

Selection of Protein Kinase Inhibitors Based on Tumor Tissue Kinase Activity Profiles in Patients with Refractory Solid Malignancies: An Interventional Molecular Profiling Study

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TRIAL INFORMATION

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- **Principal Investigator:** Henk M.W. Verheul
- **IRB Approved:** Yes

LESSONS LEARNED

- Clinically applicable tools are needed for treatment selection and repurposing of available protein kinase inhibitors (PKIs) in patients with advanced solid tumors refractory to standard treatment.
- Using a tyrosine kinase peptide substrate microarray, observed inhibitory activity in vitro could not sufficiently predict clinical benefit of treatment with the selected PKI.

ABSTRACT

Background. This exploratory molecular profiling study determined the feasibility and benefit of the selection of protein kinase inhibitors (PKIs) based on kinase activity profiling in patients with refractory solid malignancies.

Methods. Adult patients with biopsy-accessible refractory solid tumors were eligible. Per patient, the inhibitory potency of sunitinib, dasatinib, erlotinib, sorafenib, everolimus, and lapatinib was determined in tumor lysates from fresh biopsies using a tyrosine kinase peptide substrate microarray. The most active PKI in this in vitro assay was selected for treatment.

Results. Thirteen patients were enrolled in the feasibility part and underwent tumor biopsy. Of 12 patients in whom kinase activity profiling was performed, 11 started treatment with a selected PKI: dasatinib in 8, sunitinib in 2, and erlotinib in 1 patient(s). Eight patients were evaluable for response. One patient had stable disease (SD) >4 months on sunitinib; one patient had SD at 6 weeks but progressive disease (PD) at 12 weeks. The remaining patients had PD after 6 weeks of treatment.

Conclusion. Kinase inhibition profiles of multiple PKIs can be reliably determined using fresh tumor biopsies from patients with refractory solid tumors. However, the current in vitro

microarray selection approach insufficiently predicted clinical benefit of PKI treatment in these patients. *The Oncologist* 2018;23:1135–e118

DISCUSSION

Compared with the increased availability of molecular targeted therapies, including numerous protein kinase inhibitors (PKIs), the development of clinical tests to identify patient subgroups most likely to benefit from these therapies is lagging behind. A particular clinical need exists for tools to enable selection of multitargeted PKIs and for patients with advanced solid tumors refractory to standard treatment, who could benefit from repurposing of available drugs. Several potentially useful tumor-profiling platforms such as peptide and (reverse phase) protein microarrays have been suggested to infer kinase activity for treatment stratification or target identification [1–6]. Pre-clinical and clinical data have shown some indications that a 144-tyrosine kinase peptide substrate microarray may be of value for treatment selection [7, 8]. Hypothesizing that microarray-based kinase activity profiling may be a potential clinical tool for PKI treatment selection in patients refractory to

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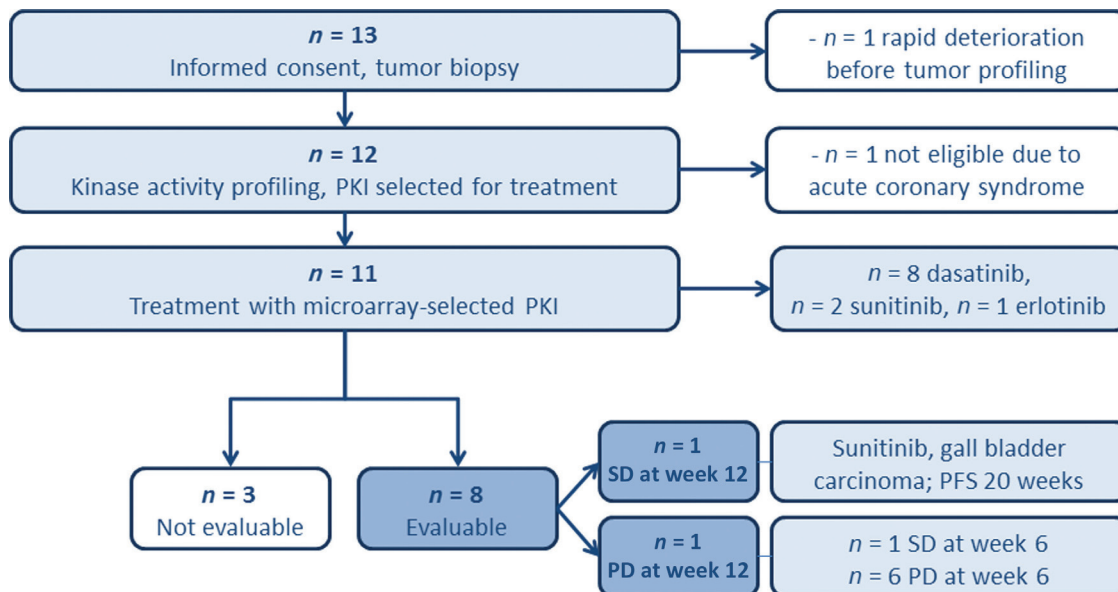


