

# Emerging Systemic Therapeutic Approaches for Personalized Medicine in Squamous Cell Carcinoma of the Lung

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## Abstract

During the past decade, a number of novel agents developed for the treatment of advanced NSCLC had, by coincidence, shown survival benefit predominantly among patients with nonsquamous histology, namely pemetrexed (anti-folate), bevacizumab (VEGF pathway inhibition), erlotinib/gefitinib (EGFR receptor tyrosine kinase inhibitors) and crizotinib (ALK receptor tyrosine kinase inhibitor). This has sparked a heightened interest in discovering key molecular aberrations that may be relevant for the treatment of squamous cell carcinoma (SCC) of the lung, a histologic subtype that represents approximately 25% of lung cancer cases diagnosed globally. This article highlights the most promising recent discoveries and targeted agents in development that may be relevant for the treatment of SCC of the lung.

## Introduction

During the past decade, a number of novel agents developed for the treatment of advanced NSCLC had, by coincidence, shown survival benefit predominantly among patients with nonsquamous histology, namely pemetrexed (anti-folate), bevacizumab (VEGF pathway inhibition), erlotinib/gefitinib (EGFR receptor tyrosine kinase inhibitors) and crizotinib (ALK receptor tyrosine kinase inhibitor) [1-5]. This has sparked a heightened interest in discovering key molecular aberrations that maybe relevant for the treatment of squamous cell carcinoma (SCC) of the lung, a histologic subtype that represents approximately 25% of lung cancer cases diagnosed globally [6]. This article highlights recent discoveries and targeted agents in development that may be relevant for the treatment of SCC of the lung.

## Fibroblast Growth Factor Receptor (FGFR)

The fibroblast growth factor family of 22 ligands variably interacts with 4 highly conserved transmembrane FGFR tyrosine kinases. Dysregulated signaling have been identified in various malignancies, via amplification, point mutation or translocations, which contribute to carcinogenesis such as increased proliferation, anti-apoptosis, cell migration and angiogenesis [7]. Examples include activating FGFR2 point mutations in endometrial carcinomas [8], FGFR2 amplification and point mutations in gastric carcinomas [9,10], FGFR3 activating point mutations in bladder carcinomas [11], FGFR3 overexpression arising from t(4;14)(p16;q32) translocation in multiple myeloma [12], FGFR4 amplification and point mutations in rhabdomyosarcomas [13], as well as amplification of FGFR1, FGFR2 and FGFR4 in breast cancer [14,15]. More recently, genomic analyses have shown frequent high level of FGFR1 amplification in a region of chromosome segment 8p12 by FISH in approximately 20% of SCC of the lung found in smokers [16]. More significantly is that this amplification underlies sensitivity to treatment with small molecule FGFR kinase inhibitors [16,17]. Few cases of FGFR2 point mutations in SCC of the lung have also been reported [18,19]. Nonetheless, wild type FGFR2 is functionally relevant as it cooperates with SOX2, which is commonly amplified in SCC of the lung, to achieve the latter's oncogenic potential [20]. Moreover, FGFs are frequently coexpressed with FGFR1 or FGFR2 in NSCLC, suggesting presence of autocrine signaling which can be inhibited by FGFR small molecule TKI. In contrast, cell lines lacking FGF/FGFR

co-expression are not affected [21]. Specific selectivity for FGFR alone maybe a disadvantage compared to ability to cross-inhibit the related PDGFR- $\alpha$  kinase, as the latter maybe relevant in certain model systems exhibiting FGFR overexpression arising from non-focal chromosome 8p12 amplification [16]. More-over, co-occurrence of other activated signaling pathways, such as constitutively activated MAPK pathway may underlie intrinsic resistance to FGFR1 inhibition [17]. Due to the high degree of homology between VEGFR2, PDGFR and FGFR kinase domain, a number of oral multikinase inhibitors in clinical use in fact demonstrates inhibition of FGFR in nanomolar concentrations as well albeit across a wide range (Table 1). A number of small molecule inhibitors have subsequently been developed to have more potent selectivity for FGFR kinase, such as dovitinib and brivanib. Indeed, there is suggestion that objective tumor response is better in FGF2-positive relative to FGF2-negative tumors in the dose-escalation phase I trial of brivanib [22]. Nonetheless, VEGF pathway inhibition remains clinically relevant with these agents, as hypertension is often seen as an adverse effect in early clinical trials [23-25]. Otherwise, nausea, vomiting, diarrhea are commonly encountered across all agents. In contrast to other multikinase inhibitors, incidence of all-grade hand-foot skin reaction (HFSR) is < 5% for pazopanib, nintedanib and the more selective FGFR inhibitors such as dovitinib, brivanib. A somewhat unique pharmacokinetic feature of dovitinib discovered based on dosing schedules utilized in the early phase I studies was an over proportional increase in dose and exposure relationship beyond 400 mg/day of continuous daily dosing. Population pharmacokinetic/pharmacodynamic modeling suggested that intermittent dosing could prevent prolonged drug accumulation and lead to better tolerance and thus currently the 5-days on/2-days off dosing schedule for dovitinib at 500 mg/day is employed in ongoing monotherapy studies [26].

