

ted to Biotechnological Innovation

# P13.108.D: Low-level constitutional mosaicism in breast cancer patients

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### **Background / Objectives**

#### Methods

- **Mosaicism** refers to the presence of two or more genetically distinct cell populations within an individual's body. In some cases, individuals may carry a **mosaic germline variant** in a breast cancer-associated gene, such as *BRCA1* or *BRCA2*.
- **Mosaicism** is just one aspect that can contribute to the overall risk of developing **breast cancer.**
- The development of **next-generation sequencing (NGS)** technologies has revealed a significant contribution of **mosaic variants** to cancer predisposition genes.
- In this study we describe the occurrence of very low-level constitutional mosaicism in breast cancer predisposition genes.

A cohort of **patients** diagnosed with **breast cancer** and referred to our laboratory for genetic testing using a **NGS panel of 52 genes** (*APC, ATM, ATR, AXIN2, BAP1, BARD1, BMPR1A, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A, CHEK2, EPCAM, FANCA, FANCL, FANCM, GALNT12, GEN1, HOXB13, MEN1, MLH1, MRE11, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NTHL1, PALB2, PMS2, POLD1, POLE, PPP2R2A, PTEN, RAD50, RAD51B, RAD51C, RAD51D, RET, RNF43, RPS20, SMAD4, SMARCA4, STK11, TP53, VHL*) was evaluated for the occurrence of **very low-level constitutional mosaicism** in breast cancer predisposition genes. In all cases suspected of mosaicism, DNA was isolated from the **buccal swab** to confirm the state of mosaicism.

#### Results

- **NGS** analysis of **7 patients** diagnosed with breast cancer in peripheral blood and buccal swab DNA revealed low-level constitutional mosaicism variants in **four genes**.
- In the NF1 gene the following variants were detected

		Probe target info	□ AllSamples			ReferenceSamples		
			BR2 NORM BR2 BLOOD		BR2 SALIVA	R1 R2		R3
		n/a	100%	100%	100%	100%	100%	100%
		n/a	100%	100%	100%	100%	100%	100%
⊡ CAS (n=5)	DSI D - Bolati	n/a			Warning			
	FSLP - Rolati	n/a						
	RSO - Refere	n/a				OK OK		
	PPO - Poforo	n/a						
		12,031 785913	0.97	0.81	0.81			
L 13q (n=40)	BDCA2-Op	13-031 787593	1	0.01	0.89	0.99	1.03	0.99
	BDCA21	13-031 787801	1.01	0.02	0.05	0.00	1.05	0.97
	BDCA2-1	13-031 788599	0.99	0.02	0.87	0.99	1.00	0.99
	BDCA2-2	13-031.700000	0.98	0.01	0.87	0.00	1.02	0.00
	BRCA2-3 (WT.	12.021 701251	0.00	0.75	0.00	1.01	0.98	1.01
	BRCAZ-S	12-021 797209	1.01	0.73	0.85	1.01	1.01	1.01
	DRCA2-4	12-021 700240	0.97	0.76	0.76	0.99	1.01	0.99
	BRCA2-5	12 021 700240	0.07	0.70	0.70	0.55	1.03	1
	BRCAZ-0	12 021 700077	0.50	0.75	0.02	0.00	1 01	0.00
	DRUAZ-7	13-031.730077	0.96	0.76	0.75	1.01	0.00	1.01
	DRCA2-8	12 021 002112	0.00	0.70	0.76	0.00	1.00	0.00
	DRCA2-9	12 021 00/726	1.01	0.76	0.00	0.00	1.02	0.55
	BRCAZ-10	13-031.004730	1.01	0.74	0.70	0.55	1.01	0.55
	BRCAZ-10	13-031.003233	1.01	0.77	0.70	1	1 01	
	BRCA2-10	13-031.600400	0.99	0.74	0.82	1	1.01	
	BRCA2-11	13-031.808469	0.97	0.8	0.8	0.00	1.01	0.00
	BRCA2-11	13-031.8034/3	0.98	0.70	0.79	0.99	1.03	0.99
	BRCA2-11	13-031.810175	0.96	0.79	0.79	0.99	1.01	0.99
	BRCA2-11	13-031.811428	0.96	0.77	0.77	1.01	0.00	1.01
	BRCA2-11	13-031.812494	0.96	0.74	0.74	1.01	0.98	1.01
	BRCA2-11	13-031.813228	0.95	0.7	0.79	0.99	1.01	0.99
	BRCA2-12	13-031.816/01	0.94	0.78	0.92	-	0.99	
	BRCA2-13	13-031.8189/3	0.05	0.7	0.83	0.00	1.02	0.00
	BRCA2-14	13-031.82/123	0.95	0.78	0.78	0.99	1.02	0.99
	BRCA2-15	13-031.828630	0.99	0.75	0.77	-	1.01	
	BRCA2-16	13-031.829982		0.74	0.77	1.01	0.99	1.01
	BRCA2-17	13-031.834/44	1 00	0.77	0.79	1.01	0.99	1.01
	BRCA2-18	13-031.835551	1.02	0.8	0.78		0.99	
	BRCA2-19	13-031.842557	0.99	0.83	0.77		0.99	
	BRCA2-20	13-031.843080	0.98	0.8	0.81	0.00	1	0.00
	BRCA2-21	13-031.848828	1.01	0.75	0.88	0.99	1.01	0.99
	BRCA2-22	13-031.851549	0.95	0.78	0.78		0.99	
	BRCA2-23	13-031.851892	0.95	0.79	0.8	1.01	0.99	1.01
	BRCA2-24	13-031.852214	0.95	0.75	0.72	1.01	0.98	1.01
	BRCA2-25	13-031.86/008	0.98	0.78	0.81	1.01	0.98	1.01
	BRCA2-26	13-031.869059	0.95	0.75	0.77	1.02	0.97	1.02
	BRCA2-27	13-031.870386	0.96	0.75	0.8	1.01	0.98	1.01
	BRCA2-27	13-031.8/0/6/	1	0.77	0.78	1		
	BRCA2-27	13-031.871519	0.99	0.77	0.78	0.99	1.02	0.99
	N4BP2L1-3	13-031.8/9393	0.96	0.78	0.79	1.01	0.97	1.01
⊡ 22q (n=3)	CHEK2-1	22-02/.46///1	1.01	1.02	0.96	0.99	1.01	0.99
	CHEK2-9	22-02/.42585/	0.98	1.09	1.07	1.01	0.99	1.01
	CHEK2-11 (M	22-02/.421828	0	0	0	0	0	0
Ξ	Reference	01-214.084389	1.04	0.98	0.94	1	1	1
References	Reference	02-166.608624	1.01	1.11	1.13	1.01	0.97	1.01
	Reference	05-132.03/610	0.95	0.98	1	1	0.99	1
	Reference	06-152.423833	1.02	1.02	0.99	0.99	1.03	0.99
	Reference	10-032.800088	0.93	0.95	0.98	1.02	0.9/	1.02
	Reference	15-046.521228	1.01	0.97	0.94	0.99	1.02	0.99

