plots were produced for changes from baseline by dose. Changes in the median levels of the plasma biomarkers at each time point were analyzed using a Mann–Whitney test (P < 0.05 considered statistically significant).

In tumor samples, c-Met phosphorylation, c-Met expression, and ERK phosphorylation were assessed using IHC and summarized descriptively by dose level/schedule, treatment cycle, and overall, using the product of the percentage of cells staining positive and the corresponding intensity score. This information was also summarized descriptively by cellular location (membrane, nuclear, and cytoplasm), if available, by dose level/schedule, treatment cycle, and overall. The percentage of subjects with amplified versus non-amplified MET in their tumor samples, as measured by FISH, were summarized by cancer type (if necessary), dose level/schedule, treatment cycle, and overall. Individual and mean products of the percentage of cells staining positive and the corresponding intensity score of the above tissue markers were displayed in a scatter plot for each assessment for changes from baseline by dose.

Preliminary antitumor activity (best overall tumor response, duration of response and duration of stable disease) was summarized by cancer type, dose level/schedule, and overall.

Results

Patient characteristics

Between February 2009 and August 2011, 45 patients were enrolled; of these, 5 patients did not meet the inclusion/exclusion criteria and an additional 6 subjects discon-
dued before being dosed [5 patients due to disease related AEs (pain, n = 2; cord compression, anemia and hemoptysis, bowel obstruction, n = 1 each; 1 patient was withdrawn due to rapid progressive disease). Thirty-four patients were dosed with golvatinib. The most common tumor type was CRC (n = 15) and 65% had received 2 or 3 prior systemic therapies (Table 1).

Exposure, dose escalation, and MTD

All patients who received at least one dose of study drug were evaluable for safety (n = 34). During dose escalation, two subjects failed to complete at least 75% of dosing during cycle 1 for reasons other than toxicity and were not evaluable for DLT (one subject in each of the 200 and 400 mg dosing cohorts). Golvatinib was escalated through 5 dose levels: 100 (n = 3), 200 (n = 6), 270 (n = 4; 1 not evaluable), 360 (n = 3), and 450 mg (n = 2). The first DLT was observed at the 200 mg dose level: a grade 3 increased γ-glutamyltransferase (GGT) and ALP. Two further DLTs were observed at the 450 mg dose level: 1 patient experienced repeated grade 2 fatigue after dose interruption for the same and a second patient experienced grade 3 fatigue. The dose was then deescalated to an intermediate dose of 400 mg where 7 patients (1 not evaluable) were treated to define this as the MTD (no DLTs were observed). This dose was also selected on the basis of the convenience of dosing with 4 × 100 mg tablets, as opposed to 3 × 300-, 1 × 50-, and 1 × 10 mg tablets. A further 9 subjects were treated at this dose level of 400 mg once daily in the MTD expansion cohort (for further safety evaluation, and assessment of pharmacokinetic, pharmacodynamic biomarkers and preliminary antitumor activity of golvatinib). Overall, patients completed a median of 2 cycles of golvatinib (range, 1–8). Two patients completed >6 cycles of study drug.

Safety and tolerability

The majority of patients (94%) experienced at least one treatment-related AE. As Table 2 shows, the most common treatment-related AEs with an incidence >10% (n, %) were: diarrhea (20, 58.8%), nausea (17, 50%), vomiting (15, 44.1%), fatigue (14, 41.2%), decreased appetite (11, 32.4%), elevated ALT (11, 32.4%), elevated AST (7, 20.6%),

<table>
<thead>
<tr>
<th>Table 1. Patient characteristics</th>
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<tr>
<td>Total, n (%); N = 34</td>
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<tr>
<td><strong>Characteristics</strong></td>
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<tr>
<td>Median (range) age, y</td>
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<tr>
<td>Gender</td>
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<td>Male</td>
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<td>ECOG PS</td>
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<td>3</td>
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<td>4</td>
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<td>5–8</td>
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<tr>
<td>Tumor types</td>
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<tr>
<td>Colorectal</td>
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<tr>
<td>Lung</td>
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<td>Renal</td>
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<td>Esophageal</td>
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<td>Melanoma</td>
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<td>Othersa</td>
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*aOthers included peritoneal, peripheral nerve, mesothelioma, bile duct, parotid gland, bladder, and unknown origin.
was 45 hours. Median steady-state pharmacokinetic parameters, no formal statistical analysis was performed to assess dose proportionality. The half-life increased with dose. Because of the small numbers of patients, based on AUC(0–t) and steady-state exposure (fatigue with anorexia) and 450 mg (vomiting).