Figure 1. Two of thirteen patients who gave informed consent could not start treatment; one patient progressed rapidly before completion of tumor profiling, and one patient became ineligible after profiling. Three patients for whom dasatinib was selected were not evaluable for response due to early clinical progression ($n = 2$) and patient's refusal of selected treatment ($n = 1$).

Abbreviations: PD, progressive disease; PFS, progression-free survival; PKI, protein kinase inhibitor; SD, stable disease.

standard treatment, we performed a molecular profiling study to select treatment with a registered PKI by in vitro assessment of their inhibitory effect on kinase activity profiles using lysates obtained from fresh tumor biopsy.

Adult patients with biopsy-accessible disease of an advanced solid malignancy, for whom no standard treatment was available, were eligible. Sunitinib, dasatinib, sorafenib, erlotinib, lapatinib, and everolimus were analyzed for their inhibition of kinase activity. Extrapolation of in vitro inhibitory potency to their presumed clinical activity was based on an algorithm considering, per drug, the number of significantly inhibited peptides and percentage of inhibition. The most potent PKI in this assay was then selected for treatment.

Thirteen patients were enrolled. Kinase activity profiling was performed for 12 patients; dasatinib was selected for 9 patients, sunitinib for 2 patients, and erlotinib for 1 patient. Eight of eleven patients who subsequently initiated the selected treatment were evaluable for response. One patient

with biliary tract cancer had stable disease (SD) on sunitinib for more than 4 months. One patient treated with dasatinib showed SD at 6 weeks but progressive disease (PD) at 12 weeks; the remaining patients had PD at first evaluation (Fig. 1). Based on our findings after 11 treated patients that dasatinib was selected in 75% of patients but resulted in clinical benefit in <10% of patients within 6 weeks, we concluded by statistical means that the chance for the trial to succeed to stage II according to prespecified criteria was <1%. The trial was therefore prematurely halted.

In conclusion, we here show that PKI inhibition profiles can be reliably determined using needle biopsies from patients with refractory solid tumors. However, the microarray-based selection strategy was insufficient in predicting clinical benefit upon treatment with the selected PKI. We anticipate that the concentrations used in this in vitro assay should be re-evaluated based on achieved PKI tumor concentrations in patients.

TRIAL INFORMATION

| | |
|-----------------------------------|--|
| Disease | Advanced cancer/solid tumor only |
| Stage of Disease/Treatment | Metastatic/advanced |
| Prior Therapy | No designated number of regimens |
| Type of Study – 1 | Phase II |
| Type of Study – 2 | Interventional molecular profiling study |
| Primary Endpoint | Feasibility and clinical benefit rate (CBR), defined as the partial response (PR), complete response (CR), and SD rate after 12 weeks, of treatment selection by tumor kinase activity profiling |
| Secondary Endpoint | Progression-free survival (PFS) ratio (PFS_2/PFS_1) of a PKI selected by kinase activity profiling (PFS_2) compared with the PFS of the treatment regimen on which the patient progressed prior to study inclusion (PFS_1) |