c.2294\_2295del, p.(Arg765Hisfs\*2) (Figure 1) and c.3197+1G>A at 31% and 32%, respectively.

- A gross deletion of the genomic region the full coding sequence of the *BRCA2* gene (Figure 2).
- Also, the variant c.1117G>T, p.(Glu373\*) was identified in *PTEN* at 25%.
- Finally, in *TP53* mosaicism was identified in variants: c.814delinsCTT, p.(Val272Leufs\*74) (32%), c.916C>T, p.(Arg306\*) (32%) and c.722C>G, p.(Ser241Cys) (31%).



**Figure 1**. Example of a patient with a pathogenic variant in *NF1* gene in 31%. This is a deletion of two nucleotides from exon 19 of the *NF1* mRNA (c.2294\_2295del), causing a frameshift after codon 765. It creates a novel stop codon 2 amino acid residues later [p.(Arg765Hisfs\*2)] and is expected to result in a truncated, non-functional protein. The mutation database ClinVar contains an entry for this variant (Variation ID: 846756). For these reasons, this variant has been classified as pathogenic.

**Figure 2**. The clinically significant variant c.(?\_-1)\_(134+1\_135-1)del was identified in the *BRCA2* gene. This is a gross deletion of the genomic region the full coding sequence of the *BRCA2* gene has been identified. However, half-quantitative analysis of the *BRCA2* gene,

## Conclusion

- In this study we report cases of low-level constitutional mosaicism in breast cancer predisposition genes and emphasize the importance of deep sequencing in breast cancer patients.
- Clinical laboratories should establish procedures to ensure the detection of mosaic variants and strategies for the verification of the results from additional material (buccal swabs, saliva or fibroblasts).

shows that this deletion was not detected in all cells of the patient, indicating the presence of somatic mosaicism. Isolated whole-gene deletions (PMID: 22762150, 21120943, 29310832) as well as larger copy number events that include this gene (PMID: 15548676) have been reported in individuals with personal and family history of breast and/or ovarian cancer. The mutation database ClinVar contains entries for this variant (Variation ID: 584385). For these reasons, this variant has been classified as Pathogenic. In order to confirm the somatic mosaicism, DNA was isolated from the buccal swab of the patient. The presence of CNV in buccal swab was investigated by use the MLPA method (Multiplex Ligation-dependent Probe Amplification, MRC Holland; PMID: 10978226). The same pattern of the deletion of entire gene was detected in the buccal swab which confirms the state of mosaicism.

#### References

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