Table 2. Grade 1/2 treatment-related AEs with an overall rate of >10%

<table>
<thead>
<tr>
<th>Treatment-related AEs</th>
<th>100 mg (n = 3)</th>
<th>200 mg (n = 6)</th>
<th>270 mg (n = 4)</th>
<th>360 mg (n = 3)</th>
<th>400 mg (n = 16)</th>
<th>450 mg (n = 2)</th>
<th>Total (N = 34)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diarrhea</td>
<td>0</td>
<td>3 (50.0)</td>
<td>3 (75.0)</td>
<td>2 (66.7)</td>
<td>10 (62.5)</td>
<td>2 (100.0)</td>
<td>20 (58.8)</td>
</tr>
<tr>
<td>Nausea</td>
<td>1 (33.3)</td>
<td>2 (33.3)</td>
<td>1 (25.0)</td>
<td>0</td>
<td>13 (81.3)</td>
<td>0</td>
<td>17 (50.0)</td>
</tr>
<tr>
<td>Vomiting</td>
<td>0</td>
<td>1 (16.7)</td>
<td>1 (25.0)</td>
<td>0</td>
<td>11 (68.8)</td>
<td>2 (100.0)</td>
<td>15 (44.1)</td>
</tr>
<tr>
<td>Fatigue</td>
<td>0</td>
<td>3 (50.0)</td>
<td>0</td>
<td>1 (33.3)</td>
<td>8 (50.0)</td>
<td>2 (100.0)</td>
<td>14 (41.2)</td>
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<tr>
<td>Decreased appetite</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1 (33.3)</td>
<td>9 (56.3)</td>
<td>1 (50.0)</td>
<td>11 (32.4)</td>
</tr>
<tr>
<td>Elevated ALT</td>
<td>0</td>
<td>1 (16.7)</td>
<td>2 (50.0)</td>
<td>2 (66.7)</td>
<td>4 (25.0)</td>
<td>2 (100.0)</td>
<td>11 (32.4)</td>
</tr>
<tr>
<td>Elevated AST</td>
<td>0</td>
<td>1 (16.7)</td>
<td>1 (25.0)</td>
<td>1 (33.3)</td>
<td>2 (12.5)</td>
<td>2 (100.0)</td>
<td>7 (20.6)</td>
</tr>
<tr>
<td>Dry skin</td>
<td>2 (66.7)</td>
<td>1 (16.7)</td>
<td>0</td>
<td>1 (33.3)</td>
<td>0</td>
<td>0</td>
<td>4 (11.8)</td>
</tr>
<tr>
<td>Dysgeusia</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>3 (18.8)</td>
<td>1 (50.0)</td>
<td>4 (11.8)</td>
</tr>
</tbody>
</table>

All patients were evaluable for pharmacokinetic analysis, and pharmacokinetic parameters are summarized in Table 3. Peak exposures were achieved within 4 to 6 hours after a single dose of golvatinib. Golvatinib exposures, based on AUC(0–1) and steady-state C_{ss,max} generally increased with dose. Because of the small numbers of patients at each dose level and the high variability in pharmacokinetic parameters, no formal statistical analysis was performed to assess dose proportionality. The half-life was 45 hours. Median steady-state t_{ss,max} occurred approximately 2 to 4 hours after dosing. Trough concentrations increased between days 2 and 8 but remained relatively constant across days 8, 15, and 22. Steady-state plasma concentrations were achieved between days 8 and 22. Peak-to-trough fluctuation values ranged from 48.6% to 82.9%. Mean accumulation ratios based on peak exposure (C_{ss,max}) ranged from 1.74 to 2.84 and those based on total exposure [AUC(0–1)] ranged from 3.01 to 4.65, indicating moderate accumulation at steady state (Fig. 1). The apparent volume of distribution (V/D) ranged between 325 and 707 L. Urine excretion after a single dose (0.93%–2.4%) and at steady state (3.59%–4.91%) was low, consistent with minimal renal excretion.

