Genetic variants predict recurrence of bladder cancer, patient survival

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Scientists at The University of Texas M. D. Anderson Cancer Center have discovered genetic variations in the inflammation pathway that reduce the likelihood of recurrence and increase survival of patients with non-muscle invasive bladder cancer (NMIBC) who are treated with mainstream therapy.

Patients with risk-reducing genotypes were 84 percent less likely to have their disease recur after treatment with Bacillus Calmette-Guerin (BCG), the prevailing immunotherapy to prevent high-risk NMIBC patients from developing recurrence. The recurrence-free median survival time among these patients was 96.7 months compared with 47 months among those with the more typical genotype, the team reported at the 100th Annual Meeting of the American Association for Cancer Research.

"The future purpose of this kind of study is personalized cancer therapy," said senior author Xifeng Wu, M.D., Ph.D., a professor in the Department of Epidemiology at M. D. Anderson. "This genetic information is an essential step toward constructing a blueprint that will determine treatment response and follow-up strategy."

Currently, the primary treatment for NMIBC is transurethral resection - surgical removal of the tumor tissues from bladder - combined with chemotherapy or immunotherapy such as BCG injection. Overall, the recurrence rate is around 50 percent over four years.

In this study of 596 patients at M. D. Anderson, 46 percent of those who

had a common genotype of the inducible nitric oxide synthase (iNOS) gene experienced a recurrence after receiving maintenance BCG therapy. Only 22 percent of patients with the variant-containing genotypes had a recurrence with the same treatment. The results suggest that BCG may be more effective when administered to individuals with genotypes containing the variant allele of the iNOS gene.

"We aimed to determine why some patients respond to BCG and others don't," said lead author Hushan Yang, Ph.D., a postdoctoral fellow in the Department of Epidemiology at M. D. Anderson.

Yang and his colleagues evaluated 59 single nucleotide polymorphisms (SNPs) in 35 major inflammation genes. Using a combined analysis, they stratified patients into multiple risk groups. Those patients in the high-risk group were found to have a median survival time of only 13.5 months, while those in the low-risk group were recurrence free for more than 96.7 months.

"Once validated, the next step will be to create a risk prediction model," said Wu. "Combining the information we have with other aspects such as clinical, epidemiological and behavioral variables, as well as tumor characteristics, patient characteristics and other genetic information will allow treating physicians to know whether their patient is likely to respond to therapy or experience a recurrence."

Source: University of Texas M. D. Anderson Cancer Center (news : web)