

# Risk prediction of metastasis through study of circulating tumor cells

Apostolou P.<sup>1</sup>, Papasotiriou I.<sup>1</sup>

<sup>1</sup> Research Genetic Cancer Centre S.A. (R.G.C.C. S.A.). Industrial Area of Florina GR53100, Florina, Greece

**Introduction:** The study of circulating tumor cells (CTCs) has been rapidly increased the last decade, as this entity of cells is implicated in cancer prognosis and progression. CTCs constitute a non-homogeneous population of cells, with metastatic ability. The present study tested the gene expression profile of genes involved in metastasis in particular organs, in CTCs from cancer patients representing different cancer types and stages.

**Materials & Methods:** Blood samples were randomly collected from 35 patients, suffering from different types of cancer (Figure 1). CTCs were isolated by using enrichment protocols and cellular and molecular based assays were used to enumerate them and study their expression profile (Table 1). All the reactions were performed in triplicates. A normal sample as well as a commercial reference cancer RNA were used as control.

**Results:** The CTCs number is increased according to the stage of the disease, in the majority of the samples. Furthermore, in samples with higher CTCs number, the expression of markers is increased. Breast samples express markers for metastasis in general as well as in liver, bone and lung. Prostate samples overexpress genes correlated with pleura, skin, bone and lung metastasis. In ovarian cancer samples, metastasis was predicted to pleura, skin, brain and lung. Metastasis in general and brain was predicted for squamous cancer samples. The rest samples, did not reveal a distinct and/or repeatable pattern.

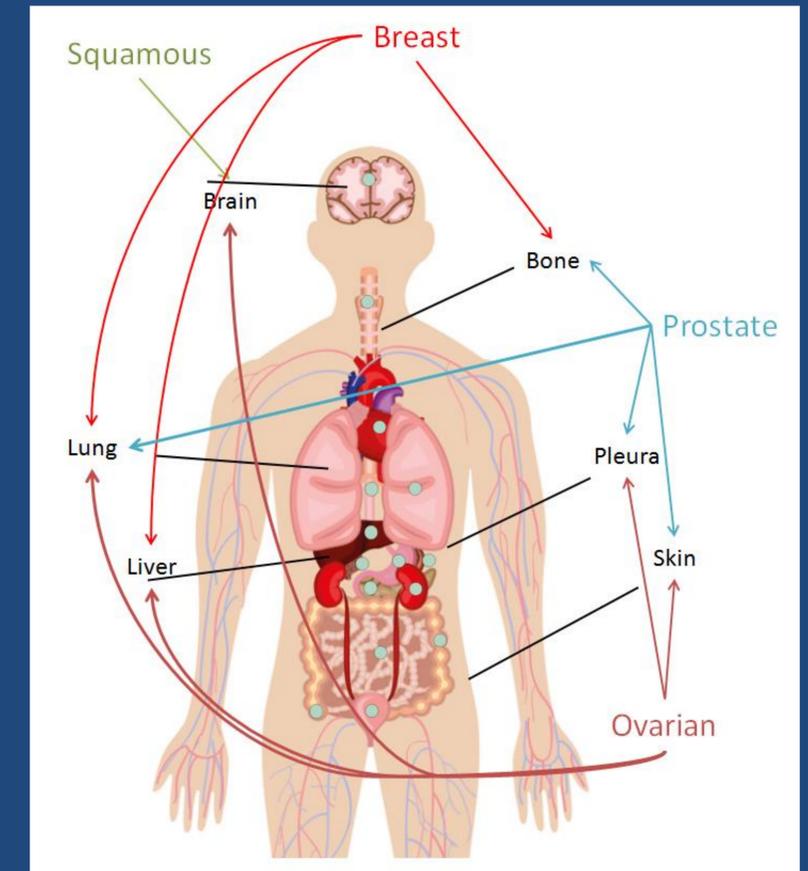


Figure 2: Metastasis prediction according to cancer type

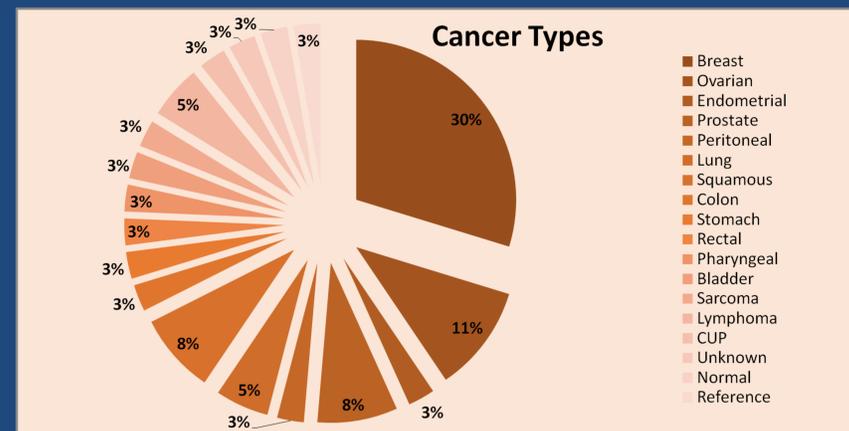


Figure 1: Distribution of samples according to their cancer type

Metastasis location	Marker	Metastasis location	Marker
General	TGF-β R2	Bone	BMPR1A
	ITGB-4 R		BMPR1B
	ITGB-5 R		BMPR2
	ITGB-6 R		CXCR4
Lung	IGF-R2	Skin	RANK
	ERK1		BST-2
Brain	ERK2	Liver	CCR7
	STAT-3		CXCR4
	CX3CR1		TRAIL-R2
Pleura	DSC-2		FAS R
	CCR6		HGFR
	MSLN		

Table 1: Genes correlated with metastasis in particular organs

**Selected References:**

- Zhou, L., Dicker, D.T., Matthew, E., El-Deiry, W.S., and Alpaugh, R.K. (2017). Circulating tumor cells: silent predictors of metastasis. F1000Res 6.
- van Dalum, G., Holland, L., and Terstappen, L.W. (2012). Metastasis and Circulating Tumor Cells. EJIFCC 23, 87-97.

**Disclosure of Potential Conflicts of Interest**

None of the authors of the above study has declared any conflict of interest  
e-mail: office@rgcc-gelab.com

**Conclusion:** The study of CTCs is of primary importance for the scientific community. Among same cancer type samples, different metastasis profiles were revealed, demonstrating that analysis of CTCs and particularly, their enumeration in comparison with their expression profile might be useful to focus the following up and screening to specific organs.