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Pharmacodynamic studies

Circulating biomarker studies. Twenty-five patients had evaluable measurements on circulating biomarkers for analysis. Increases in the median levels of the plasma biomarkers, c-Met, VEGFR2, uPAR, and Ang-2 were observed after treatment with golvatinib: a Mann–Whitney test demonstrated statistically significant increases (P < 0.05) for c-Met on days 2, 8, 15, and 22, for VEGFR2 on days 8, 15, and 22,
for uPAR on days 8 and 22, and for Ang-2 on day 22. However, there was no correlation with dose (Fig. 2).

**Tumor pharmacodynamic analysis.** Eight patients underwent tumor biopsies at baseline (patients 1019, 1020, 1021, 1022, 1024, 1025, 1026, and 1028). All biopsies were evaluated by FISH (for MET gene copy number, representative images are shown in Fig. 3A and C) and by IHC (for expression levels of c-Met protein, representative images are shown in Fig. 3D and F). In addition, paired (pre- and postdose) biopsies were evaluable in 4 patients at the MTD (patients 1019, 1020, 1024, and 1026). These four paired biopsies were evaluated by IHC for levels of phospho-c-Met (p-c-Met) and phospho-ERK (p-ERK) c-Met (Tyr1234/1235) and for levels of phosphorylation of ERK (Thr202/Tyr204).

An increase in MET gene copy number was seen in 2 patients with papillary RCC (patient 1020) and CRC (patient 1028; Fig. 3B and C); in both patients this was associated with high levels of c-Met protein expression by IHC (Fig. 3E and F). The increase of MET gene copy number in the patient with papillary RCC (patient 1020) was associated with an increase in the copy number of chromosome 7 (possibly a polysomy of chromosome 7; Fig. 3B). The trisomy of chromosome 7, where both the HGF and MET genes reside, has been reported in the literature to occur frequently in papillary RCC (39). Patient 1028 with CRC also demonstrated amplified the MET gene. Six patients (1019, 1021, 1022, 1024, 1025, and 1026) did not show an increase in MET gene copy number (a representative image of a tumor without MET gene amplification, patient 1022, is shown in Fig. 3A). Consistent with normal MET gene copy number, the level of c-Met protein expression in patient 1022 was low (Fig. 3D). IHC analysis in paired pre- and postdose biopsies showed a posttreatment decrease in p-c-Met in 2 patients (Fig. 3G and I; patients 1020 and 1024). Patient 1020 was the patient with papillary RCC with an increased copy number of chromosome 7 and MET gene who demonstrated a reduction in the number of cells staining positive for p-c-Met from 46% to 3.7%. Patient 1024, with CRC, demonstrated a decrease in cells expressing p-Met, from 40% to 17%. In patients 1019 (diagnosed with melanoma) and 1026 (diagnosed with carcinoma of unknown primary), levels of p-c-Met were barely detectable pretreatment and did not change with treatment. However, in patient 1026 (carcinoma of...
Figure 3. Immunohistochemical assessment of c-Met protein expression and FISH analysis of MET gene copy number (expanded MTD cohort 400 mg). Changes in levels of p-c-Met and p-ERK in pre- and posttreatment tumor biopsies.
unknown primary) there was a decrease in the level of p-ERK after dosing with golvatinib, from 52% to 2% (Fig. 3H and I).

Response evaluation

Thirty-one patients were included in the efficacy population. There were no complete responses. One patient with transitional cell carcinoma of the bladder (patient 1022) demonstrated an unconfirmed partial response with a 35% decrease in the target lesions by RECIST after cycle 2. Six patients demonstrated stable disease (SD) lasting ≥85 days (range, 85–237 days). The patient with SD lasting 237 days had an esophageal carcinoma treated at 200 mg.

Two patients with SD lasting 50 (patient 1020, RCC) and 54 days (patient 1024, CRC) demonstrated downregulation of p-c-Met (Fig 3G and I). Patient 1026 (CUP) who demonstrated downregulation of p-ERK was not evaluable for response.

