CHARACTERIZING THE POTENTIAL INTERPLAY BETWEEN NUCLEOTIDE EXCISION REPAIR AND R-LOOPS

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R-loops have been a focus of interest in genomics due to their non-canonical structures and unclear roles on genomes of many organisms. While R-loops contribute to gene expression and efficient transcriptional termination, they cause genome instability under certain conditions. They are formed when an RNA anneals with its complementary DNA strand. A DNA:RNA hybrid is formed and the other strand of DNA is left single-stranded (ssDNA). To date, there was no clear knowledge on R-loops' tendency for UV damage formation or how these DNA:RNA hybrid and ssDNA structures affect nucleotide excision repair (NER), the primary mechanism to cope with UV-induced DNA damage. Therefore, we aimed to shed light on the relationship between R-loops and UV damage occurrence and repair using R-loops' positions on human and Arabidopsis genomes, and Damage-seq and XR-seq data that provided positions of UV damages and repair events, respectively. By comparing the R-loop-forming locations with damage and repair occurrences, we observed that the repair efficiency on R-loops was better than their surrounding regions. However, when ATAC-seq read count normalization eliminated the impact of R-loops being on open chromatin, lower repair efficiency on R-loop centers and 5' regions, but higher repair efficiency on 3' regions were observed. Because this repair profile might not be valid for each R-loop, we created heatmaps of relative repair where we could group R-loops with similar repair profiles. As a result, four different relative repair profiles were observed. We also checked the damage occurrence on R-loops and saw that in general, R-loops receive less damage than their surroundings, while there were also four different damage profiles within subgroups of R-loops. Further analysis will be conducted based on these results to explain what is behind differential repair and damage profiles on R-loops and better understand the roles of R-loops on our genomes.