Additional Details of Endpoints or Study Design

Based on the CBR of approximately 10% observed in phase I studies of the registered PKIs used in this study, we hypothesized that the microarray-based selection would increase the CBR of PKI treatment in this patient population refractory to standard treatment from 10% to 25%. Based on Simon's two-stage optimal trial design, it was calculated that 43 patients (18 in stage I and 25 in stage II) needed to be treated. The interim analysis after stage I required demonstrated clinical benefit for at least 3 of 18 patients to proceed to stage II, in which 25 more patients would be included. If at least 8 of the total 43 patients would demonstrate clinical benefit, the null hypothesis that this treatment selection strategy is only effective in 10% of patients would be rejected. If in stage I ≤ 2 of the 18 patients would have clinical benefit at 12 weeks of treatment, the study would be terminated due to lack of acceptable clinical benefit (efficacy) of this approach. Based on these considerations, this trial was calculated to have 80% power to detect CBR of 25% versus the null rate of 10% with a 5% Type I error rate.

| | |
|--------------------------------|---|
| Investigator's Analysis | Level of activity did not meet planned endpoint |
|--------------------------------|---|

DRUG INFORMATION FOR PHASE II STANDARD (TREATMENT SELECTION) ARM**Drug 1**

| | |
|-----------------------------------|---------------------|
| Generic/Working Name | Sunitinib |
| Dose | 50 mg per flat dose |
| Route | p.o. |
| Schedule of Administration | Once daily |

Drug 2

| | |
|-----------------------------------|----------------------|
| Generic/Working Name | Erlotinib |
| Dose | 150 mg per flat dose |
| Route | p.o. |
| Schedule of Administration | Once daily |

Drug 3

| | |
|-----------------------------------|----------------------|
| Generic/Working Name | Sorafenib |
| Dose | 400 mg per flat dose |
| Route | p.o. |
| Schedule of Administration | Twice daily |

Drug 4

| | |
|-----------------------------------|---------------------|
| Generic/Working Name | Dasatinib |
| Dose | 70 mg per flat dose |
| Route | p.o. |
| Schedule of Administration | Twice daily |

Drug 5

| | |
|-----------------------------------|---------------------|
| Generic/Working Name | Everolimus |
| Dose | 10 mg per flat dose |
| Route | p.o. |
| Schedule of Administration | Once daily |

Drug 6

| | |
|-----------------------------------|------------------------|
| Generic/Working Name | Lapatinib |
| Dose | 1,250 mg per flat dose |
| Route | p.o. |
| Schedule of Administration | Once daily |

PATIENT CHARACTERISTICS

| | |
|---|---|
| Number of Patients, Male | 7 |
| Number of Patients, Female | 5 |
| Stage | IV |
| Age | Median (range): 62 (26–69) |
| Number of Prior Systemic Therapies | Median (range): 2 (1–3) |
| Performance Status: ECOG | 0 – 3 1 – 9 2 – 0 3 – 0 Unknown – |

Cancer Types or Histologic Subtypes

Colorectal cancer 5
 Cholangiocarcinoma 3
 Gallbladder cancer 1
 Pancreatic cancer 1
 Germ cell cancer 1
 Synovial sarcoma 1

PRIMARY ASSESSMENT METHOD

| Title | Total patient population |
|---|---|
| Number of Patients Screened | 13 |
| Number of Patients Enrolled | 12 |
| Number of Patients Evaluable for Toxicity | 12 |
| Number of Patients Evaluated for Efficacy | 8 |
| Evaluation Method | RECIST 1.0 |
| Response Assessment CR | $n = 0$ |
| Response Assessment PR | $n = 0$ |
| Response Assessment SD | $n = 1$ |
| Response Assessment PD | $n = 7$ |
| (Median) Duration Assessments PFS | 6 weeks |
| Outcome Notes | According to the study design, a stopping rule would apply if <3 of 18 patients in stage I would have clinical benefit at 12 weeks of treatment. However, based on our findings after 11 treated patients that dasatinib was selected in 75% of patients, resulting in clinical benefit in <10% of patients within 6 weeks, we concluded by statistical means that the chance for the trial to succeed to stage II according to prespecified criteria was <1%. Therefore, the trial was prematurely halted. As a consequence, the secondary objective to determine the PFS ₂ /PFS ₁ ratio of microarray-selected PKI treatment became futile as well. |