Discussion

This phase I study defined the MTD of golvatinib, an RTK inhibitor of c-Met, Ron, c-KIT, and Eph receptors, as 400 mg administered orally, once daily, in 28-day cycles. The DLTs were fatigue and raised ALP and GGT. Fatigue was common and not insignificant, occurring in 50% of patients at the MTD, and resulted in a dose reduction in 2 patients treated at this dose level. Other frequently occurring AEs were diarrhea, nausea, and vomiting, which were manageable with supportive therapy. A concurrent phase I study using a twice-daily dosing schedule defined a MTD of 400 mg per day (200 mg twice-daily; ref. 40). The toxicity profile was also similar, with DLTs of elevated ALT (n = 1) and nausea, vomiting, and anorexia (n = 1). In our study, although pharmacokinetic linearity was not shown in view of the small numbers and variability, peak $C_{\text{max}}$ and AUC$_{(0-t)}$ increased with dose. Although not tested in this study, but based on the results of a previous healthy volunteer study, food effect differences in golvatinib exposure were modest and considered clinically insignificant (41). The results of this latter study became available with 2 patients remaining on our study and so for pharmacokinetic assessments, all patients were dosed on an empty stomach.

Paired pre- and posttreatment biopsies were evaluable in 4 patients at the MTD and provided preliminary evidence of target inhibition and downstream pathway modulation. Two of 4 patients, with papillary RCC and CRC, demonstrated a detectable decrease in the number of cells staining positive for p-c-Met. One patient with carcinoma of unknown primary demonstrated downregulation of p-ERK posttreatment. Pharmacodynamic analysis of plasma biomarkers showed an increase in the median levels of plasma biomarkers, in particular soluble c-Met and a marker of angiogenesis, Ang-2. Limited conclusions can be drawn regarding these results of circulating pharmacodynamic analyses, given the small number of patients; however, elevated soluble c-Met suggested inhibition of the c-Met receptor while Ang-2 is a marker of angiogenesis. We have no pharmacodynamic data from this or other clinical studies of golvatinib that demonstrate an inhibitory effect on Eph signaling. Golvatinib was originally developed as a tyrosine kinase inhibitor (TKI) of c-Met, but was subsequently found to be a potent inhibitor of EphB4 and Tie2 in preclinical studies (37). However, preclinical data using unique in vitro assay systems of two-dimensional and three-dimensional endothelial cells/pericyte coculture sprouting assays demonstrated that the EphB4 inhibitory activity of golvatinib disrupted anti-VEGF therapy-resistant tumor vasculature in a combination with lenvatinib [a TKI of VEGFR1–3, FGFR1–4; PDGFRa, RET, and KIT (42)]. We can however confirm that the unbound concentration of golvatinib at $C_{\text{min,ss}}$ (400 mg) of 55.35–67.65 ng/mL, equivalent to 0.0707–0.086 μmol/L, is above the IC$_{50}$ of 0.015 μmol/L for EphB4 (data on file, Eisai).

This study provides some evidence that golvatinib is associated with clinical and pharmacodynamic activity in patients with advanced cancers. Although there were no complete or partial responses, 2 of 3 patients with pharmacodynamic evidence of target modulation (patient 1020 with papillary RCC and patient 1024 with CRC) demonstrated SD lasting ≥50 days. However, what is not clear from our work is the duration of pharmacodynamic modulation of cancer cells. It is possible that if this pharmacodynamic effect were sustained, more clinically meaningful outcomes may have been demonstrated.

Despite the evidence of target modulation, the efficacy of golvatinib as a single agent was limited. Further dose escalation was prevented by fatigue which, although not uncommon with RTK inhibitors, is difficult to manage. An intermittent dosing schedule may be conceivable, but the impact on pharmacodynamic effects would have to be closely assessed. The observation of elevated Ang-2 levels raises the hypothesis that angiogenesis may represent a mechanism of resistance to targeting c-Met, and it is possible that simultaneous targeting of both c-Met and angiogenic signaling may yield a greater therapeutic benefit. Preclinical data cited previously certainly support the combination therapy of golvatinib and lenvatinib, which may be promising to overcome anti-VEGF therapy resistance (43). A phase I/II study of golvatinib in combination with lenvatinib is presently underway.

