



Are erlotinib and gefitinib interchangeable, opposite or complementary for non-small cell lung cancer treatment? Biological, pharmacological and clinical aspects

Giuseppe Bronte^{a,1}, Christian Rolfo^{b,1}, Elisa Giovannetti^c, Giuseppe Cicero^a,
Patrick Pauwels^d, Francesco Passiglia^a, Marta Castiglia^a, Sergio Rizzo^a,
Francesca Lo Vullo^a, Eugenio Fiorentino^e, Jan Van Meerbeek^f, Antonio Russo^{a,*}

^a Medical Oncology, Department of Surgical and Oncology Sciences, University of Palermo, Palermo, Italy

^b Phase I-Early Clinical Trials Unit, Oncology Department and Multidisciplinary Oncology Center Antwerp (MOCA) Antwerp University Hospital, Edegem, Belgium

^c Department Medical Oncology, VU University Medical Center, Amsterdam, The Netherlands

^d Molecular Pathology Unit, Pathology Department and Multidisciplinary Oncology Center Antwerp (MOCA) Antwerp University Hospital, Edegem, Belgium

^e Surgical Oncology, Department of Surgical and Oncology Sciences, University of Palermo, Palermo, Italy

^f Thoracic Oncology, Multidisciplinary Oncology Center Antwerp (MOCA) Antwerp University Hospital, Edegem, Belgium

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Contents

| | |
|---|-----|
| 1. Introduction | 301 |
| 1.1. Definition of EGFR-TKIs drugs | 301 |
| 1.2. EGFR Pathway | 301 |
| 2. Biological bases of EGFR-TKIs treatment | 301 |
| 2.1. EGFR mutational status and resistance mutations | 301 |
| 2.2. EGFR-TKIs mechanisms of action | 302 |
| 2.3. Biological hypotheses to explain the differences between erlotinib and gefitinib | 303 |
| 3. Pharmacokinetics | 304 |
| 3.1. Bioavailability | 304 |
| 3.2. Metabolism and clearance | 305 |
| 4. Clinical aspects | 305 |
| 4.1. Comparison of clinical trials results (first line, second line and maintenance) | 305 |
| 4.1.1. Use in pretreated patients | 305 |
| 4.1.2. Use for first-line treatment | 306 |
| 4.1.3. Use as maintenance treatment | 307 |
| 4.2. Directly comparing studies | 308 |
| 4.3. Possibility of sequential administration of the two drugs | 309 |
| 4.4. Toxicity | 310 |
| 5. Conclusions | 310 |
| Reviewers | 311 |
| Acknowledgements | 311 |
| References | 311 |

* Corresponding author at: Department of Surgical and Oncological Sciences, Section of Medical Oncology, University of Palermo, Via del Vespro 129-90127 Palermo, Italy. Tel.: +39 091 6552500; fax: +39 091 6554529.

E-mail address: antonio.russo@usa.net (A. Russo).

¹ Both authors contributed equally to this work.

Abstract

Gefitinib and erlotinib are the two anti-epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKIs) approved for treatment of advanced NSCLC patients. These drugs target one of the most important pathways in lung carcinogenesis and are able to exploit the phenomenon of ‘oncogene addiction’, with different efficacy according to EGFR gene mutational status in tumor samples. Gefitinib has been approved only for EGFR mutation bearing patients regardless the line of treatment, while erlotinib is also indicated in patients without EGFR mutation who undergo second- or third-line treatment. Some studies evaluated the main differences between these drugs both for direct comparison and to improve their sequential use. In particular, toxicity profile resulted partially different, and these observations may be explained by several molecular and pharmacokinetic features. Therefore, this review integrates preclinical data with clinical evidences of TKIs to guide the optimization of currently available treatments in advanced NSCLC patients.

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Keywords: Lung cancer; Gefitinib; Erlotinib; Tyrosine kinase; EGFR; NSCLC

1. Introduction

1.1. Definition of EGFR-TKIs drugs

The management of NSCLC patients can today take advantage from the use of innovative targeted agents, such as erlotinib and gefitinib. The rationale for the efficacy of these small tyrosine kinase inhibitor (TKI) molecules lies in the so called “oncogene addiction” hypothesis, according to which some mutations that occur in specific oncogenes may render cancer cell survival strictly dependent on that aberrant gene [1,2]. Thus, drugs that are able to inactivate the mutated gene offer a new important strategy in the treatment of selected subgroups of tumors.

Gefitinib and erlotinib are orally active EGFR TKIs with different structure, as also reflected by the different molecular weight (446.9 Da and 429.9 Da, respectively). These drugs are ATP competitors at the ATP-binding pocket in the intracellular domain of EGFR [3]. As a consequence of this inhibition, cellular proliferation, angiogenesis, tumor invasion, and metastatic potential are inhibited. Gefitinib is available as film-coated tablets that contain 250 mg of active compound. Erlotinib tablets are available in three dose strengths: 25 mg, 100 mg, and 150 mg.

1.2. EGFR Pathway

Epidermal growth factor receptor (EGFR) is a transmembrane protein with cytoplasmic kinase activity that transduces growth signaling from the extracellular environment to the cell. The EGFR gene is located on the short arm of chromosome 7 (7p11.2) and encodes a 170 kDa type I transmembrane growth factor receptor [4]. EGFR belongs to the HER/erbB family receptor tyrosine kinases, which includes HER1 (EGFR/erbB1), HER2 (*neu*, erbB2), HER3 (*erbB3*) and HER 4 (*erbB4*). The interaction of EGFR extracellular domain with specific ligands induces a homo-dimerization (or hetero-dimerization with other HER family members) that causes the activation of the TK domain resulting in tyrosine autophosphorylation. Multiple signaling pathways are then activated, including RAS/RAF/ERK/MAPK and PI3K/AKT pathways [5]. These pathways regulate several

intracellular processes such as proliferation, invasion, cellular repair, protection from injury and anti-apoptosis [6].

2. Biological bases of EGFR-TKIs treatment

2.1. EGFR mutational status and resistance mutations

Until April 2004 it was unclear how to identify NSCLC patients who would benefit from the use of erlotinib or gefitinib. The data from the retrospective analysis of BR.21 trial about erlotinib in pretreated patients suggest that never-smokers and patients with EGFR-positive tumors might experience an enhanced benefit from erlotinib compared to placebo [7]. Higher response rates were also associated with patient characteristics such as never-smoking status, female gender, adenocarcinoma histotype, and East Asian race. Nevertheless it was clear from the outset that not all patients responded in the same way to the treatment with these drugs. Then, two research groups from Boston revealed that EGFR gene mutations in the kinase domain are strongly associated with TKIs sensitivity [8–10].

The sensitizing mutations to TKIs treatment fall within EGFR kinase domain and are activating mutations. To date four main types of EGFR activating mutations have been identified: point mutation in exon18 (G719X, G719S, G719A), deletions in exon19, insertions in exon20, and point mutation in exon21 (L858R and L861Q). The most frequent mutations are exon19 deletions (over 20 variant types) and leucine-to-arginine mutation at codon 858 in exon21 (L858R), accounting for 90% of all EGFR mutations. Several cell-based studies demonstrated that these mutations increased autophosphorylating activity on intracellular tyrosines determining the activation of a subset of downstream effectors. In addition, the mutant kinases are more sensitive to inhibition by gefitinib and erlotinib, which seems to reflect their increased drug affinity [11].

