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LETTER

Small molecules against B-RAF (BRAF) Val600Glu (V600E) single mutation

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Dear editor

We have read with great interest the paper by Tang and Chen[1] published in the most recent issue of the *International Journal of Nanomedicine*, in which the authors describe the protocol by which scientists constructed the ideal BRAF (V600E)-modeled structure through homology modeling and introduced the method of structure-based docking or virtual screening from a large compound database. They concluded that BRAF (V600E) has a quite prominent structural or conformational variation when compared to the wild-type BRAF protein by matrix of root mean square fluctuation and principal component analysis. On the basis of structure-based virtual screening, ligand-based quantitative structure activity relationship models, and molecular dynamics simulation, we recommend aknadicine and 16beta-hydroxy-19s-vindolinine N-oxide as potent compounds for developing novel inhibitors in the future.

The v-raf murine sarcoma viral oncogene homolog B1 (BRAF) gene is mutated in 40%–60% of melanomas, the most common being the V600E mutation, which leads to activation of the mitogen activated protein kinase (MAPK) pathway.[2] BRAF is a member of the RAF family of serine/threonine protein kinases. This family consists of three kinases, ie, ARAF, CRAF (RAF-1), and BRAF, of which the latter has the highest basal kinase. BRAF functions to regulate the MAPK/ERK pathway, which is conserved in all eukaryotes. The RAS/RAF/MEK/ERK pathway acts as a signal transducer between the extracellular environment and the nucleus. Extracellular signals such as hormones, cytokines, and various growth factors interact with their receptors to activate the small G-proteins of the RAS family. BRAF-mutated tumors have a poor response to traditional chemotherapy and a poor prognosis in melanoma, thyroid, and colon cancers.[3–5] Targeted therapies are of great interest for these types of cancer, and elucidation of the structure and functions of BRAF kinase is the subject of much ongoing research. The approach of targeting oncogenic kinases has been successful in the treatment of cancers with activating mutations in the kinase gene that drives their progression. It is likely that our evolving understanding of BRAF genetics and signaling will allow further personalization of cancer therapy with the goal of improving clinical responses.

We are confident that the results reported Tang and Chen[1] have brought progress to the field, but targeting a malignant cell with a monotherapy protocol is expected to fail and thus lead to clinical relapse of the disease. Thus, combination therapy is likely to be the most effective management plan for the treatment of BRAF-mutated tumors. Many BRAF-specific inhibitors display a cytostatic response inducing senescence and are susceptible to acquired resistance. Therefore, combination with traditional chemotherapeutic agents seems to be more effective than either treatment alone.

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Author contributions

All authors have made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in either drafting the communication or revising it critically for important intellectual content; gave final approval of the version to be published; and agree to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

Disclosure

The authors report no conflicts of interest in this work.

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Authors' reply

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Dear editor

The RAS/RAF/MEK/ERK pathway is the most significant signal cascade when discussing the etiology of malignant melanoma. BRAF(V600E) is the most destructive single mutation which may lead to advanced or metastatic melanoma. Knowing the molecular characteristics and structural variation of BRAF(V600E) protein when compared to wild-type BRAF protein by molecular dynamics simulation helps us to understand how the mutant protein amplifies the phosphorylation and metamorphic character.[1]

There are many mechanisms of resistance with regard to existing BRAF inhibitors. RAS or MEK mutation is one of the acquired responses conferring drug resistance. Gln61 (Q61) mutation of N-ras or Cys121 (C121) mutation of MEK is an example of drug resistance. Our previous study entitled "Molecular insight and resolution for tumors harboring the H-ras(G12V) mutation" investigated the H-ras protein single mutation and reported that H-ras(G12V) mutation offered a stable condition for excess signal transduction. Our subsequent studies have focused on N-ras and MEK single mutation. Through structure-based analysis, ligand-based analysis, or molecular dynamics simulation, we can explore the differences between these wild-type and mutant proteins, and provide possible resolution for tumors harboring N-ras or MEK mutation.[2]

In addition to acquired resistance, a compensatory increase in activity of microphthalmia-associated transcription factor is involved in adaptive resistance. Further, BRAF mutations are not detected in approximately 50% of melanoma lesions. Cyclin-dependent kinase 2 is the alternative target for drug management of these melanoma patients. Our previous study entitled "Drug design of cyclin-dependent kinase 2 inhibitor for melanoma from traditional Chinese medicine" elaborated another possible therapy for advanced or metastatic melanoma.[3]

Disclosure

The authors report no conflicts of interest in this work.

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