ADVERSE EVENTS

All Cycles

| Name | NC/NA | 1 | 2 | 3 | 4 | 5 | All grades |
|-----------------------|-------|----|----|-----|----|----|------------|
| Thromboembolic event | 87% | 0% | 0% | 13% | 0% | 0% | 13% |
| Fatigue | 75% | 0% | 0% | 25% | 0% | 0% | 25% |
| Noncardiac chest pain | 87% | 0% | 0% | 13% | 0% | 0% | 13% |

Only grade ≥ 3 adverse events that were potentially related to the study treatment are shown. Treatment with dasatinib caused more significant toxicity compared with sunitinib and erlotinib (Common Terminology Criteria for Adverse Events grade ≥ 3 adverse events in 3/8 vs. 0/3 patients, respectively).

Abbreviation: NC/NA, no change from baseline/no adverse event.

ASSESSMENT, ANALYSIS, AND DISCUSSION

| | |
|----------------------------------|---|
| Completion | Study terminated before completion |
| Terminated Reason | Did not fully accrue |
| Investigator's Assessment | Level of activity did not meet planned endpoint |

This study represents the first attempt to predict the clinical activity of six approved protein kinase inhibitors (PKIs) in individual patients based on their in vitro activity in lysates from fresh-frozen tumor biopsies, followed by selection of the most active agent for personalized treatment. Adult patients with

progressive, measurable, and biopsy-accessible disease of an unresectable and/or metastatic solid malignancy refractory to standard treatment, with Eastern Cooperative Oncology Group performance status of 0–2 were eligible. Tumor needle biopsies were taken with up to three passes under ultrasound-

computed tomography guidance. Biopsies with $\geq 50\%$ tumor cells upon hematoxylin and eosin staining were considered representative. Kinase activity profiling was performed using a tyrosine kinase peptide substrate microarray (PamChip) consisting of 144 peptide substrates (PamGene, Hertogenbosch, The Netherlands), including phosphorylation sites for epidermal growth factor receptor, vascular endothelial growth factor receptor, and platelet-derived growth factor receptor (Fig. 2) [9]. Per patient, sunitinib, sorafenib, erlotinib, dasatinib, everolimus, and lapatinib were analyzed in vitro for their inhibition of kinase activity; the most potent PKI in this assay was then selected for treatment (Fig. 3). PKIs were prescribed according to standard dose and schedule. Treatment was continued until disease progression or unacceptable toxicity.

Thirteen patients, of whom five had metastatic colorectal cancer and four biliary tract cancer, were enrolled in the study and underwent tumor needle biopsy (Table 1). Kinase activity profiling was performed for 12 patients; dasatinib was selected for 9 patients, sunitinib for 2 patients, and erlotinib for 1 patient. Eleven patients subsequently initiated the selected treatment after a median of 17 days following tumor biopsy (Fig. 1). Algorithm scores for the selected PKIs are shown in Table 2. Eight of eleven patients who started treatment with the microarray-selected PKI were evaluable for response. One patient reached the endpoint of clinical benefit at 12 weeks of treatment. This patient with gallbladder carcinoma had stable disease >4 months on selected treatment with sunitinib. Of note, this drug has shown a 50% disease control rate in 54 patients with advanced, chemotherapy-refractory biliary tract cancer but with a median duration of disease control of only 2.4 months [10]. Although we showed that this selection strategy was technically and clinically feasible in this patient population, this resulted in a relative selection preference for dasatinib without subsequent evidence of clinical activity in the patients who went on to receive this drug. Therefore, after treatment of 11 patients, the study was halted for lack of drug selection and clinical activity and a calculated probability of less than 1% for the trial to succeed to stage II.