Despite the efficacy of EGFR-targeted therapy in NSCLC, almost all patients develop resistance to these drugs, with a mean duration of the response ranging between 3 and 7 months [12,13]. Beyond all the activating mutations that confer sensitivity to TKIs, there are indeed other point

mutations that may determine resistance to TKIs treatment. The most common resistance mutation is the T790M (substitution of threonine to methionine on codon 790), which falls into exon20. This mutation cause the insertion of a bulky methionine over the ATP binding pocket, blocking access to EGFR-TKIs but not to ATP [14]. Because of its significant role in affecting TKIs activity, the T790M should also be evaluated before the beginning of the treatment. This mutation has been thought to cause resistance by sterically blocking binding of TKIs such as gefitinib and erlotinib, but this explanation is in contrast with the fact that it remains sensitive to structurally similar irreversible inhibitors. Subsequent studies showed that T790M mutation increased the affinity of the receptor for ATP [15] and that T790M mutants retain low-nanomolar affinity for TKIs, in particular gefitinib [14]. This mutation occurs in cis of the same allele as the original activating mutations (it may be either an exon19 deletion or an exon21 L858R mutation). Interestingly, data from a recent study have unraveled the predictive value of T790M [16]. This study analyzed 95 patients enrolled in EURTAC trial for T790M end P53 mutations, EML4-ALK translocation and BIM mRNA expression levels. The results showed that OS for patients with T790M mutations was 40.1 months in those with high BIM levels and 15.4 months in patients with low/intermediate BIM levels ($P=0.04$). These findings should lead to the design of studies of treatment based on the presence of the EGFR T790M mutation and BIM expression levels. In addition to the EGFR T790M mutation, there are other uncommon secondary resistance mutations, such as T854A in exon21 [17], as well as L747S [18], and D761Y [19], both in the exon19. T854A mutation has a comparable effect to that of T790M; L747S is thought to shift the equilibrium toward the active conformation of the receptor, while D761Y may affect the catalytic cleft of the receptor [20] (Figs. 1–4).

2.2. EGFR-TKIs mechanisms of action

Both gefitinib and erlotinib exert their action by interacting with EGFR ATP binding pocket and thereby blocking the signal transduction. EGFR mutations make the cancer cells more sensitive to these drugs through the phenomenon of “oncogene addiction”, which provides a rationale for molecular targeted therapy. The blockade of this pathway leads to tumor cell death, while sparing EGFR wild type cells. Despite many studies support the concept of this phenomenon, the underlying biological and molecular mechanisms are not yet clear. Zhou and collaborators have recently developed a mathematic model of EGFR-associated signaling network to investigate possible molecular mechanisms of tumor cell death [21].

EGFR activation results in the initiation of different cellular pathways. In response to several stimuli (toxic environmental stimuli or receptor occupation by the ligands EGF, transforming growth factor- α and neuregulins), the EGFR forms homo- or heterodimers with other family members and

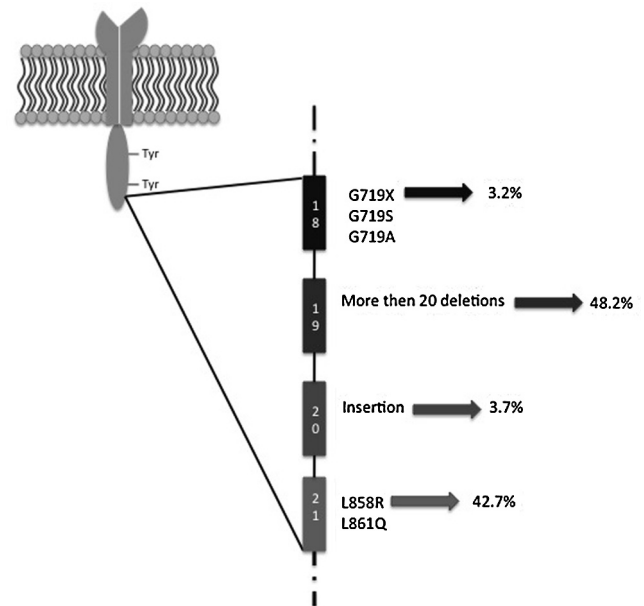


Fig. 1. EGFR activating mutation. The main mutation types identified in EGFR gene are: point mutation in exon18 (G719X, G719S, G719A), deletions in exon19, insertions in exon20, and point mutation in exon21 (L858R and L861Q). Point mutation in exon18 and insertions in exon20 account for 4% of all EGFR mutations; the most frequent mutations are exon19 deletions (over 20 variant types) and leucine-to-arginine mutation at codon 858 in exon21 (L858R), accounting for 90% of all EGFR mutations.

all the possible complexes between ErbB family members have been already identified [22]. The three heterodimers that are most frequently formed are ErbB-2/ErbB-3, ErbB-2/ErbB-4, and ErbB1/ErbB-4 and the different ability to form homo- and heterodimers is dictated by receptors expression levels. Receptor dimerization is followed by activation of intrinsic protein tyrosine kinase activity and tyrosine phosphorylation. These lead to the formation of phospho-tyrosine residues that enable receptor to recruit adaptor proteins such as Shc and Grb2 [23]. Several studies have also shown that the phosphorylation of specific tyrosine residues is able to recruit specific cytosolic proteins, and then activate different pathways [11]. For example Purvis and collaborators [24] assumed that phosphorylated Y1068 (pY1068) binds mainly to Gab-1 and Grb2 while phosphorylated Y1173 (pY1173) binds preferentially to Shc. This introduces the concept that differential signaling is headed by the phosphorylation of different tyrosine residues that transduce signal through distinctive/diverse pathways. Once bound to the receptor Shc and Grb2 recruit SOS that promotes the replacement of GDP by GTP in Ras, thereby activating Ras. This activation in turns lead to the phosphorylation of Raf and hence the MAPK pathway is activated. Conversely, the interaction of the EGFR with Gab-1 leads to the recruitment of phosphatidylinositol 3-kinase (PI3K), which induces the activation of AKT pathway by transforming PIP2 in PIP3 [25–29]. An internal process of negative feedback regulates both these pathways. In fact, activated ERK can also phosphorylate the protein SOS

