DISCUSSION

In routine practice, to identify genotype-specific subsets of patients can lead to successful treatment with appropriate kinase inhibitors and determine survival outcomes differed among genotypes. In the present study, we demonstrated our experience on EGFR and ALK mutation analyses (6–9).

Although it has been shown that smears can be used effectively for DNA extraction for EGFR mutation assays, use of a cell block is recommended for cytology specimens and in our practice, we gained enough tumour DNA from cell blocks. Pyrosequencing is a sensitive method for the detection of mutations in DNA isolated from paraffin embedded tissues.

The previously reported EGFR mutation rates of NSCLC in the Turkish population were given 4% and 7%. The EGFR mutation rate we have found is 11.8%. This difference can be explained by the study cohort which contains only adenocarcinomas and it is known that adenocarcinomas have EGFR mutations more than other histologic subtypes of lung carcinomas. We also used only tumours that contained part of the formalin-fixed paraffin-embedded tumour tissue slides. In previous studies on the Turkish population, the slide examination and preparation was not clear. Another reason could be the detection technique we used, because in previous studies dideoxy sequencing was used for EGFR mutation analyses and it is known that pyrosequencing is superior to dideoxy sequencing in the detection of EGFR mutations (10–12).

Soda *et al* reported an inversion on chromosome arm 2p resulted in the creation of an EML4 - ALK fusion gene in lung cancer in 2007 (13). The EML4-ALK fusion gene was identified in 5 of 75 (7%) NSCLC patients examined. Subsequent studies have indicated that the prevalence of EML4 - ALK fusion gene is about 2 % to 7% of all NSCLCs with enrichment in adenocarcinomas in never or light smokers (3, 4). In this study, we found ALK gene rearrangement as 17.4%. This result is quite different from the existing data. It could be

explained by the number of patients that we were studied are low and we choose the adenocarcinoma patients without EGFR mutations.

Male predominance is evident in our study cohort (F/M=1/4). It could be the explanation of male predominance in EGFR and ALK mutated cases. In the current study, metastatic lung adenocarcinoma tissues demonstrated EGFR and ALK mutations more than the tumours obtained from primary site. We detected EGFR mutations in exons 18, 19 and 21 which are associated with TKI sensitivity. Although, we did not know the EGFR and ALK status of primary tumour tissues that we found EFGR and ALK mutations on metastatic counterparts, it seems reasonable to repeat molecular testing in metastatic lung adenocarcinomas (4, 9).

CONCLUSION

Metastatic adenocarcinomas demonstrated EGFR mutation more than primary tumours; therefore, repeating molecular testing in metastatic lung adenocarcinomas may uncover newly acquired molecular alterations.

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Author Contributions

IH Ozbudak conceived paper, oversaw data collection, conducted data analysis, wrote manuscript and approved final version. M Ozcan participated in study design, data analysis and interpretation, revised manuscript and approved final version. G Ozbilim participated in study design, data analysis, revision of manuscript and approved final version. The authors declare that they have not received any financial support and that there are no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

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