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Newer orally administered small molecule inhibitors currently in development with even better selectivity for FGFR include LY2874455, BGJ398, and AZD4547. BGJ398's selectivity for FGFR 1-3 was demonstrated *in vivo* by dose-dependent inhibition of bFGF-stimulated angiogenesis but no corresponding impairment of VEGF-induced angiogenesis [27]. Phase I study of this agent is ongoing, with the study design reflecting the recognition that rationale-based, biomarker-driven patient enrichment design is ethical and feasible even in early clinical development of targeted agents. This phase I study, which started in 12/2009, is limited to patients with tumor that have FGFR1 or FGFR2 amplification or FGFR3 mutations. It started enrolling FGFR1-amplified NSCLC patients in the first quarter of 2011. Similarly, the phase I study of AZD4547, started in 9/2009, is recruiting only patients with tumors that have FGFR1 or FGFR2 amplification or overexpression. LY2874455, which is a dominant pan-FGFR inhibitor, exhibits approximately 6-9 fold selectivity on inhibition of FGF-over VEGF-mediated signaling *in vivo*. No appreciable blood pressure changes were seen in murine models at doses that achieve inhibition of xenograft growth, which can inhibit FGFR by 90% but VEGFR2 at <50% [28]. A phase I study which started recruiting patients in 12/2010 with advanced malignancies is ongoing. Ponatinib is a multikinase inhibitor that was developed to inhibit both native (IC<sub>50</sub> 0.37 nM) and mutant forms of bcr-abl, including T351I (IC<sub>50</sub> 2 nM) in patients with chronic myelogenous leukemia [29]. Preclinical models demonstrate its ability to inhibit growth of FGFR1-amplified squamous cell lung cancer xenografts as well as greater potency in inhibiting all activated forms of FGFR1-4 compared to dovitinib, brivanib, cediranib and nintedanib [30]. Common toxicities, reported in the phase II PACE study in CML, showed rash, myalgia, abdominal pain, headache, arthralgia and thrombocytopenia which reflect class-effects of bcr-abl inhibitors. Unusual severe adverse event include pancreatitis [31]. Thus, whether this agent can achieve meaningful antitumor efficacy for FGFR-driven solid malignancies along with acceptable safety profile in lung cancer patients, many of whom have comorbidities, is unknown. Other clinical trials of small molecule FGFR inhibitors specifically in SCC of the lung involve nintedanib- one is an ongoing phase I/II

study which started in April 2011 combining nintedanib with cisplatin and gemcitabine as first-line therapy (NCT01346540). The second is a planned phase I study combining nintedanib and everolimus in all solid tumors with an expansion phase for patients with FGFR1-amplified NSCLC (NCT013492960).