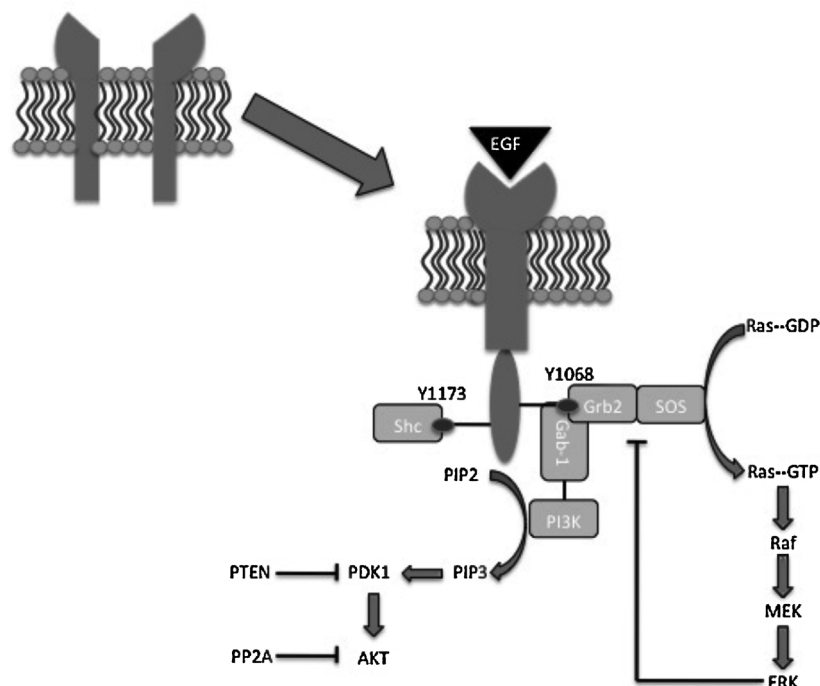


Fig. 2. EGFR pathway: Receptor dimerization lead to the activation of intrinsic protein tyrosine kinase activity and tyrosine phosphorylation. The phosphorylation of different tyrosine residues enables the receptor to recruit adaptor protein such as Shc and Grb2. Phosphorylated Y1068 (pY1068) binds mainly to Gab-1 and Grb2 while phosphorylated Y1173 (pY1173) binds preferentially to Shc. The recruitment of SOS promotes the replacement of GDP by GTP in Ras, thereby activating Ras. This activation in turns lead to the phosphorylation of Raf and hence the MAPK pathway is activated. Instead the interaction of the EGFR with Gab-1 leads to the recruitment of phosphatidylinositol 3-kinase (PI3K), that by transforming PIP2 in PIP3 induces the activation of AKT pathway.

inducing the dissociation of Grb2-SOS from the receptor. PIP3 and Akt are instead dephosphorylated by PTEN and PP2A, respectively. P38 is an important pro-apoptotic effector that can be activated by a variety of environmental stresses, among them the most important is the stress due to reactive oxygen species (ROS). Numerous studies have shown that stimulation of neoplastic cells with EGF can induce ROS production thus activating P38 [30]. The acute inactivation of EGFR results in a drastic decline of p-ERK and AKT and a delayed increase of P38. This finally results in a rapid decrease of proliferative stimuli and an increase of pro-apoptotic signals in addicted cancer cells [31].

Orally administered gefitinib or erlotinib are taken up by cancer cells, and they reversibly and competitively inhibit the binding of ATP to the phosphate-binding loop. By the inhibition of ATP binding to EGFR, the EGFR-TKIs therefore block auto-phosphorylation and the activation of downstream signaling pathways, leading to the inhibition of cell proliferation and the induction of apoptosis in cancer cells [32].

2.3. Biological hypotheses to explain the differences between erlotinib and gefitinib

The analysis of clinical data suggests a difference in the effectiveness of erlotinib and gefitinib. We present hypotheses on the biological basis of this difference to improve the understanding of TKIs' biological function. We hypothesize that the different response to gefitinib and erlotinib may depend on

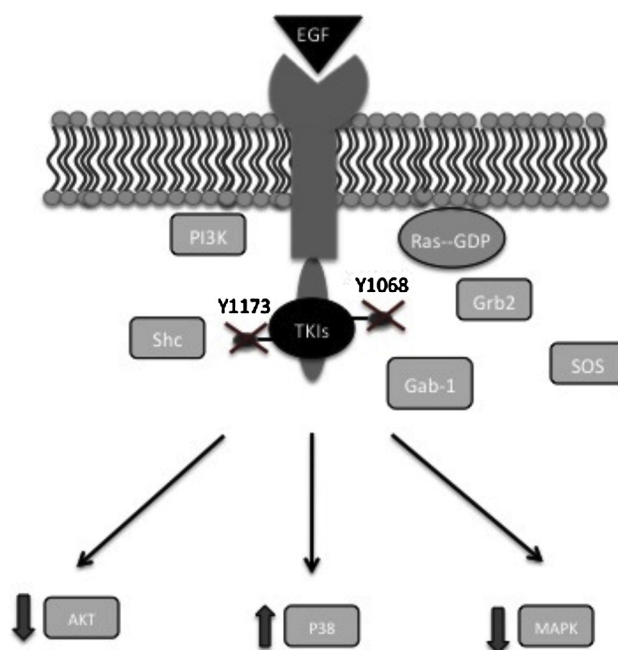


Fig. 3. TKIs supposed mechanism of action. Orally administered gefitinib (or erlotinib) is taken up by cancer cells, and it reversibly and competitively inhibits the binding of ATP to the phosphate-binding loop. By the inhibition of ATP binding to EGFR, EGFR-TKIs therefore block auto-phosphorylation and the activation of downstream signaling pathways, leading to the inhibition of cell proliferation and the induction of apoptosis in cancer cells.

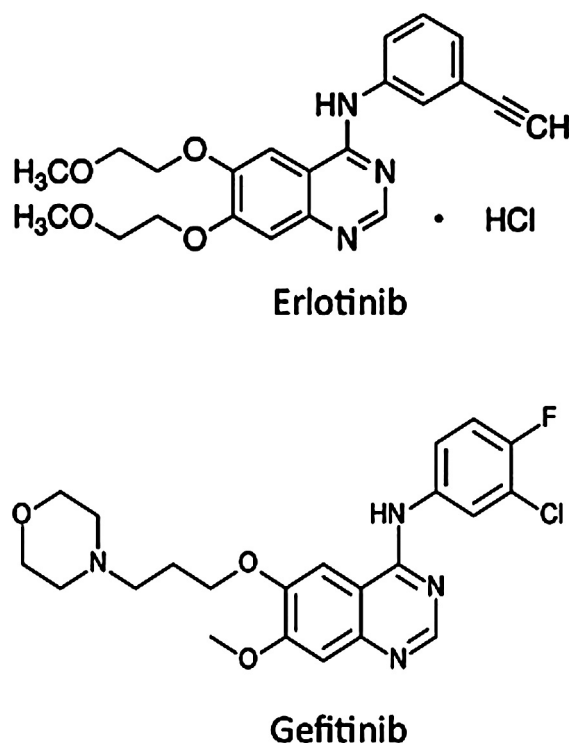


Fig. 4. Erlotinib and gefitinib chemical structures. Erlotinib and gefitinib (molecular mass 429.9 and 446.9 respectively) are both based on a 4-anilino-quinazoline kinase pharmacophore and exhibit similar pharmacokinetic characteristics in patients after oral administration, with extensive metabolism primarily by cytochrome P450 3A4 in liver.

the effects of various EGFR mutations on receptor structure, primarily on catalytic site. This hypothesis is supported by Yun and collaborators, stating that the effect of the mutations on inhibitor binding site is important, because they cluster around the catalytic cleft and differences in inhibitor sensitivity of the mutants have been reported [15]. This study suggests that mutations L858R and G719S have a different effect on the sensitivity to gefitinib, showing that L858R binds more tightly to gefitinib compared to G719S mutant. This markedly tighter binding of gefitinib to L858R mutant could explain its effectiveness against cells bearing this mutation. In particular L858R transformed Ba/F3 cells are significantly more gefitinib-sensitive than G719S transformed cells [32]. These data show that intrinsic differences in the inhibitor binding affinity of the altered EGFR kinases might explain the differential sensitivity of cell lines and tumor cells bearing L858R and G719S proteins.

