Background: Breast cancer in very young women (35 years or less) (BCVY) represents a small percentage (<5%) but its impact is very large on their personal, professional and emotional lives. BCVY is a more aggressive disease, and has poorer prognosis than that of older women and shows clinical differential characteristics. In this study, we wanted to validate our previous analysis (Peña-Chilet et al., BMC Cancer, 14:529, 2014) with data freely available from a large study (Dvinge et al., Nature, 497 (7449):378-82, 2012).

Methods: We have downloaded microRNA (miRs) data of 1302 Breast Tumors from Cambridge Breast Unit under European Genome Archive (www.ebi.ac.uk/ega) with EBI access EGAD00010000438. The biomarker used is microRNAs, a small RNA molecule with regulatory functions, which have proved very efficient in the classification of tissues and cancers. The work involved the re-analysis of the microRNA data from Agilent Technologies Inc. using R/Bioconductor tool for its versatility. We have use 35 years or younger and older than 65 years to separate two groups of breast cancer patients resulting in 33 BCVY and 712 of older counterparts. We have analyzed the putative gene targets and pathways implicated using GO Ontology and Reactome.

Results: We present the clinical and molecular characteristics of the two groups. Our molecular analysis from 853 miRs showed that 56 of them were deregulated in BCVY (31 upregulated and 25 downregulated). Nine of the upregulated (29%) belong to the polycluster miR-17/92. Some of their described gene targets are PTEN, E2F1-3 family, TGF-b, Smad2-4, BCL2L1 among others. Another 7 (22%) to the miR-515 family. Within the downregulated group we would like to highlight the mir-29 y mir-30 families (representing 28 % of the group): miR-29c*, miR-29c, miR29b, y miR-30a*, miR-30c, miR-30b y miR30e. Described gene targets are CDK6 and IGF1R. Several cellular and metabolic processes seem to be involved in the deregulation of BCVY affecting cell cycle, apoptosis and metastasis.

Conclusions: We have been able to find a singular miR profile in breast tumors of young patients. Although the individual miRs do not fully coincide with our original results, the signaling pathways altered are convergent.

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