### PI3K (phosphoinositide 3-kinase) Pathway

The PI3K signaling pathway has a prominent role in regulating cancer cell growth and survival [32]. Class I PI3Ks are comprised of 4 isoforms of the catalytic p110 subunit:  $\alpha$ ,  $\beta$ ,  $\delta$  and  $\gamma$ , with the cell proliferation and growth principally the function of the p110 $\alpha$  isoform. p110 $\alpha$  (as well as the  $\beta$  and  $\gamma$  isoforms) are in turn regulated by p85-like regulatory subunits. Akt, the main effector, is activated downstream to PI3K, which in turn results in signaling chiefly through mTORC1. The mechanism of AKT activation by PI3K is regulated by the phosphatase and tensin homologue deleted on chromosome 10 (PTEN) tumor suppressor gene [33]. The PI3K pathway can be activated horizontally by inputs via receptor tyrosine kinase and G protein-coupled receptor signaling (e.g. Ras family) or constitutively by genetic abnormalities. Somatic activating mutations in the *PIK3CA* gene, which encodes for the catalytic p110 $\alpha$  subunit of PI3K, have been described in various malignancies such as colorectal, ovarian cancers, including lung cancers [34]. This has been reported to occur in approximately 2-4% of NSCLC and in approximately 1-10% of squamous cell lung carcinomas, with the most common mutations being in the helical domain encoded by exon 9 (E542 K, E545K) which interfere with p85 $\alpha$  binding and in the kinase domain encoded by exon 20 (H1047R, H1047L) [35-37]. Preclinical as well as early clinical studies have shown that presence of PIK3CA mutations in cancer cells confer treatment sensitivity to single-agent PI3K pathway inhibitors [34,38]. Presence of PIK3CA amplification, found in 43-65% of SCC of the lung, appears to be mutually exclusive with the presence of PIK3CA mutations [37,39]. The oncogenic effects of PIK3CA mutations however appear greater compared to PIK3CA amplification [37], suggesting that therapeutic effects of PI3K inhibitors will be greatest against tumors with mutant PIK3CA relative to PIK3CA-amplified tumors. Preclinical studies have

Drug	FGFR1	FGFR2	FGFR3	FGFR4	VEGFR2	Reference
	IC <sub>50</sub> (nM)					
Nintedanib	47	63	122	451	21	[29]
	69	37	108	610		[82]
Brivanib	165	202	530	2023	4.2	[29]
	15	32	52	>1000		[83]
Dovitinib	16	50	53	341	5.4	[29]
	13	21	18	470		[83]
Cediranib	5	33	36	697	<1	[29]
	26					[84]
Ponatinib	2	2	18	8	1.5	[29]
Sunitinib	437	852	314		34	[81]
Sorafenib	64	825	1019		28	[81]
Pazopanib	80	350	138		15	[81]
Axitinib	231				0.2	[85]
LY2874455	2.8	2.6	6.4	6	7	[28]
AZD4547	0.2	2.5	1.8	165		[86]
BGJ398	0.9	1.4	1	60	180	[27]
Regorafenib	202				4.2†	[87]
XL228	8	2	3			[88]

\*Data may vary between different references for the same compound due to differences in assay methodology. References that compare potency across various agents are preferentially cited when available. † murine VEGFR2

**Table 1:** Comparison of FGFR/VEGFR kinase inhibition profile of various FGFR inhibitors\*.

shown that resistance to PI3K inhibitors in PIK3CA-mutant tumors maybe mediated by presence of activated RAS/RAF/MEK pathway [40]. Of relevance is that while PIK3CA mutations frequently coexist with EGFR or K-ras mutations in lung adenocarcinomas [41], this is not the case with pure SCC of the lung [35]. Loss of PTEN is associated with PI3K pathway activation and this molecular event is found in 24-44% of NSCLC tumors as assessed by absent PTEN protein expression as determined by IHC, and up to 75% if cases with weak PTEN expression were included [42,43]. Published results show discordant data on the association of PTEN loss with tumor stage in SCC of the lung [43,44]. Nonetheless, genetic aberrations as a mechanism of PTEN loss, such as by mutation or homozygous deletion, are rare in lung cancer. Epigenetic silencing, such as promoter methylation, may partially explain some cases [42,43]. Recent data suggests that inactivation of p110 $\beta$  can counteract the effect of PTEN loss and that a pan-PI3K inhibitor will have greater antitumor efficacy compared to a isoform-specific PI3K inhibitor without activity against p110 $\beta$  although responses can still be seen [45,46].

The Akt family of kinases is comprised of 3 isoforms, Akt1, Akt2 and Akt3. There is relative specificity in each isoform's regulation of cellular processes, such as anti-apoptosis/cell survival for Akt1, maintenance of glucose homeostasis for Akt2 and brain development for Akt3. However, considerable overlap exists in their function such that functional isoform-specific signaling may be irrelevant with aberrant Akt activation [47]. The oncogenic E17K mutation in exon 4 of the plekstrin homology (PH) domain of Akt1 occurs in 6-8% of colorectal and breast malignancies [48]. While rare in NSCLC, it appears to be primarily found in squamous cell lung carcinoma, reported in 1-1.5% of squamous cell lung cancers [35,49,50]. This mutation is associated with increased membrane localization which results in increased autophosphorylation of AKT1, increased levels of cyclin D1 and reduced the sensitivity to an allosteric Akt kinase inhibitor [48,50]. The occurrence of AKT1 mutation and PIK3CA mutations are generally mutually exclusive events [48,51].