Moreover, the combination of two different mutations could confer resistance to a TKI but improve sensitivity to the other one. In particular, an EGFR mutation E884K, in combination with L858R, was identified in a patient with advanced lung cancer who progressed on erlotinib maintenance therapy, and subsequently had leptomeningeal metastases that responded to gefitinib [33].

Several other EGFR mutations might also play a relevant role in this context and further studies are necessary

to investigate this possibility. More than 75 different EGFR kinase domain residues have been reported to be altered in NSCLCs. Using transfection of an YFP-tagged fragment of the EGFR intracellular domain (YFP-EGFR-ICD), followed by immunofluorescence microscopy analysis, recent studies demonstrated that the exon 20 insertions Ins770SVD, Ins774HV N771GY and A767-V769 confer increased kinase activity, but no sensitivity to erlotinib at clinically available concentrations [34]. However, a more recent study showed that sensitivity to erlotinib and gefitinib differed among several EGFR mutations at exon 19 [35]. Moreover, gefitinib and erlotinib seems to have slightly different activity also for the wild-type EGFR receptor, since response rates of gefitinib in NSCLC with wild-type EGFR range from 0 to 6.6% in several phase III trials [36–39], while the response rate of erlotinib in NSCLC with wild-type EGFR was 7% in the BR.21 study [40]. Although one should be cautious in interpreting these results since the detection method of EGFR mutations varied from study to study, further studies with standardized methods may help the clinician in patient management and may also improve the research of new and more potent TKIs selective for specific mutations.

Finally, several research groups are investigating the possible role of EGFR polymorphisms in the response and toxicity to TKIs treatment [41]. Germline polymorphisms can be easily assessed in blood samples, and candidate polymorphisms in EGFR have been correlated with outcome in NSCLC patients treated with gefitinib or erlotinib [42]. In particular, EGFR -191C/A, -216 G/T, and R497K polymorphisms have been associated with gastrointestinal toxicity both in gefitinib and erlotinib-treated patients, while AKT1-SNP4 A/A genotype seems to be a candidate biomarker of primary resistance, when using gefitinib in NSCLC patients [43], but not in the pharmacogenetic analysis of the BR.21 randomized phase III clinical trial of erlotinib [44]. Despite these intriguing findings, the small sample size, together with the interethnic differences, and the retrospective nature of most pharmacogenetic studies, make it difficult to draw any clear conclusions regarding the role of these biomarkers in determining the differential clinical outcome or toxicity in gefitinib and erlotinib treatment. Hopefully, the accurate planning of new prospective trials, the increased knowledge of key mechanisms affecting drug distribution/activity, and the use of novel technologies, including genome-wide approaches, may provide critical and essential tools to improve our insights in EGFR-TKIs mechanisms of action, in order to optimize these treatments in selected NSCLC patients.

3. Pharmacokinetics

3.1. Bioavailability

After oral assumption erlotinib is slowly absorbed and reaches its maximum plasma concentration after 3–4 h with a mean bioavailability of 60%. One study provided an estimate of the absolute bioavailability of 59%. At a dose of

150 mg daily erlotinib keep an area under curve (AUC) of 38,420 ng.h/ml [45]. This value is about seven-fold higher than those which could be obtained by administering therapeutic doses of gefitinib. Thus, the standard dose of erlotinib yields a higher exposure, and a patient should receive >3-fold recommended dose of gefitinib, which is 250 mg, to obtain drug concentrations equivalent to those achievable by erlotinib.

The solubility of both erlotinib and gefitinib is pH-dependent. Agents that alter gastric pH, such as H₂-receptor antagonists and proton-pump inhibitors can substantially reduce the plasma levels of EGFR TKIs, and their concomitant use should be avoided. Moreover, both the bioavailability and the AUC of erlotinib increase considerably when the drug is ingested with food [46]. Erlotinib has an oral bioavailability of 60% when taken on an empty stomach. Conversely, when taken with food, erlotinib has a bioavailability of nearly 100%, which potentiates side effects. Therefore, erlotinib should be taken at least 1 h before or 2 h after a meal. After 7–8 days erlotinib concentrations reach steady-state and its elimination half-life is 31 h. Erlotinib is evenly distributed in the plasma and tumor tissue (plasma: tumor ratio = 1:1). Binding to plasma proteins is approximately 95% bound to serum albumin and alpha-1 acid glycoprotein (AAG) of the serum. For erlotinib a 30% dose reduction is allowed. This dose reduction regards 6–16% of patients because of side effects.

In contrast, food does not affect the absorption of gefitinib. The absorption after oral administration is moderately slow and peak plasma concentrations are obtained after 3–7 h from administration, with elimination half-life of 48 h, and mean bioavailability of 60%. This drug is distributed extensively in tissues, and plasma protein binding is approximately 90% [47].

3.2. Metabolism and clearance

Erlotinib and gefitinib are metabolized primarily by CYP3A4 and less by CYP3A5 and CYP1A1 [48]. Erlotinib is metabolized primarily in the liver by different cytochrome enzymes (especially by CYP3A4), but intestinal and lung cancer cells could partly contribute to its catabolism. Moreover, cigarette smoking induces CYP1A1 and has been correlated with a reduction in erlotinib exposure after a therapeutic dose [49].

Erlotinib excretion is >90% by stools and the rest by kidney. Less than 2% of delivered dose is excreted as unchanged drug. Also gefitinib is excreted mainly as metabolites in stools, with renal elimination accounting for <4% of the administered dose.

However, erlotinib lipophilicity is about 3-times lower than gefitinib. This could help to explain some of the differences in pharmacokinetic and pharmacodynamic properties of the two compounds, since a greater lipophilicity also leads to a higher susceptibility to the action of catabolic mechanisms, an increase in biliary excretion and a decrease in

plasma concentrations of free drug. In fact erlotinib is less exposed to hepatic cytochrome enzyme action, resulting in a slower clearance.

The factors related to the patient that showed a correlation with the pharmacokinetics of erlotinib were serum total bilirubin, Alpha-1 Acid Glycoprotein (AAG) and current smoking. Increased serum concentrations of total bilirubin and AAG concentrations were associated with a reduced erlotinib clearance. An interesting data on the pharmacokinetics of erlotinib is given by its interaction with smoke, so that smoker's drug exposure is reduced by 50–60% and the maximum tolerated dose is increased to 300 mg [49]. For this reason smoking cessation should be suggested before treatment starts.

4. Clinical aspects

EGFR-TKIs represent the mainstream target therapy in NSCLC lung cancer, leading to improvements in PFS and OS when used as upfront treatment in patients whom tumors harbor EGFR mutations [50]. Instead of chemotherapy, which induces limited benefit on a large proportion of NSCLC patients, targeted drugs are able to obtain a higher benefit on a limited number of selected patients, with a lower toxicity and a better quality of life. Therefore targeted drugs improve the concept of tailored therapy, which will lead to new algorithms taking into account clinical characteristics, histology, molecular profiling such as genomics, and individual genes pattern. It represents the new frontier of cancer treatment without using chemotherapeutic drugs, even if, at this time, these progresses have had only a limited impact on the overall outcome, and chemotherapy remains the only possible treatment for the most part of NSCLC patients [51].

