Managing Hodgkin Lymphoma

How should genome sequencing data be applied in the clinical practice of HL?

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Hello! My name is Dr. Anas Younes, and I am the Chief of Lymphoma Service at the Memorial Sloan Kettering Cancer Center and Professor at Weill Cornell Medical College in New York. Today, I will be covering highlights from my educational session at ICML, also known as the Lugano Lymphoma Meeting, focusing on clinical applications of genome studies. What I presented at the educational session is how we are now trying to apply genome sequencing data into clinical practice. One application is to fine-tune the diagnosis of lymphomas. Frequently, the pathologists can look under microscope, do immunohistochemistry and FISH studies, and still there is no clear-cut classification. That is where sometimes the genome studies can contribute to refine these rather unusual histological presentations. I have provided some examples about how we fine-tune the case with primary mediastinal large-cell lymphoma based on the genetic sequencing data. The other application is mainly to select patients for treatment strategies, and at the Lugano meeting, there was a beautiful presentation by Frank Morschhauser. He presented the data with the EZH2-targeted agents, where he showed that if you target patients with follicular lymphoma with tumors that have EZH2 mutations, the response rate is 93%, whereas if you treat patients with follicular lymphomas without the mutation, the response rate is significantly lower, as I remember is 30%, still not bad, but it is significantly lower. That is where we want to move with these genetic analyses to select patients for a certain therapy that can produce a higher response rate. There are talks and discussions about basket protocols for lymphomas where you can stratify patients into different buckets based on the genomics analysis. The third potential application is to look at minimal residual disease or circulating tumor DNA after treatment, mainly after induction therapy, mainly to determine whether the presence or absence of circulating tumor DNA would predict a clinical response or cure. If the presence of circulating tumor DNA after induction therapy predicts, let's say relapse, should we act on it? This is an evolving field. I think this concept is currently being incorporated in different clinical trials, but this will take a few years before we sort out the significance of these observations. Thank you for viewing this activity.