The first-generation PI3K inhibitors, such as wortmannin and LY294002 have been used extensively in preclinical models but are poorly soluble and toxic, likely due to off-target effects against unrelated enzymes such as polo-like kinases [52]. As both p110 $\alpha$  and p110 $\beta$  mediate signals downstream of insulin receptor, hyperglycemia/diabetes is a mechanism-based class effect of PI3K inhibitors. Other

common side effects reported include rash, mucositis, fatigue and diarrhea. Various PI3K inhibitors have been developed and are in clinical development (Table 2). CAL-101 (also known as GS-1101) is a potent p110 $\delta$ -selective inhibitor being developed for hematological malignancies, with promising role as well in chronic inflammatory diseases as well since p110 $\delta$  is mainly expressed in leukocytes [53]. Phase I study of GSK1059615 was terminated prematurely due to lack of sufficient exposure following single- and repeat-dosing [54]. GDC-0941, an oral reversible pan-inhibitor of Class I PI3K, is currently being evaluated in a multi-arm randomized phase II study in combination with carboplatin and paclitaxel, with or without bevacizumab, as first-line treatment (NCT01493843) in molecularly unselected NSCLC based on promising phase Ib results of this combination, particularly in the squamous subset of patients [55]. A prerequisite is the availability of archival or fresh tissue which will be used to conduct biomarker assessments. BKM120, an oral reversible pan-PI3K inhibitor exhibited preferential inhibition of PIK3CA mutant tumors, in contrast to either Kras or PTEN mutant models in preclinical studies [56]. Mood alteration such as anxiety and depression were reported in up to 20%, likely due to its ability to cross the blood-brain barrier [57]. There is an ongoing two-stage randomized phase II study of BKM120 as second line agent in comparison with docetaxel for SCC of the lung with evidence of activated PI3K pathway in archival/fresh biopsy specimen (NCT01297491). Currently being planned is a phase II study of BKM120 in various tumor types, including NSCLC, which have PIK3CA mutations E542K, E545K, H1047R, H1047L (NCT01501604). XL147 is another oral reversible pan-PI3K inhibitor which is being evaluated in a phase I study in combination with carboplatin and paclitaxel as treatment for advanced solid tumors including NSCLC (NCT00756847). Phase I single-agent study showed a confirmed partial response in a patient with NSCLC with wildtype PIK3CA but PTEN status is unknown. Pharmacodynamic studies in post-treatment biopsies shows reduction in pERK, which is notable as phosphorylation of ERK1/2 and MEK1/2 are generally not inhibited by these agents [58,59]. PX-866 is an oral irreversible pan-inhibitor of Class I PI3K synthetically derived from wortmannin though with ten-fold greater potency and nearly 3-fold less hepatotoxicity in murine toxicology studies relative to wortmannin [60]. A phase I single-agent study showed transaminase elevation as one of the dose-limiting toxicities [61]. It is currently being evaluated in randomized phase II study in combination with docetaxel versus docetaxel alone in patients with

Drug	p110 $\alpha$	p110 $\beta$	p110 $\delta$	p110 $\gamma$	mTOR	Reference
GDC-0941	3	33	3	75		[89,90]
PX-866	6	>300 uM	3	9		[91]
BKM120	52	166	116	262	2866	[56]
XL147	39	383	36	23	>15000	[92]
ZSTK474	16	44	5	49		[93]
CAL-101	>100 uM	1820 uM	70	1240		[94]
CH5132799	14	120	500	36	1600	[62]
PF-04691502	1.8	2.1	1.6	1.9	16	[64]
PF-05212384	0.4	6	8	6	1	[65]
GSK2126458	0.019	0.13	0.024	0.06	0.18	[95]
XL765	39	113	43	8	157	[96]
BEZ235	4	75	7	5	21	[97]
SF1126	356	736	3225	1774	1060	[98]
GDC-0980	5	27	7	14	17	[99]

**Table 2:** Comparison of kinase inhibition profile of various PI3K inhibitors (IC<sub>50</sub> in nM).



advanced NSCLC or squamous cell carcinoma of the head and neck (NCT01204099).