The first clinical trials evaluating the TKIs efficacy in the treatment of NSCLC patients date back to 2003–2005. On the basis of encouraging pre-clinical results, some phase III studies were designed to evaluate the efficacy of gefitinib and erlotinib in combination with the chemotherapeutic second-line treatment [12,52] and the first-line [53–55]. However these results were clearly negative. More recently, a further phase III study [56], evaluated the addition of erlotinib to first-line cisplatin-gemcitabine chemotherapy in stage IIIB–IV NSCLC patients. The authors concluded that erlotinib with concurrent cisplatin-gemcitabine shows no benefit compared to chemotherapy-naive NSCLC patients.

4.1. Comparison of clinical trials results (first line, second line and maintenance)

4.1.1. Use in pretreated patients

On the basis of encouraging results emerging from phase II studies, which showed a good activity profile of gefitinib and erlotinib as second/third line treatment in terms of response rate (RR), two randomized phase III trials comparing the efficacy of both drugs versus placebo were conducted [57,58].

Table 1

Randomized phase III trials of comparison of TKI vs. placebo in pre-treated patients with advanced NSCLC.

| Clinical trials | BR.21 [36] | ISEL [37] |
|---|---|-----------------------|
| Treatment | Erlotinib vs. placebo | Gefitinib vs. placebo |
| Median OS 6.7 vs. 4.7 months (HR: 0.73; <i>p</i> : 0.001) | 5.6 vs. 5.1 months (HR: 0.89; <i>p</i> : 0.1) | |

In particular BR21 study, which enrolled 731 patients with NSCLC in second/third line treatment, achieved the primary endpoint, overall survival (OS), with an extension of 42% of the median survival in the erlotinib group compared with placebo (OS: 6.7 vs. 4.7 months, HR: 0.73, *p*: 0.001).

A multivariate subsequent analysis of the study showed a greater RR in the erlotinib arm in a subgroup of patients selected on the basis of certain clinical characteristics (women, non-smokers, Asian race, adenocarcinoma). These characteristics are associated with a higher probability of EGFR gene mutation, but BR21 data showed a statistically significant benefit even in the subgroup of male patients, smokers, squamous histology, leading to the drug registration with indication for treatment of 2–3 line in NSCLC patients not selected on the basis of clinical or biomolecular features.

With regard to gefitinib, the phase III trial which compared gefitinib vs. placebo in the treatment of 2nd–3rd line NSCLC patients, ISEL [58], didn't reached the primary endpoint (OS: 5.6 months in the gefitinib arm vs. 5.1 in the placebo arm, HR: 0.89, *p*: 0.1), although subgroup of analysis showed a statistically significant advantage in favor of gefitinib in patients with certain clinical characteristics (i.e. women, Asian, not smokers, adenocarcinoma), as described above. Indeed the rate of responses obtained with gefitinib in the ISEL study (8%) is very similar to the one obtained with erlotinib in BR21 (9%), and the progression-free survival (PFS) as well as the OS data seem overlapping.

The different final results achieved in these two studies could be attributed to the different chemosensitivity of the two selected populations. In fact, one of the inclusion criteria of the ISEL trial was that patients had a progressive disease within 90 days from the last cycle of performed chemotherapy, so that about 45% of patients in the ISEL study had a PD as the best response to treatment compared to 18% of the patients in BR21 study (Table 1).

Four following clinical trials compared gefitinib versus docetaxel in second line treatment. The INTEREST study [59], designed as a noninferiority trial, enrolled 1466 patients

after 1–2 chemotherapy regimens not selected on the basis of clinical or molecular characteristics, reaching their objective in full (HR: 1.02 96% CI: 0.905–1.15), with a median survival of 7.6 months for gefitinib vs. 8 months for CT. Also the study SIGN [60] showed similar results in terms of OS (7.5 months vs. 7.1 months for gefitinib and docetaxel respectively), as well as the two Asian studies ISTANA [61] and V15-32 [38], in which the higher median survival (14.1 months), can be regarded as the general treatment outcomes in unselected East Asian patients, while the results of INTEREST may represent general treatment outcomes in Western countries. A recent meta-analysis [62] summarizes and reinforces the results that emerge from individual studies, not showing a statistically significant difference in OS and PFS between treatment with gefitinib and docetaxel in the 2nd–3rd line; but a higher RR%, a better toxicity profile and a better quality of life were associated with gefitinib treatment, so that the authors conclude that it would be preferable to docetaxel.

Next, three randomized phase III trials compared erlotinib and chemotherapy in the treatment of 2nd–3rd line NSCLC patients not selected on the basis of clinical or biomolecular characteristic. In the TITAN trial [63], which compared erlotinib vs. docetaxel or pemetrexed, OS (primary endpoint) was similar in the two treatment arms (5.3 months in erlotinib arm vs. 5.5 months in the CT arm, HR: 0.95, *p*: 0.73). In a similar study [64], in patients treated with erlotinib vs. pemetrexed, time to progression (TTP) seems not different between the two treatment arms, while primary endpoint data (OS) of TAILOR study, comparing erlotinib vs. docetaxel, are not yet available, although some partial results of the study, concerning the secondary endpoint (PFS) presented at ASCO 2012, seem to highlight a benefit in favor of docetaxel (HR: 0.69, 95% CI: 0.52–0.93) (Table 2).

4.1.2. Use for first-line treatment

The strong evidences concerning EGFR gene activating mutations and their correlation with the efficacy of TKI, prompted several clinical trials to evaluate the use of these drugs in the first-line treatment of NSCLC patients in Asia. The Phase III study IPASS [39] compared gefitinib vs. carboplatin–paclitaxel in a population of patients selected on the basis of clinical features (Asian, non-smoking, adenocarcinoma), demonstrating non-inferiority of gefitinib vs. standard chemotherapy in terms of PFS (5.7 vs. 5.8 months), which was the primary endpoint, as well as for OS (18.6 vs. 17.3 months), with a tolerability profile and a better quality-of-life in patients treated with gefitinib.

Table 2

Randomized phase III trials of comparison of TKI vs chemotherapy in pre-treated patients with advanced NSCLC.

| Clinical trials | INTEREST [38] | SIGN [39] | ISTANA [40] | V15-32 [41] | TITAN [43] | TAILOR |
|-----------------|-----------------------------|-------------------------|---------------------------------|-------------------------------|-------------------------------|-------------------------|
| Treatment | Gefitinib vs. docetaxel | Gefitinib vs. docetaxel | Gefitinib vs. docetaxel | Gefitinib vs. docetaxel | Erlotinib vs. doc/pem | Erlotinib vs. docetaxel |
| Median OS | 7.6 vs. 8 months (HR: 1.02) | 7.5 vs. 7.1 months | 14.1 vs. 12.2 months (HR: 0.87) | 11.5 vs. 14 months (HR: 1.12) | 5.3 vs. 5.5 months (HR: 0.95) | Not yet available |

Subsequently the analysis of subgroups selected on the basis of molecular factors [65] showed a statistically significant advantage in favor of gefitinib in the subgroup of patients harboring EGFR gene activating mutations, both in terms of PFS (HR: 0.48, $p < 0.0001$) and RR (43% vs. 32%, $p < 0.001$), whereas no difference was observed regarding OS. Similar results were reported in a randomized phase III Korean study, FIRST SIGNAL [66], which compared gefitinib vs. cisplatin–gemcitabine combination, not showing any difference between the two treatment arms (PFS 6.1 vs. 6.6 months) in the general population selected on the basis of clinical features, while a statistically significant difference in favor of gefitinib was observed in the subgroup of EGFR mutated patients (PFS 8.7 vs. 6.7 months).

