COMPARATIVE GENOMIC HYBRIDIZATION STUDIES ON MESOTHELIOMA SHOW A PARALLEL FATE OF 1p21-1p22 AND 9p21 BANDS, AND A CHROMOSOMALLY STABLE SUB-GROUP

<u>Melaiu Ombretta¹</u>, Bracci Elisa¹, Cristaudo Alfonso², Bonotti Alessandra², Foddis Rudy², Mutti Luciano³, Gemignani Federica¹, Landi Stefano¹

¹Department of Biology, University of Pisa, Pisa, 56126, Italy; ²Department of Endocrinology and Metabolism, Orthopedics and Traumatology, Occupational Medicine, University of Pisa, Pisa, 56126, Italy; ³Mutti Luciano, Laboratory of Clinical Oncology, Vercelli National Health Trust, Vercelli, 13100, Italy. (e-mail: slandi@biologia.unipi.it)

Malignant Pleural Mesothelioma (MPM) is a cancer whit a poor prognosis. Unfortunately, robust conclusions on the landscape of the chromosomal rearrangements could not be made, given the limited sample sets studied. In order to improve the knowledge on the field, we collected (pooled) all the results deriving from studies on comparative genomic hybridization (CGH). This allowed a better description and novel insights on the alterations occurring in 179 MPM tissues (74 epithelioid, 48 sarcomatoid, 57 biphasic) and 8 cell lines (4, 1, and 3, respectively). Some chromosomal bands were involved in aberrations with a frequency exceeding 20% for -1p21, -9p, -14q, and -22q for the epithelioid, -4, +5p, +8q21 \rightarrow ter, -9p, -13, and -14q for the sarcomatoid, and -9p, -14q, and -22q for the biphasic type. We found a statistical significant association between losses at 9p21 and 1p21-1p22 (21% of the samples showed a contemporary loss of the two chromosomal bands, $P=7.74 \times 10^{-8}$). The association held also within each histological group. These findings suggest an underlying mechanism related to MPM tumorigenesis. Finally, 15% of epithelioid, 13% of sarcomatoid, and 13% of biphasic MPM tissues did not show genomic alterations. Interestingly, previous studies suggested a less aggressive behavior of MPM in relation to a low degree of chromosomal alterations. However, according to our review of the literature, only few studies considered this aspect. More studies are warranted to understand whether chromosomal rearrangements could be included as diagnostic and prognostic biomarker in the clinical practice.