Pre-clinical studies on the therapeutic potential of all-trans-retinoic acid in the personalized treatment of gastric cancer

How to cite:

For guidance on citations see FAQs.

© 2022 Luca Guarrera

https://creativecommons.org/licenses/by/4.0/

Version: Poster

oro.open.ac.uk
All-trans retinoic acid (ATRA), the active metabolite of vitamin A, is the first example of targeted therapeutics and it is successfully used in the treatment of acute promyelocytic leukaemia (APL). In combination with chemotherapy or arsenic trioxide, ATRA induces complete remission in >90% of APL patients and remission is maintained for at least 5-7 years in the majority of cases. These exceptional clinical results have raised interest in the potential of ATRA as an anti-tumour agent also for solid tumours, with particular reference to diseases which are devoid of viable therapeutic options, like gastric cancer (GC).

Gastric cancer (GC) is a heterogeneous type of tumour. Hence, personalized use of ATRA in the clinics calls for the identification of the subtypes responsive to ATRA-based therapeutic protocols, and the development of a diagnostic tool capable of predicting ATRA-sensitivity.

Gastric Cancer is a relatively heterogeneous type of cancer and can be divided into four groups (CIN, EBV, GS and MSI) according to the gene-expression/gene-mutational profiles. We developed a gene-expression model (ATRA-21) which is associated to and confident. Although GCs have a predicted low sensitivity to ATRA, interestingly, the GS and EBV groups are high responders according to the high ATRA-21 similarity score. Based on these results, a finer subdivision from transcriptional point of view was obtained. In order to validate these results, it may be useful to discriminate transcriptional differences between the 2 groups. In literature, there are several works where subdivisions have been made on the basis of the transcriptomic profile of gastric carcinomas.

An optimal idea would be to investigate the most appropriate method, and to identify a genomic signature explaining the molecular differences. Moreover, the identification of a predictive model of ATRA-sensitivity and the application of the latter in tissue cultures of primary GC tumors patients is necessary.

**References**