In 2010 two randomized Japanese trials, NEJ002 and WJTOG [67,68], compared in first-line treatment of NSCLC gefitinib vs. carboplatin–paclitaxel and gefitinib vs. cisplatin–docetaxel, respectively. Patients were selected for the presence of EGFR gene activating mutations, and the results showed the clear superiority of gefitinib in this subset of patients (median PFS 10.8 months vs. 5.4 months HR: 0.30, $p < 0.001$, in the NEJ002 study, and median PFS 9.2 vs. 6.3 HR: 0.489, $p < 0.0001$ in WJTOG 3405), which determined the premature end of the trial, during the interim analysis.

In all these studies, the OS was similar in both arms, probably because of the high cross-over rate, so that almost all the patients who progressed after a first-line chemotherapy received a TKI as second-line treatment. A recent meta-analysis [69] confirms the results of studies comparing chemotherapy and gefitinib in first-line treatment showing a higher RR (72% vs. 38% OR: 4.04) and a statistically significant increase in PFS (HR: 0.45) in patients treated with gefitinib selected for EGFR gene activating mutations. On the basis of this evidence in July 2009 EMA approved gefitinib for the treatment of locally advanced or metastatic NSCLC in all treatment lines limited to patients bearing EGFR gene activating mutations. To date gefitinib is considered the best first-line option for this molecularly selected subgroup of patients.

Erlotinib was also compared to chemotherapy in first-line treatment of NSCLC patients. Two phase III randomized trials were conducted on a selected population for the presence of EGFR gene activating mutations: the OPTIMAL study [70] enrolled 154 patients in China, comparing erlotinib vs. carboplatin–gemcitabine combination, while in the EURTAC study [71] 174 Caucasian enrolled patients were randomized to erlotinib vs. platinum-based regimens. In both studies the primary endpoint has been reached with a median PFS 13.1 months in arm with erlotinib vs. 4.6 months HR: 0.16, $p < 0.0001$ (OPTIMAL study), and a median PFS 9.7 vs. 5.2 months HR: 0.37, $p < 0.0001$ (EURTAC study). Therefore erlotinib has also proven effective in first-line treatment of NSCLC patients with EGFR mutation. Moreover, it is the only EGFR TKI, which has been directly tested against chemotherapy in Caucasian patients.

A recent meta-analysis [69] included 13 randomized trials which compared TKIs and chemotherapy in first and second-line treatment of 10433 patients selected for the presence of EGFR gene activating mutations, showing a clear superiority of TKIs both in terms of ORR (67.6% vs. 32.8% RR: 2.06) and PFS (HR: 0.30), while no difference was observed regarding OS. These results are likely to be influenced by crossover treatments that formally abrogate any survival gain. Moreover, the increased benefit is statistically maintained both in untreated and in treated patients, while erlotinib appear to have a greater effect on RR and progression delay than gefitinib.

Some phase II trials have compared erlotinib vs. chemotherapy in patients with unknown EGFR mutation status, with conflicting results. A phase II trial [72] compared erlotinib vs. carboplatin–paclitaxel in the first line treatment in NSCLC patients with performance status (PS) 2, with relevant results for chemotherapy arm (RR 2% vs. 12% PFS 1.9 vs. 3.5 months, HR: 1.45, $p: 0.6$). However these results may be influenced by patient PS, which is known to influence the effectiveness of TKI, as observed in another phase II study [73], in which >75 year-old or PS2 patients were treated with erlotinib as first-line treatment, with very disappointing results (ORR: 21%, median PFS: 1.5 months; median OS: 3.2 months).

Another study on elder people (>70 years, PS0/1) [74], comparing erlotinib vs. carboplatin–vinorelbine, showed greater efficacy of chemotherapy (PFS: 4.6 vs. 2.4 months, $p: 0.0005$, RR: 28.3% vs. 7.8%, $p: 0.0001$). On the other hand, the results of a recent phase II study [75], which compared erlotinib versus single-agent chemotherapy with oral vinorelbine in elderly patients (> 70 years), showed a statistically significant advantage in favor of erlotinib (RR: 22.8% vs. 8.9%, PFS: 4.57 vs. 2.53 months, $p: 0.02$), with an increase in median PFS that was greater in patients with EGFR activating mutations gene in treatment erlotinib ($n: 9$, median 8.4 months), followed by the same mutated patients treated with vinorelbine ($n: 15$, median 3.97 months), and then in descending order by patients without mutation treated with vinorelbine and erlotinib (median 3.83 and 1.47 months respectively). These data suggest a possible prognostic value of EGFR, in addition to the already known predictive value. Furthermore, it raises the possibility of treating with biologic drugs selected subset of patients (elderly PS 0–1, ineligible for double platinum) regardless of the mutational status of EGFR, saving them from all the toxic effects of chemotherapy, and even getting a higher efficacy, is promising (Table 3).

4.1.3. Use as maintenance treatment

Two recent phase III trials evaluated the use of TKI on maintaining strategy with good results. In particular, SATURN study [76] evaluated the erlotinib efficacy in maintenance after 4 cycles of platinum-based chemotherapy, in a population of unselected patients, showing a statistically significant benefit in terms of PFS (median PFS: 12 vs. 11 weeks, HR: 0.71, $p < 0.0001$) and OS (median OS: 12

Table 3
Randomized phase III trials of comparison of TKI vs chemotherapy in first-line treatment of patients with advanced NSCLC.

| Clinical trials | IPASS [45] | FIRST-SIGNAL [47] | NEJ002 [48] | WJTOG 3405[49] | OPTIMAL [51] | EURTAC [52] | |
|-----------------|--|---|---|---------------------------------------|-----------------------------------|--|--------------------------------|
| Treatment | | Gefitinib vs. carboplatino-paclitaxel | Gefitinib vs. cisplatio-gemcitabina | Gefitinib vs. carboplatino-paclitaxel | Gefitinib vs. cisplatio-docetaxel | Erlotinib vs. carboplatino-gemcitabina | Erlotinib vs. platinum doublet |
| Median PFS | Overall population EGFR-mutation positive EGFR mutation negative | 5.7 vs. 5.8 months HR: 0.74 HR: 0.48 $p < 0.0001$ HR: 1.38 | 6.1 vs. 6.6 months HR: 0.813 8.7 vs. 6.7 months HR: 0.544 2.1 vs. 6.4 months HR: 1.419 | 10.8vs5.4 months HR: 0.36 | 9.2 vs. 6.3 months HR: 0.489 | 13.1 vs. 4.6 months HR: 0.16 | 9.7 vs. 5.2 months HR: 0.37 |
| Median OS | Overall population EGFR mutation positive EGFR mutation negative | 18.6vs17.3 months HR: 0.90 21.6 vs. 21.9 months HR: 1.00 11.2 vs. 12.7 months HR: 1.38 | 21.3vs23.3 months HR:0.932 30.6 vs. 26.5 months HR: 1.043 HR: 1.00 | 30.5 vs. 23.6 HR: 0.887 | Not available | Not available | Not available |