The (aberrant) biological activity of kinases in tumor cells is only one of the main determinants for response to treatment with PKIs. Other major contributing factors are the target specificity and affinity of the PKI for individual kinases that are biologically active and the bioavailability of the drug at the target site, in tumor cells [11, 12]. PKI bioavailability is multifactorially determined by chemical characteristics such as pH and lipophilicity that influence their intestinal uptake after oral ingestion, protein-binding capacity, and ability to cross cell membranes. The latter will determine the circulating free concentration of a specific PKI and thereby its diffusion rate into the tumor microenvironment [13]. The relative contribution of each of these determinants to response and their interplay are difficult to evaluate. We observed a striking disconnection between the potency of dasatinib in the assay and its lack of clinical activity in patients in this study. We hypothesize that the diffusion rate of dasatinib into the tumor microenvironment may be hampered by its high protein-binding capacity causing its inactivity. Moreover, other factors contribute to the mismatch between conditions in vivo and the nonphysiological in vitro test setting. Besides an overrepresentation of Src substrates on chip, the

anticipated clinical activity of dasatinib or other PKIs may be potentially overestimated by the reduced kinase specificity for the synthetic short peptides, as both the amino acid sequence context of the tyrosine phosphorylation site and the three-dimensional structure of the substrate are known to contribute to this specificity [9, 14].

It is challenging to have information on kinase or pathway activity and target specificity, affinity, and bioavailability all at one's disposal. Information of (aberrant) kinase activity in tumor cells from patients is dependent on relative abundance, energy, and phosphorylation status of the cells, which is balanced by activity of kinases and phosphatases. Information on PKI potency and selectivity for target kinases can be obtained by high-throughput screening platforms [15]. Verification of adequate PKI accumulation in tumor tissue in patients during treatment is less straightforward. Tumor concentrations are not properly reflected by circulating concentrations in blood, as we and others have previously shown [13, 16, 17]. Of interest, alternative approaches to predict tumor PKI concentrations may become available (e.g., by imaging using labelled drugs) [18, 19].

The benefits of the kinase activity-profiling microarrays used in this study over other strategies include their high-throughput usability and limited protein input requirements, enabling their implementation in clinical practice. However, label-free mass spectrometry-based tyrosine-phosphoproteomics may be a complementary approach, as this allows for more unbiased and direct inference of signaling pathway or kinase activity. We have recently shown that this approach is feasible in small clinical samples, allowing the identification of patient-specific but also PKI-specific profiles [20] (and Labots et al., unpublished data).

In conclusion, we here show that tumor needle biopsies from patients with refractory solid tumors provide sufficient tissue to reliably determine PKI inhibition profiles. However, this microarray-based PKI selection strategy was insufficient in predicting subsequent clinical benefit upon treatment with the selected PKI. We anticipate that the PKI concentrations used in this in vitro assay should be re-evaluated based on achieved PKI tumor concentrations in patients. In addition, PKI-affinity/selectivity and mass spectrometry-based (tyrosine) phosphorylation profiles may further guide development of predictive tools or biomarkers for PKI treatment benefit. Such an improved strategy is of utmost importance to realize the promise of personalized medicine for treatment selection in this high-need patient population.

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DISCLOSURES

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(C/A) Consulting/advisory relationship; (RF) Research funding; (E) Employment; (ET) Expert testimony; (H) Honoraria received; (OI) Ownership interests; (IP) Intellectual property rights/inventor/patent holder; (SAB) Scientific advisory board

