Good morning, teachers and colleagues. So this is a new trial, new upcoming trials in the germline testing and screening in lung cancer. This is the germline study which was presented in WCLC this year. That is, they evaluated the pathogenic or likely pathogenic variants in cancer predisposition genes among selected patients with adenocarcinoma. So just coming to the introduction, this was done in Latin America, Mexico. So there also the lung cancer is the leading cause of cancer-related mortality.

And that actually the mean age at diagnosis, it's engaged when compared to the Caucasians. And non-smokers, they have a higher incidence, around 50%. And they have a higher frequency of actionable genomic alterations. So there are various papers which are showing that 0.3 to 15%

had a pathogenic or pathogenic germline variance, which is influenced by either ethnicity, clinical stage, and the study criteria, which most includes the DNA repair pathways. And higher prevalence are also observed in patients with positive family history, young onset presentation, adenocarcinoma histology, and the actionable genomic alterations.

So this germline study, which was done in Mexico, it aimed to determine the prevalence of the PGVs, that is the pathologic germline variants in lung cancer, particularly the adenocarcinoma variant, using the pragmatic selection criteria for the germline genetic assessment. So coming to the methods, so it's a cross-sectional study, single-center study done in Mexican population from December 2022 to October 2023.

Selection criteria, lung cancer, adenocarcinoma with a family history that is either one first degree relative or more than or equal to two secondary relatives with lung cancer. Aged diagnosis, either less than or equal to 50 years or less than or equal to 60 with a pack year incidence less than 20 or presence of more than or equal to actionable germline

that is irrespective of the age. That is you can see here almost more than 95% covered EGFR ALK, ROS1 RED, KRAS, BRAF MET or HER2/EXON 2 insertions. So the sample is they have collected from the peripheral blood and using 144 cancer-related genes that is using the SOFIA HCS community panels they have analyzed the PGVs or the likely pathogenic variants.

364 patients were screened for lung cancer in that almost 201 patients were included in the study. So coming to the results, total number of populations 201, so 67% being female and mean age of diagnosis is 51 years. So 44% were less than or equal to 50 years and non-smokers were around 73%. So out of 201 patients, almost 91% patient had the actionable genomic alterations. That is most common being EGFR followed by ALK.

So coming to the main results, so out of 201 patients, 43 patients had the pathogenic germline variance, that is 21.4, one-fifth of the patients had. So in that PGVs, the most common being the HRR pathway which was present in 40% of the patients followed by base excision repair pathway and the rest. Tumor suppressor genes was present in around 8.3%. In that 21.4, almost clinically actionable mutations were present in around 77%.

So this slide implicates the total number of 43 patients who had the pathogenic germline variants and also the clinical characteristics also being showed in this slide. So the most common mutation which are PgVs which are seen is the ATM which was present in around 9.3% followed by the CHEK2 BLM and BRCA2 was also seen in 6.9% and TP53 you can see also it's around the second most 6.9%.

So by doing a univariate analysis, there was a trend towards some positive association in some of the factors, that is male sex, AGS in that KRAS, personality of cancer. And this was not shown in this slide. Actually, the age less than 30 years has a very strong association of having a PGV. So coming to the conclusion, so

This study showed that approximately one-fifth of the patients were found to have pathogenic germline variants by using the pragmatic selection criteria for genetic testing. And in that two-thirds of the individuals, they had variants in the DNA repair genes. That is the most common being ATM, forward weight check 2, BRCA 2, etc.

So these criteria, it may be appropriate for identifying eligible patients for germline genomic testing in low-middle-income countries and resource-limited settings. The major limitations being a single-center study which was done in Mexico with a small sample size. Another thing that even though they have detected clinically actionable mutations of around 77%, we have seen in certain cancers, other cancers like breast,

ovary, prostate or pancreas, even though the clinically actionable mutations are there, some of the drugs only work, others don't work. So in lung cancer we don't know how it is going to be. And we have some few case reports of BRCA mutation in lung cancer where the PARP inhibitors have been given, some showing positive results and some showing negative results. So we still don't know whether it is going to be clinically actionable in lung cancer. Second thing is the cost.

In low-middle income countries and resource-limited setting, it's going to be very tough. And the last thing is, even though this is, as I already mentioned, it's a single standard study where they have shown 21%. There is already one paper which was published in 2022, that is in the Asian population, where they have shown 4% of pathogenic germline variants was present. So it is...

We actually don't know the actual incidence of PGVs present. So we need a larger data including diverse population so that the actual incidence can be met and so that a selection criteria can be fit for the genetic testing and screening like those which has been present in the breast, ovarian and colorectal cancer. So still A to go. Thank you. Thank you. Thank you, Naveen.