BYL719, GDC-0032, INK-1117 are isoform-specific p110 $\alpha$ -selective inhibitors developed to potentially increase magnitude of target p110 $\alpha$  inhibition by attenuating toxicities related to modulation of the other isoforms. CH5132799 has relatively greater selectivity for p110- $\alpha$ , with approximately 2-fold greater potency against common PIK3CA mutants relative to wildtype p110 $\alpha$  [62]. It demonstrated activity against some PTEN-deficient tumors, although likely the effect will have been more pronounced in the presence of p110 $\beta$  inhibition as previously described [46]. These agents are undergoing dose-escalation monotherapy studies in unselected population with exception of an ongoing phase I study of BYL719 limited to patients with confirmed PIK3CA abnormality (mutation or amplification) (NCT01219699).

The dual ATP-competitive PI3K/mTOR kinase inhibitors have efficacy in inhibiting both mTORC1 and mTORC2 aside from the PI3K family. This is an important feature as an undesired consequence of isolated mTORC1 inhibition, such as with rapamycin analogs, is the activation of Akt due to abrogation of the negative feedback loop [63]. PF-04691502 (orally administration) and PF-05212384 (intravenously administered, also known as PKI-587) have shown effective preclinical activity against NSCLC xenograft models harboring dual PTEN deletion/EGFR mutation or dual PIK3CA mutation with either Kras or EGFR mutation [64,65]. Early phase I clinical data shows good tolerability but no objective tumor responses to date even in tumors with PIK3CA mutation [66,67]. Preclinical studies of BEZ235 show that its efficacy maybe predominantly related to its mTOR kinase inhibition, whereby at low drug concentrations (<100 nM), mTOR inhibition predominates with corresponding induction of Akt phosphorylation, which is eliminated either by exposure at a higher concentration to achieve dual mTOR/PI3K blockade (500 nM) or by the combination of an IGF-1R tyrosine kinase inhibitor [68]. Early clinical studies showed an objective tumor response in a NSCLC patient with Cowden syndrome [69]. As alluded to earlier, response to PI3K inhibitors maybe limited in PIK3CA mutants due to frequent coexistence of activated RAS/RAF/MEK pathway. Preclinical studies show that combination with a MEK inhibitor may overcome this resistance [40,56]. Moreover, the compensatory activation of ERK observed with the use of PI3K inhibitors as a mechanism of treatment resistance has been described [70]. Thus, phase I studies evaluating the combination of PI3K inhibitors with MEK inhibitors are ongoing or being planned (e.g. BKM120 with MEK162 or GSK1120212; BEZ235 with MEK162; BYL719 with MEK162; GDC0941 with GDC-0973, XL147 with MSC1936369B, PF-04691502/PF-05212384 with PD-0325901; GSK2126458 with GSK1120212).

Various oral ATP-competitive pan-AKT inhibitors, such as GSK2110183, GSK2141795, GDC-0068, and AZD5363 are in early clinical development. These agents may have activity against cancers with the E17K AKT1 mutation, in contrast to potentially reduced efficacy of allosteric inhibitors against this AKT1 mutant [48]. While downstream signaling is inhibited, the ATP-competitive pan-AKT inhibitors, as a class-effect, induce hyperphosphorylation of AKT termed 'inhibitor hijacking of kinase activation', possibly through a conformational change [71]. MK2206 is an oral PH domain-dependent allosteric inhibitor with relatively greater potency against AKT1 and AKT2 (IC 50 of 5 and 12 nM, respectively) compared to AKT3 (IC50

of 65 nM) [72]. It induces a closed or inactive conformation of AKT, abrogates AKT phosphorylation and disrupts membrane localization [73]. Adverse effects observed in early clinical trials show spectrum of side effects consisting of skin rash, nausea, hyperglycemia and diarrhea similar to PI3K inhibitors [72]. A multiarm phase II study for NSCLC implemented in the first quarter of 2011 is ongoing, which prospectively assigns patients to specific kinase inhibitors according to the result of tumor molecular profiling (NCT01306045). Patients with PIK3CA, AKT or PTEN mutations will be allocated to the MK-2206 treatment arm. In terms of predictive biomarkers, there appears to be a relationship between the presence of PIK3CA mutations or PTEN loss with sensitivity to AKT inhibitors, and the presence of activated Ras pathway with resistance which may be overcome by combination with MEK inhibitors in lung cancer models [74-76]. A phase I study evaluating the combination of MK2206 with the MEK inhibitor AZD6244 is ongoing, with expansion cohort limited to NSCLC with Kras mutations or other specific (undisclosed) mutations (NCT01021748).