Other clinical studies support this hypothesis. Phase I and II studies of foretinib, an inhibitor of both c-Met and VEGFR2, not only demonstrated immunohistochemical evidence of target modulation but also meaningful clinical responses and meaningful SD (44,45). In addition, HGF-c-MET signaling is also implicated in resistance to EGFR TKI therapy, and rational combinations with anti-EGFR therapies have also been tested. Other c-Met inhibitors such as tivantinib, cabozantinib, and onartuzumab have been combined with erlotinib to try to overcome this HGF-c-MET–mediated resistance to EGFR TKI therapy (46–48). In developing future treatment paradigms of personalized medicine, it is likely that golvatinib’s efficacy as monotherapy or in combination will be best demonstrated when...
applied to a molecularly defined patient population that is more likely to show clinical benefit. Foretinib demonstrated activity in a phase I setting in patients with papillary RCC, which is associated with activating mutations of MET. Activating mutations of MET have been shown in the germ-line of patients with hereditary papillary RCC and up to 13% of patients with sporadic papillary RCC (18). Furthermore, a majority of sporadic RCCs have a duplication of chromosome 7, where MET is located (39). An initial phase I study of foretinib indicated an efficacy signal in papillary RCC with a tolerable side-effect profile (44). A phase II study subsequently demonstrated significant activity in patients with germline MET mutations (45). A second phase II study in 74 patients with advanced gastric cancer showed SD as the best response in 15 patients (49). However, just 3 patients demonstrated MET amplification at baseline, and one of these demonstrated SD. The authors concluded that foretinib was of limited value in unselected patients with gastric cancer, and furthermore, as a single agent. Phase II and III studies of tivantinib with erlotinib in NSCLC showed evidence of clinical benefit for subsets of patients with MET high tumors. Although the phase III study was negative for the defined primary endpoint of progression-free survival (PFS) and overall survival (OS), an analysis of 40% of trial participants showed that PFS and OS were longer in patients with 2+ MET-positive immunostaining in more than 50% of cells (12, 46, 50). Likewise, a randomized phase II study of onartuzumab with erlotinib (versus placebo) in patients with advanced NSCLC demonstrated a significant PFS and OS benefit in a subset of patients with MET diagnostic-positive tumors (48). On the basis of the results of these studies, current phase III trials of tivantinib in hepatocellular carcinoma and onartuzumab with erlotinib in NSCLC are focused on MET diagnostic-positive patients.

Our study was initiated before the concept of prospective patient selection having established itself in the clinic. However, the encouraging pharmacodynamic data supported by the developmental route taken by other c-Met inhibitors suggest that this approach of patient selection can be applied to future trials of golvatinib.

In summary, this phase I study of golvatinib met its primary and secondary objectives of establishing a recommended phase II dose to take forward for further development in combination with other targeted therapies. These studies may require modification of the schedule to counteract fatigue and, more importantly, focus on enrolling MET-positive patients to maximize the pharmacodynamic effect and efficacy.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Acknowledgments
The authors thank Yuki Nishihoka, pharmacokinetic analyst, Knunal Shah, trial coordinator, and Margaret Maniscalki, editorial assistant.

Grant Support
The financial support for all study-related procedures in this clinical trial was provided by the study sponsor, Eisai, Ltd. The Drug Development Unit of the Royal Marsden NHS Foundation Trust and The Institute of Cancer Research (ICR) are supported in part by a program grant from Cancer Research UK (CRM065-C347/A18077). This work was also supported by an Experimental Cancer Medicine Centre (ECMC) Award (CRM64-C12540/A115573, to The ICR) and the National Institute for Health Research Biomedical Research Centre (NIHR BRC; joint to the Royal Marsden and ICR). The Clinical Trials Unit of University of Manchester and The Christie Hospital NHS Foundation Trust are supported by the ECAC/NIH Christie Grant Award (RD40002).

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Received February 18, 2014; revised August 7, 2014; accepted August 25, 2014; published OnlineFirst October 2, 2014.

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Clin Cancer Res  Published OnlineFirst October 2, 2014.

Updated version  Access the most recent version of this article at:
doi:10.1158/1078-0432.CCR-14-0409

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