Morphological and genetic characterization of benign primary bone tumors and their correlation with clinicopathological and radiological findings

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Background/Aim: Osteoid osteomas (OO) and osteoblastomas (OB) are common benign primary bone tumors separated by size (OO <2cm, OB >2cm). Both showing similar histological features and can mimic osteosarcoma. In contrast to OO, OB have a locally aggressive growth pattern and no pain relief after NSAID intake. Rearrangements involving FOS and FOSB were reported in both tumors. The aim of this study is to determine the diagnostic utility of epi-/genetic alterations in these tumors and to find genetic changes that can explain the different behavior of OB and OO. Methods: Retrospective analysis of OO and OB from 2000 until September 2022 was performed. Fusion analysis was done using next-generation sequencing (NGS) using Archer FusionPlex Sarcoma Panel (ArcherDX Analysis software). Methylation was performed using Illumina Infinium MethylationEPIC BeadChip technology. Our data will be compared with previously published data, including TCGA. Results: The cohort included 34 OO and 20 OB. OO occurred in the upper and lower extremity (12/34 and 16/34) and the spine (6/34). OB occurred in the spine and lower extremity equally often (each 9/20), one case in the upper extremity and the ribs. Curettage was performed in 28/34 OO and 14/20 OB, 8 (2/34 OO, 6/20 OB) underwent resection. After methylation analysis of 14 samples (8 OO, 6 OB) there is a tendency that the tumors cluster in different groups. In 10 samples fusion analysis was performed so far (9 OO, 1 OB), a FOS- or FOSB-rearrangement were detected with low confidence. In 7 cases, DNA quality was insufficient for further analysis. Discussion: Though OO and OB have the same macroscopic and histologic appearance, their behaviour is different. First data show a tendency, that OO and OB form two clusters with methylation analysis. FOS- and FOSB-rearrangement are difficult to discover by NGS, and further adjustment to the protocol is needed. As the sample size is small, further analysis will be performed to confirm our results