## Discoidin Domain Receptor 2 (DDR2)

DDR2 is a receptor tyrosine kinase that is activated by collagen binding and Src phosphorylation, thereby regulating various processes such as cell differentiation, extracellular matrix remodeling and cell migration [77,78]. Mutations in DDR2, both in the kinase domain and other regions, have been recently identified in approximately 3% of SCC of the lung based on a sequencing screen for recurrent mutations in this tumor type, with a total of 11 DDR2 mutations found in 290 samples (9 in 277 primary tumor specimen) [79]. There were no alterations in DDR2 gene copy number or protein overexpression found. This seminal finding generated significant attention as the investigators demonstrated that the mutations are oncogenic and that dasatinib, a dual src/abl kinase inhibitor, can block mutant DDR2, both kinase and non-kinase domain forms, in *in vitro* and *in vivo* preclinical models. Moreover dual inhibition of DDR2 and Src demonstrated additive efficacy against DDR2-transformed cell lines. The authors also reported that in a patient with EGFR-wildtype SCC of the lung harboring the DDR2 kinase domain mutation, treatment with a combination of erlotinib and dasatinib resulted in objective tumor response [79]. Of note, dasatinib, has the most potent activity against DDR2 (IC<sub>50</sub>=1.4 nM) compared to other kinase inhibitors such as imatinib (IC<sub>50</sub>=675 nM), nilotinib (IC<sub>50</sub>=55 nM), sorafenib (IC<sub>50</sub>=55 nM) and pazopanib (IC<sub>50</sub>=474 nM) [80,81]. Dasatinib is currently being evaluated in a phase II study as monotherapy for patients with SCC of the lung (NCT014916330).

## Conclusion

A great progress has recently been made in identifying key oncogenic aberrations in SCC of the lung. The race is on for the first pharmacologic agent with good therapeutic index that will achieve meaningful clinical benefit for patients with this diagnosis. The modulation of FGFR1 appears to hold the most promise, due to its relative prevalence and panoply of drugs in development. However, success will depend on understanding additional pharmacokinetic and pharmacodynamic factors that influence antitumor efficacy of these drugs in development. Another practical issue that faces the clinical development of these targeted therapies is the validation, in tandem, of predictive markers for treatment sensitivity and resistance. Moreover,

the assay for this biomarker should have sufficient sensitivity to detect low-frequency aberrations, either in fresh/frozen tumor or paraffin-embedded specimen, particularly as tumor cells can be heterogeneous and background material of normal tissue cannot be avoided. Ideally, this should be incorporated into a platform capable of multiplex testing a large panel of candidate genes to fully utilize the typically small quantity of tumor genetic material available, such as the Sequenom Mass ARRAY system. However, this requires dedicated technological, human and financial resources that may not be readily available for the community practitioner. Because immunohistochemical and tissue microarray methods are readily available in pathology laboratories, developing this is another feasible approach though this may be hampered by availability of relevant antibodies, optimization required and the relative tissue requirement compared to high-throughput methods even with TMAs. It is likely that with the rapid drop in cost of sequencing in line with technical advances, next-generation sequencing. As relevant is the need to understand both intrinsic and acquired resistance to therapy. This entails incorporating patient selection based on molecular profiling during the earlier phases of clinical testing as well as the need to perform multiple evaluations, such as biopsies, along each patient's treatment course that will enable elucidation of the genetic or signaling events that mediate acquired treatment resistance. More importantly, when multiple agents having similar spectrum of activity are being developed contemporaneously by different drug companies, there should be a collaborative effort in developing new study designs that will permit an efficient means of clinical testing, in a fashion akin to what has been spearheaded by the I-SPY2 investigators. This is a highly pertinent concern particularly when the patient population for clinical trials is limited by the low prevalence rate of an oncogenic drug target.

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