vs. 11 months, HR: 0.81). This advantage was higher in patients who had SD at the end of chemotherapy, compared with those who had a RP. The ATLAS study [77] evaluated the addition of bevacizumab to erlotinib after 1st line chemotherapy until progression, highlighting a statistically significant increase in PFS (HR: 0.72) and a small benefit in OS. However the trials for second early line therapy are often based on clinical criteria, such as patients with large tumors, symptomatic, PS 0–1, no severe toxicities to first-line treatment [78]. Moreover a meta-analysis [79] and a pooled analysis [80] showed that erlotinib produced significant clinical benefits (improvements in PFS and OS) with acceptable toxicity as a maintenance strategy in patients with unresectable NSCLC who had not progressed after four cycles of first-line chemotherapy, even if further studies are needed to identify patients that may obtain greater benefits from maintenance with erlotinib, and to compare its use as early second line to standard second line therapy treatment. Gefitinib was also effective on maintaining strategy in an unselected population of patients who had completed 4 cycles of platinum-based chemotherapy, regardless of the response obtained in the first-line treatment [81], with a statistically significant benefit in terms of PFS (4.8 months vs. 2.16, HR: 0.42, $p < 0.0001$) (Table 4). Finally, data suggest that both gefitinib and erlotinib produces a significant survival benefit and maintenance strategy with EGFR TKIs after first line chemotherapy is a good treatment strategy in unselected patients with advanced NSCLC, and an excellent option for patients with EGFR mutation [82].

4.2. Directly comparing studies

There are few studies performing a direct comparison between gefitinib and erlotinib. A randomized Phase II trial [83] compared the second-line treatment with gefitinib and erlotinib, in a population of patients selected on the basis of clinical favorable features (women, non-smokers, adenocarcinoma) or the presence of EGFR activating gene mutations. This trial didn't show statistically significant differences between these two drugs regardless EGFR mutational status. However, the subgroup analysis showed higher activity of both drugs in patients with EGFR-mutated (ORR: 76.5%; PFS: 11.9 months) than patients with EGFR-WT (ORR: 25%, PFS: 2.8 months, $p = 0.001$, $p = 0.08$). In patients with unknown EGFR status, the gefitinib arm achieved a 37% RR and a 4.3 months median PFS while patients in the erlotinib arm had RR of 55% and PFS of 3.1 months. The small number of patients greatly reduces the statistical power of this study and doesn't allow the identification of significant differences between the two drugs. Similar results emerge from another study [84] that compared the efficacy of both drugs as third-line treatment in a population of unselected patients either clinically or on the basis of biomolecular factors, concluding that there are no statistically significant differences, although a slight trend was observed in terms of survival in favor of erlotinib in patients treated for more than 6 months. The same

Table 4

Randomized phase III trials on TKI maintenance therapy in patients with advanced NSCLC after first line treatment.

| Clinical trials | SATURN [57] | ATLAS [58] | INFORM [60] |
|----------------------|--|--|--|
| Treatment | Erlotinib vs. placebo | Bevacizumab + erlotinib vs. bevacizumab + placebo | Gefitinib vs. placebo |
| First-line treatment | Platinum-based chemotherapy × 4 cycles | Platinum-based chemotherapy × 4 cycles + bevacizumab | Platinum-based chemotherapy × 4 cycles |
| Median PFS | 12.3 vs. 11.1 weeks HR: 0.71 | 4.8 vs. 3.7 months HR: 0.72 | 4.8 vs. 2.6 months HR: 0.42 |
| Median OS | 12 vs. 11 months HR: 0.81 | 15.9 vs 13.9 months HR: 0.90 | 18.7 vs 16.9 months HR: 0.84 |

Table 5

Clinical trials on direct comparison between gefitinib and erlotinib in patients with advanced NSCLC.

| Clinical trials | | Kim ST et al. [61] | Kim ST et al. [63] | Wu WS et al. [64] | Wu JY et al. [65] |
|-----------------|------------------------|---|--|--|--|
| Treatment | | Gefitinib vs. erlotinib (second-line treatment) | Gefitinib vs. erlotinib (pre-treated patients) | Gefitinib vs. erlotinib (all lines of treatment) | Gefitinib vs. erlotinib (all lines of treatment) |
| ORR | Overall population | 47.9% vs. 39.6% <i>p</i> : 0.269 | 38% vs. 32.2% <i>p</i> : 0.273 | 41.9% vs. 42% <i>p</i> : 1.0 | 46.4% vs. 35.5% <i>p</i> : 0.004 |
| | EGFR-mutation positive | | | 51% vs. 57.7% | 61.9% vs. 75.4% <i>p</i> : 0.069 |
| | EGFR-mutation negative | | | 13.3% vs. 25% | 12.8% vs. 13.9% <i>p</i> : 0.84 |
| Median PFS | Overall population | 4.9 vs. 3.1 months <i>p</i> : 0.336 | 4.7 vs. 2.7 months <i>p</i> : 0.06 | 7.6 vs. 7.9 months <i>p</i> : 0.47 | 5 vs. 2.9 months <i>p</i> : 0.102 |
| | EGFR-mutation positive | | | 10.5 vs. 10.3 months <i>p</i> : 0.32 | |
| | EGFR-mutation negative | | | 2.3 vs. 4.5 months <i>p</i> : 0.03 | |

results of equal efficacy/toxicity in second/third-line treatment are confirmed by another study [85], conducted on 342 patients not selected on the basis of clinical or molecular factors. Conversely, a retrospective study [86] that compared the efficacy of gefitinib and erlotinib in patients with lung adenocarcinoma and known EGFR mutational status demonstrated a statistically significant difference between the two treatment arms in favor of erlotinib in EGFR-WT patients (RR: 25% vs 4%, *p*: 0.0064; PFS: 4.5 vs. 2.3 months, *p*: 0.03), while no differences were observed in patients with EGFR gene activating mutations. However, no differences were found in terms of OS.

Finally, a previous retrospective study [87] compared gefitinib and erlotinib treatment in a population of 716 patients with advanced NSCLC in all lines of treatment, showing no statistically significant differences between these two drugs in the different lines, regardless of EGFR mutational status. Additional informations about the current use of these two different drugs in clinical practice, showed that erlotinib would be used much more frequently than gefitinib in the treatment of male patients, smokers, not adenocarcinoma histology (*p* < 0.001); both drugs are used more in 1st line rather than in 2nd or 3rd line, but gefitinib is much more used than erlotinib in this indication (63% vs. 38%, *p* < 0.001). This is certainly due to the fact that erlotinib has not been indicated in first-line treatment of NSCLC patients, although all studies compared with chemotherapy have made

a clear superiority of erlotinib in patients with activating mutations of the EGFR gene (Table 5).

