Identification of alternative splice variants in the transcriptome of Squamous Cell Carcinoma of the Cervix and Adenocarcinoma of the Cervix

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Abstract

The uterine cervix is the initial portion of the uterus that communicates with the vaginal canal. In this region, cervical cancer can develop, which is a type of tumour that most affect women nowadays. There are many subtypes of cervical cancer: about 70% of the new cases are identified as cervical squamous cell carcinoma (SCC), 20% of the cases are adenocarcinoma (ADC), and the rest is composed by mixed tumours. Even though there are definite subtypes, the treatment administered for both SCC and ADC is the same, which compromises response and remission of ADC, the worst prognostic subtype. Since they are molecularly heterogeneous, it is still an ongoing challenge to distinguish ADC and SCC through their expression profile. The clarification of their expression profiles could complement their immunohistochemical diagnostic, help differentiate the subtypes, and possibly find new pharmacological targets differentially expressed in ADC. Since other studies have primarily focused on canonical transcripts, we propose that annotated and/or new alternative splice variants could help clarify and build the expression profile of these cervical cancer subtypes. Accordingly, our objective is to find differentially expressed alternative splice transcripts in ADC and SCC transcriptome. We obtained the RNA-Seq profile of 8 SCC and 3 ADC. After trimming using Trimgalore, mapping onto the human genome using Hisat2, and read count using htseq, we performed differential expression using DESeq2 using the default protocol. We used CLASS2 to identify and annotate the alternative splice variants, including previously uncharacterized, of two different long non-coding RNA. One of which is expressed only in SCC, but with variation within samples, which could confirm the heterogeneity of cervical cancer subtypes as proposed by other research groups. The other lncRNA is shown only in ADC samples, which could be a prospect of a biomarker. Further statistical analysis are needed to confirm these primary observations.

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