COMPARATIVE STUDY OF RESPONSE OF CHONDROSARCOMAS TO X-RAYS, AND CORRELATION WITH THEIR GENETIC CHARACTERIZATIONS

Girard N\textsuperscript{1,2}, Aury-Landas J\textsuperscript{1,2}, Morgane Barreau\textsuperscript{1,2}, Lhuissier E\textsuperscript{1,2}, Baugé C\textsuperscript{1,2} and Boumediene K\textsuperscript{1,2}

\textsuperscript{1}Normandie Université, France; \textsuperscript{2}UNICAEN, EA4652 MILPAT, Caen, France

INTRODUCTION Chondrosarcomas (CHS) are malignant tumors of bone that produce hyaline cartilage matrix. Primary CHS is the second most frequently primary malignant tumor of bone after osteosarcoma, and represents about 25% of bone sarcomas. CHS is considered as highly resistant to both chemotherapy and radiations, making surgical resection the only curative treatment. However, mechanisms of resistance are not well understood.

OBJECTIVES This project aims to investigate resistance mechanism to radiotherapy. We compared the response of five different chondrosarcomas cell lines to X-rays radiation. To understand why chondrosarcomas have differential responses to X-rays, we performed full exome analysis.

DISCUSSION/RESULTS Cell lines derived from human chondrosarcomas can be classified according to their sensibility to X-rays within 3 groups: X-rays induced both apoptosis and senescence in the most sensitive group, whereas they induce only apoptosis or senescence for the intermediate group. No death could be detected for the most resistant group.

In addition, we generated an average of 4.9 Gb of sequence per cell line. On average, 56 000 variants were identified per exome, including 1700 new variants. After filtration, 166 to 339 non-synonymous variants exon per line have a deleterious functional impact on the predicted protein. Of interest, we found eight mutated genes in the cell lines in which apoptosis is observed after irradiation with X-rays. Their putative roles in resistance/sensibility of chondrosarcoma cell lines is under investigation.

CONCLUSION We show that chondrosarcomas cell lines respond differently to X-ray. In addition, our study is the first one which extensively characterize commonly used human CHS cell lines by exome sequencing. Our preliminary results provide essential genetic information on radiation resistance mechanisms X through the identification of genes potentially involved in the response to radiation.