REFERENCES

1. Piersma SR, Labots M, Verheul HM et al. Strategies for kinome profiling in cancer and potential clinical applications: Chemical proteomics and array-based methods. *Anal Bioanal Chem* 2010;397:3163–3171.
2. Perner F, Schnoder TM, Fischer T et al. Kinomics screening identifies aberrant phosphorylation of CDC25C in FLT3-ITD-positive AML. *Anticancer Res* 2016;36:6249–6258.
3. van der Sligte NE, Scherpen FJ, Meeuwssen-de Boer TG et al. Kinase activity profiling reveals active signal transduction pathways in pediatric acute lymphoblastic leukemia: A new approach for target discovery. *Proteomics* 2015;15:1245–1254.
4. van Oostrum J, Calonder C, Rechsteiner D et al. Tracing pathway activities with kinase inhibitors and reverse phase protein arrays. *Proteomics Clin Appl* 2009;3:412–422.
5. Sereni MI, Baldelli E, Gambara G et al. Kinase-driven metabolic signalling as a predictor of response to carboplatin-paclitaxel adjuvant treatment in advanced ovarian cancers. *Br J Cancer* 2017; 117:494–502.
6. Baldelli E, Calvert V, Hodge A et al. Reverse phase protein microarrays. *Methods Mol Biol* 2017; 1606:149–169.
7. Versele M, Talloen W, Rockx C et al. Response prediction to a multitargeted kinase inhibitor in cancer cell lines and xenograft tumors using high-content tyrosine peptide arrays with a kinetic read-out. *Mol Cancer Ther* 2009;8:1846–1855.
8. Sikkema AH, Diks SH, den Dunnen WF et al. Kinome profiling in pediatric brain tumors as a new approach for target discovery. *Cancer Res* 2009;69: 5987–5995.
9. Labots M, Gotink KJ, Dekker H et al. Evaluation of a tyrosine kinase peptide microarray for tyrosine kinase inhibitor therapy selection in cancer. *Exp Mol Med* 2016;48:e279.
10. Yi JH, Thongprasert S, Lee J et al. A phase II study of sunitinib as a second-line treatment in advanced biliary tract carcinoma: A multicentre, multinational study. *Eur J Cancer* 2012;48:196–201.
11. Lemeer S, Zorgiebel C, Ruprecht B et al. Comparing immobilized kinase inhibitors and covalent ATP probes for proteomic profiling of kinase expression and drug selectivity. *J Proteome Res* 2013;12: 1723–1731.
12. Rovithi M, Verheul HMW. Pulsatile high-dose treatment with antiangiogenic tyrosine kinase inhibitors improves clinical antitumor activity. *Angiogenesis* 2017;20:287–289.
13. Gotink KJ, Broxterman HJ, Labots M et al. Lysosomal sequestration of sunitinib: A novel mechanism of drug resistance. *Clin Cancer Res* 2011;17:7337–7346.
14. Amanchy R, Periaswamy B, Mathivanan S et al. A curated compendium of phosphorylation motifs. *Nat Biotechnol* 2007;25:285–286.
15. Marx H, Lemeer S, Schliep JE et al. A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. *Nat Biotechnol* 2013;31:557–564.
16. Lankheet NA, Schaake EE, Burgers SA et al. Concentrations of erlotinib in tumor tissue and plasma in non-small-cell lung cancer patients after neoadjuvant therapy. *Clin Lung Cancer* 2015;16:320–324.
17. Petty WJ, Dragnev KH, Memoli VA et al. Epidermal growth factor receptor tyrosine kinase inhibition represses cyclin D1 in aerodigestive tract cancers. *Clin Cancer Res* 2004;10:7547–7554.
18. Mammatas LH, Verheul HM, Hendrikse NH et al. Molecular imaging of targeted therapies with positron emission tomography: The visualization of personalized cancer care. *Cell Oncol (Dordr)* 2015; 38:49–64.
19. Yaqub M, Bahce I, Voorhoeve C et al. Quantitative and simplified analysis of 11C-erlotinib studies. *J Nucl Med* 2016;57:861–866.
20. Labots M, van der Mijn JC, Beekhof R et al. Phosphotyrosine-based-phosphoproteomics scaled-down to biopsy level for analysis of individual tumor biology and treatment selection. *J Proteomics* 2017; 162:99–107.

