



3 - NEW ADVANCES IN THE DIAGNOSIS OF GONADOTROPH TUMOURS

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Resumen

Introduction: Gonadotroph tumours (GT) are the most common subtype of silent PitNETs. The diagnosis of this subtype of tumours is established after surgery. There are no reliable markers of aggressiveness to predict their clinical course and, moreover, immunohistochemistry (IHC) usually classifies GT as null cell tumours.

Objectives: To correlate molecular, immunohistochemical and biochemical gonadotropin expression, to quantify the gene expression of transcription factors of gonadotroph lineage and to correlate molecular data with demographic, clinical and radiological variables.

Methods: 34 molecularly identified GT were selected from PitNET collection of the Biobank of the Alicante Health and Biomedical Research Institute. Demographic, clinical, biochemical (pre-surgical concentrations of FSH and LH), IHC (protein expression of FSH and LH) and molecular variables (expression of FSH, LH, ESR1, SF1 and GATA2) were studied.

Results: 13 patients (38.2%) were women and 21 (61.8%) men. The average age was 58.9 ± 15.4 years. The most prevalent neurophthalmological manifestation was the oculomotor manifestation (58.8%) followed by headache (38.2%). 24 tumours (70.6%) were invasive. GT showed higher expression of GATA2 gene (10.590 ± 9.309) compared with SF1 (0.619 ± 0.284) and ESR1 (0.225 ± 0.271). We observed a statistically significant correlation between gene and IHC expression of FSH ($r = 0.380$, $p = 0.024$). Protein expression of FSH correlated positively with pre-surgical concentrations of FSH ($r = 0.45$, $p < 0.01$). Tumour size correlated negatively with FSH gene expression ($r = -0.44$, $p < 0.01$).

Conclusions: The positive correlation between pre-surgical levels of FSH and the IHC expression of FSH would allow anticipate the diagnosis of GT before surgery. The quantification of expression gonadotroph-lineage transcription factor genes could help diagnose these tumours.