This trend in the use of these two TKIs could be explained by the two major comparing studies between TKIs and placebo in 2nd-line treatment (ISEL and BR21), which demonstrated an exclusive benefit of erlotinib in unselected population, and no benefit of gefitinib. However, in contrast to this finding, there are evidences from 4 studies that compared the efficacy of gefitinib versus docetaxel in the second-line for unselected population, as well as the data of the studies that have directly compared erlotinib and gefitinib in 2nd–3rd-line, suggesting the absolute equivalence of the two treatments. In this regard it may be appropriate to review and re-modulate the directions to the rigid use of the two drugs in different lines of treatment with the aim of being able to guarantee to the patient the highest number of treatment options.

Finally, we are eager to know the results of the only Asian trial currently underway evaluating the direct comparison between gefitinib and erlotinib in the treatment of first-line treatment with NSCLC patients.

4.3. Possibility of sequential administration of the two drugs

Several studies (retrospective, prospective, case reports) evaluated erlotinib efficacy in patients who had a PD after

first-line treatment with gefitinib, showing controversial results. Two clinical trials [88,89], in patients selected according to specific clinical characteristics (women, non-smokers, adenocarcinoma) reported very low response and survival rates (RR: 25%, median PFS: 1.5 months). Conversely, another study [90], which assessed erlotinib in patients with the same clinical characteristics, reported significantly higher response rate (RR: 57%), if we consider those patients who had a disease control during treatment with gefitinib. Similar data were reported in two other studies (DCR 55% and 50%) [91,92]. Studies on patients selected for EGFR mutation status showed higher RR (50%) and DCR (75%) in EGFR-WT patients, who obtained a previous response to gefitinib [92], and no statistically significant benefit in patients who developed resistance to gefitinib [93]. A pooled analysis summarizes the data emerging from individual studies evaluating sequential treatment with erlotinib after failure of gefitinib or erlotinib [94]. It concludes that a statistically significant benefit could be achieved in patients selected on the basis of specific clinical features, who experienced a long-term disease control during treatment with gefitinib, intended as a median PFS of at least 6 months. However the authors suggest that the EGFR mutational status couldn't be considered a predictor of response for erlotinib after gefitinib failure. A careful analysis of response and survival data reported in these studies show a slight trend of effectiveness in favor of patients with EGFR-WT. From this observation we could argue that the biomolecular mechanisms of acquired resistance to gefitinib are common to both these TKIs. In particular, the T790M EGFR mutation and MET amplifications are the most frequent causes of acquired resistance to both these EGFR TKIs.

Besides the higher equivalent erlotinib dose (the dose administered coincides with MTD, while the dose of gefitinib is equal to 1/3 MTD) and the lower IC50 compared to gefitinib are possible explanations for the theory of different sensitivity of tumor cells to the two drugs which is observed in patients with EGFR WT. Another hypothesis to explain this phenomenon regards the initial presence of both sensitive and resistant clones to TKI. The resistant clones could increase during TKI treatment inducing acquired drug resistance. The amount of resistant clones could be reduced during subsequent chemotherapy, thus yielding new sensitivity to TKIs. This theory might also explain the results emerging from studies which evaluated the re-administration of gefitinib after failure of the same on the front lines, reporting DCR of 27% and a median PFS 13.8 months [95]. However, we could hypothesize that the clones resistant to gefitinib might not be resistant to erlotinib, or be incompletely resistant, because of the presence of unknown mutations and different profiles of resistance/sensitivity to the two drugs.

4.4. Toxicity

The analysis of data from individual studies about toxic effects of TKIs show a good tolerability profile of both drugs, with an incidence of adverse events significantly lower

with respect to chemotherapy (61–13% for chemotherapy vs. gefitinib $p < 0.001$; dose reduction of 35% vs. 16% for gefitinib; in the IPASS study, and 65% vs. 17% for erlotinib; dose reduction of 53% vs. 6% for erlotinib in the OPTIMAL). The treatment with these drugs is associated with a significantly lower incidence of myelosuppression, nausea, vomiting, fatigue, neurotoxicity. The most common toxic effects most frequently encountered in the course of treatment with TKIs are rash, diarrhea and asymptomatic hypertransaminasemia generally mild to moderate, while severe toxicities are uncommon. Although the toxicity profile is almost comparable in both drugs, a phase II study [83] comparing the efficacy/toxicity of these two drugs in the 2nd-line showed a higher incidence of moderate-to-severe rash in patients treated with erlotinib (43% vs. 10.4%), as well as a higher incidence of fatigue. However these toxicities didn't affect the dose-intensity or quality of life in the two treatment arms. A recent meta-analysis [96] has analyzed over 24 trials, showing a statistically significant association between rash and clinical efficacy of treatment with TKIs (OS: HR:0.30, $p < 0.00001$; PFS: HR:0.50, $p < 0.00001$), so that the authors conclude that the rash can be considered an independent predictor of effectiveness for TKI treatment, particularly for patients with EGFR unknown mutational status. However, a careful analysis of the studies reported in this meta-analysis and other studies in the literature including the recent study of Lilembaum et al. [72] highlights a difference regarding skin toxicity. In fact, treatment with erlotinib is associated with a higher incidence of moderate-to-severe skin-rash, which seems to be associated with a statistically significant outcomes (ORR, PFS, OS), not always demonstrable during treatment with gefitinib, which is rather more frequently responsible for mild–minimal skin toxicities. These differences, though slight, there certainly appear relevant and worthy of in-depth in subsequent work.

5. Conclusions

In the last years the introduction of the anti-EGFR TKIs gefitinib and erlotinib represented the most important innovation for the treatment of advanced NSCLC. Infact these drugs are able to target the main pathway involved in lung cancer development and progression, the EGFR-mediated signaling transduction pathway. Furthermore TKIs allow sparing these patients from chemotherapy and subsequent quality-of-life-impairing toxicities. However in the first-line treatment only patients bearing EGFR gene activating mutations could achieve more benefit than chemotherapy.

Since gefitinib and erlotinib have different structure and subsequently different affinity with their receptor, toxicity frequency, but similar efficacy results, we postulated that these drugs could be partially interchangeable in the decision making for EGFR-mutated advanced NSCLC patients who will undergo a cancer treatment. However these two molecules are not identical, and we carefully evaluated

available information about a comparison between these drugs, as well as on a possible complementary role in the overall management of these patients.

The biological, pharmacological and clinical differences of anti-EGFR TKIs should represent the starting point for further studies, at different levels. For instance the clinical results divergence should be related to molecular differences, which might be evaluated using new standardized procedures. This should prompt the development and validation of predictive tests to select the best drug for each patient. The evaluation of the possible sequential use of gefitinib and erlotinib is another key point in the clinical setting, since it would allow widening the treatment options.

Since the main goal of advanced cancer treatment is represented by prolongation of lifetime together with quality-of-life preservation, we envision that novel biological and pharmacological insights leading to the optimal use of currently available targeted drugs could achieve better results than chemotherapy in the future clinical management of NSCLC patients.

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Dr Juan Iovanna, INSERM, Unité 624, Stress Cellulaire, Parc Scientifique et Technologique de Luminy, Marseille Cedex 9, F-13288, France.

Dr Wainer Zoli, Istituto Scientifico Romagnolo per lo Studio e la Cura dei Tumori (I.R.S.T.), via P. Maroncelli 40, I-47014 Meldola (FC), Italy.

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