FIGURES AND TABLES

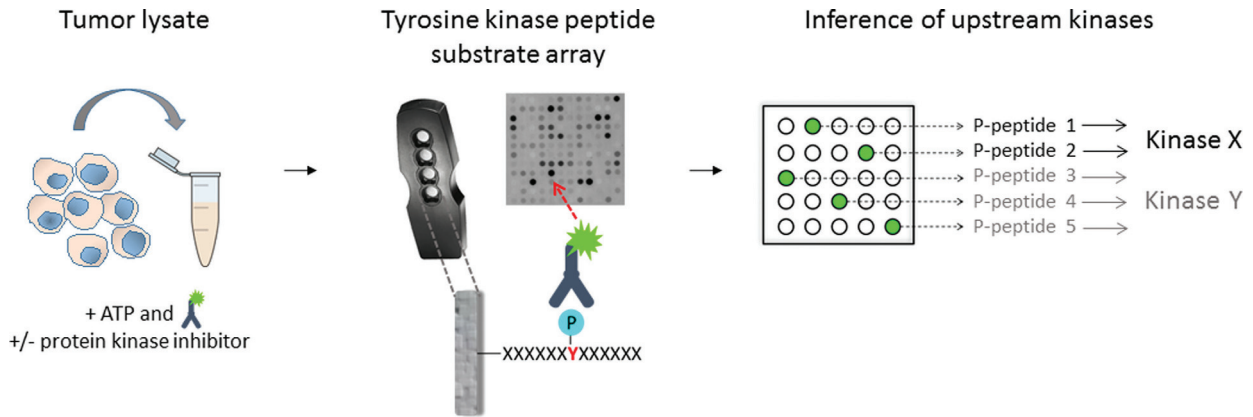


Figure 2. Kinase activity measurement based on the PamChip (tyrosine kinase peptide substrate) microarray using a PamStation12 instrument. Per patient, control and inhibition samples were measured in triplicate using 5 µg lysate protein input per sample. Each run, based on three chips with four microarrays each, allows for simultaneous measurement of 12 samples. Shortly before application on the microarray, tumor lysate is mixed with kinase reaction buffer, containing the fluorescein-labeled antiphosphotyrosine antibody pY20 as well as ATP, for phosphate transfer. In addition, for the inhibition samples, protein kinase inhibitors (PKIs) were spiked to the sample mix. Hereafter, incubation of the microarrays at 30°C is started for 60 cycles, during which the sample mix is transferred through the porous array once per minute. As a result of lysate kinase activity, (target) peptide substrates on chip will be phosphorylated at the tyrosine residue (Y), leading to phosphotyrosine formation, to which the fluorescein-labeled antibody will bind. A 12-bit charge-coupled device camera monitors fluorescence intensities resulting from binding of the antiphosphotyrosine antibody over time. End levels of signal intensity, expressed in arbitrary units, after 60 minutes of incubation were determined for PKI-spiked and control lysates. For each PKI, the percentage inhibition for all 144 peptide substrates on chip was calculated by dividing the mean end-level signal intensity of the PKI-spiked sample triplicates by the mean end-level signal intensity of the control sample triplicates (end-level intensity PKI/control). Peptide phosphorylation inhibition was considered to be significant if the *p* value calculated from a Student’s *t* test was <.05. Kinase enzymatic activity can be inferred from recorded intensity of peptide phosphorylation over time. XXXXXYXXXXX denotes peptide sequence context with tyrosine (Y) substrate flanked by six other amino-acids. Abbreviations: ATP, adenosine triphosphate; P-peptide, phosphorylated peptide.

| Inhibition, % | Number of significantly inhibited peptide substrates per PKI | | | | Algorithm score | Interpretation of PKI activity | Treatment selection |
|---------------|--|-------|-------|------|-----------------|--------------------------------|---------------------|
| | 1–10 | 11–20 | 21–30 | > 30 | | | |
| 0 | 0 | 0 | 0 | 0 | 0 | Absent | – |
| 1–20 | 0 | 1 | 2 | 2 | 2–3 | Intermediate | + |
| 21–40 | 1 | 2 | 3 | 3 | 4–5 | High | + |
| 41–60 | 2 | 3 | 3 | 4 | ≥6 | Very high | + |
| >60 | 3 | 4 | 4 | 4 | | | |

Figure 3. Per PKI, extrapolation of the ex-vivo potency to their (potential) activity in patients was based on an algorithm considering the number of significantly inhibited peptides (columns) with, in the rows, their individual average percentage of inhibition (left). A PKI was considered to demonstrate no (significant) phosphorylation inhibition if the sum of the scores obtained from the algorithm was 0, low inhibition if the sum of the scores was 1, intermediate if 2 or 3, high if 4 or 5, and very high inhibition if this score was ≥6. In vitro, a PKI should at least result in intermediate phosphorylation inhibition to be considered significant and to thus be selected for therapy (right). In case ≥2 PKIs would display intermediate to very high inhibition, the agent with the highest cumulative score was selected for treatment of the patient. In case of equal scores, the least toxic drug was selected for treatment. Abbreviation: PKI, protein kinase inhibitor.

Table 1. Patient characteristics

| Patient ID | Age, years | Gender | Diagnosis | Selected PKI | Response at week 12 | Response at week 6 | PFS in weeks | Grade ≥ 3 toxicity (possibly related) |
|------------|------------|--------|--------------------|--------------|---------------------|--------------------|--------------|--|
| 1 | 63 | M | Rectal cancer | Dasatinib | NE ^a | NE ^a | NE | |
| 2 | 62 | F | Colon cancer | Dasatinib | PD | SD | 12 | Deep venous thrombosis |
| 3 | 68 | M | Rectal cancer | Dasatinib | NA ^b | NA ^b | NA | |
| 4 | 57 | M | Cholangiocarcinoma | Dasatinib | NE ^a | NE ^a | NA | Pain right flank; Fatigue |
| 5 | 38 | M | Germ cell cancer | Erlotinib | PD | PD | 6 | |
| 6 | 57 | F | Colon cancer | Dasatinib | PD | PD | 6 | Fatigue |
| 7 | 26 | M | Synovial sarcoma | Dasatinib | PD | PD | 6 | |
| 8 | 64 | F | Cholangiocarcinoma | Dasatinib | PD | PD | 6 | |
| 9 | 57 | M | Pancreatic cancer | Sunitinib | PD | PD | 6 | |
| 10 | 69 | F | Gallbladder cancer | Sunitinib | SD | SD | 20 | |
| 11 | 62 | F | Cholangiocarcinoma | Dasatinib | PD | PD | 6 | |
| 12 | 66 | M | Colon cancer | Dasatinib | NE ^c | NE ^c | NE | |

Patients for whom peptide microarray-based kinase activity profiling was performed.

^aPatient not evaluable due to rapid deterioration.

^bNot applicable; patient turned ineligible after profiling.

^cPatient not evaluable, declined treatment after profiling.

Abbreviations: 6, PFS is 6 weeks; F, female; ID, identification; M, male; NA, not applicable; NE, not evaluable; PD, progressive disease; PFS, progression-free survival; PKI, protein kinase inhibitor; SD, stable disease.

Table 2. Summary algorithm scores

| Patients with selected PKI, <i>n</i> | Median algorithm score (range) for PKI in the test | | |
|--------------------------------------|--|-------------------|---------------|
| | Dasatinib | Sunitinib | Erlotinib |
| Dasatinib, <i>n</i> = 9 | 8.2 (6–10) | 5.0 (3–6) | 2.5 (1–5) |
| Sunitinib, <i>n</i> = 2 | 8.5 (8–9) | 9.5 (9–10) | 8.0 (7–9) |
| Erlotinib, <i>n</i> = 1 | 6 (NA) | 6 (NA) | 7 (NA) |

Table displays the selection algorithm scores for the PKIs dasatinib, sunitinib, and erlotinib (columns), reflecting their in vitro inhibitory potency, in the 12 patients (rows) for whom kinase activity profiling was performed. The median selection algorithm score for dasatinib in all 12 patients was 8 (range 6–10). In the nine patients for whom dasatinib was selected, this was 8.2, whereas the median score for sunitinib was 5.0 and 2.5 for erlotinib. For the two patients with sunitinib as most active drug in vitro, differences between the top three drugs were smaller. In these patients, the median algorithm score was 9.5 for sunitinib, 8.5 for dasatinib, and 8.0 for erlotinib.

Data for lapatinib, everolimus, and sorafenib are not shown; the median algorithm selection score of these drugs in all 12 patients was 1 (range 0–6).

Abbreviations: NA, not applicable; PKI, protein kinase inhibitor.

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