Association of the rs2234909 variant of the FGFR3 gene with colorectal cancer in a Mexican population

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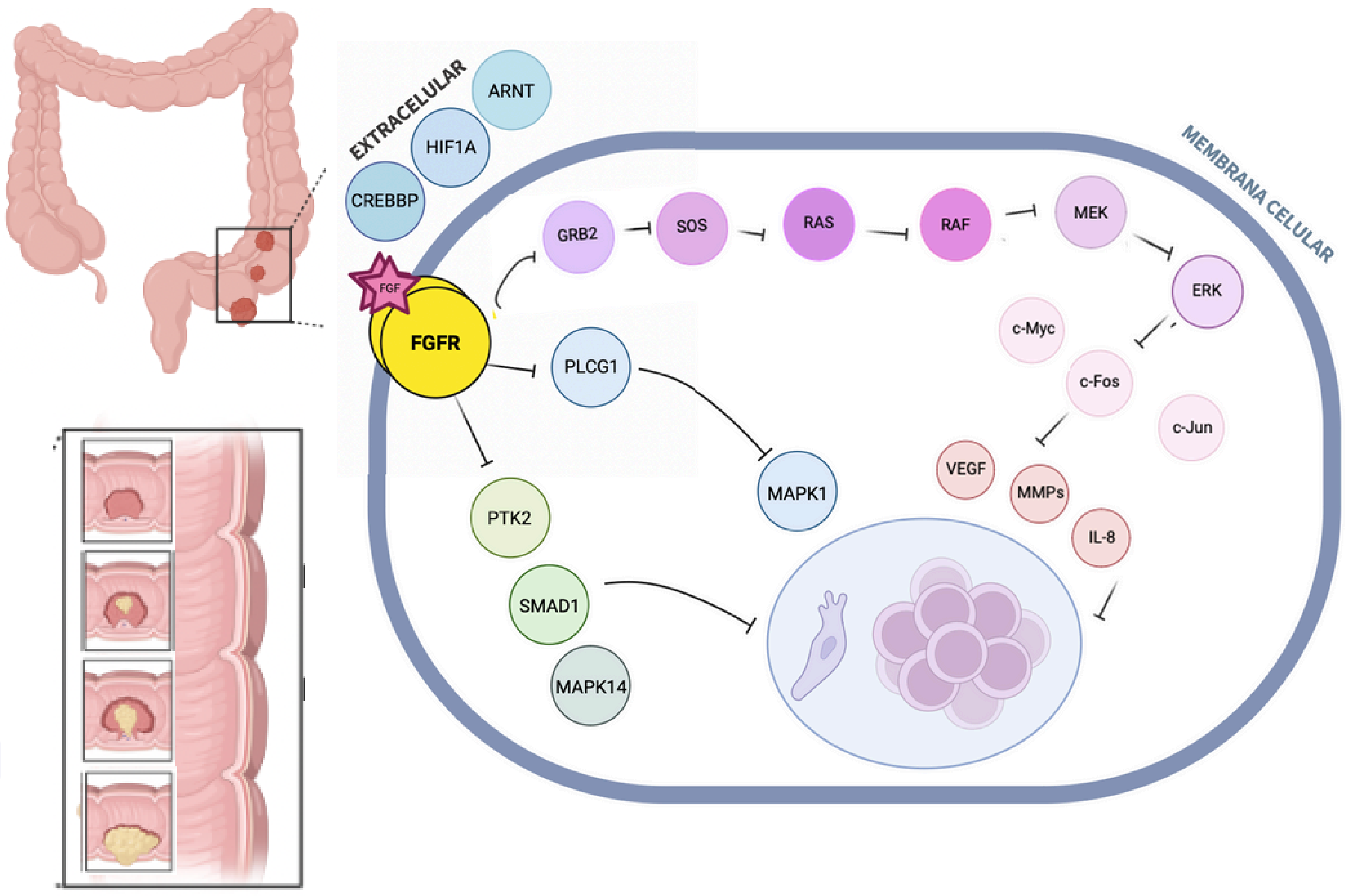
Background

Colorectal cancer (CRC) ranks as the third most common malignancy worldwide and the leading cause of cancer-related mortality in 2024. While previous studies have explored the role of intracellular genes in CRC development, there is limited evidence regarding the involvement of fibroblast growth factor receptors (FGFR), particularly *FGFR3*[1,2].

This gene, located on chromosome 4p16.3, consists of 19 exons and plays a key role in cell cycle regulation. Three high-variability regions, or hotspots, have been identified within the gene, with exon 7 being the most significant—accounting for approximately 88% of reported mutations[3,4].

Exon 7 encodes the IgIII domain, which is essential for the formation of receptor isoforms via alternative splicing, affecting ligand-binding specificity. The synonymous variant rs2234909, located in exon 7 (codon 294), involves a T>C transition (p.Asn294Asn)[5,6].

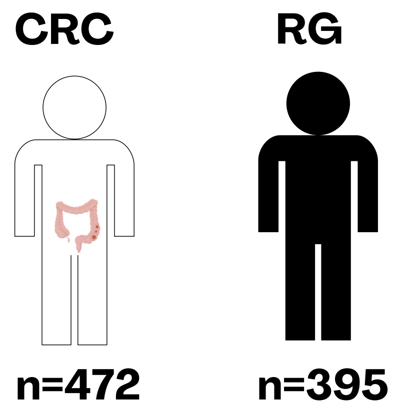
Although it does not change the amino acid sequence, it may promote disulfide bond formation between adjacent monomer receptors or induce structural changes in the tyrosine kinase domain, leading to ligand-independent dimerization[7,8].

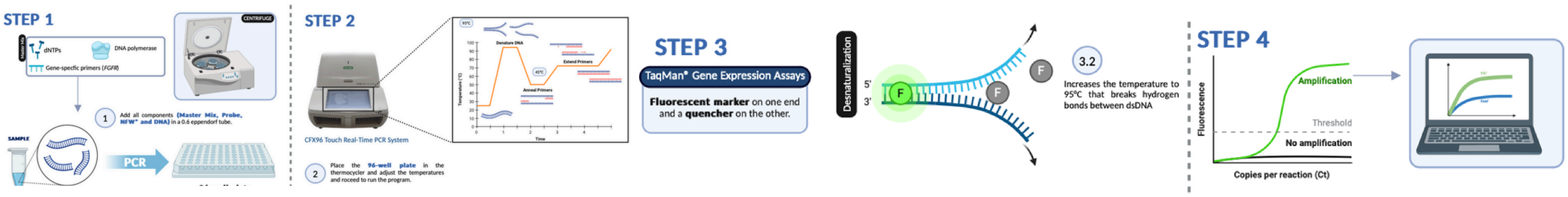


Objetive

To analyze the association between the *FGFR3* rs2234909 variant and CRC in the Mexican population.

Materials and Methods





1. Add all components **(Master Mix, Probe, NFW* and DNA)** in a 0.6 eppendorf tube.

2. Place the **96-well plate** in the thermocycler and adjust the temperatures and roceed to run the program.

Fluorescent marker on one end and a **quencher** on the other.

3.2 Increases the temperature to 95°C that breaks hydrogen bonds between dsDNA

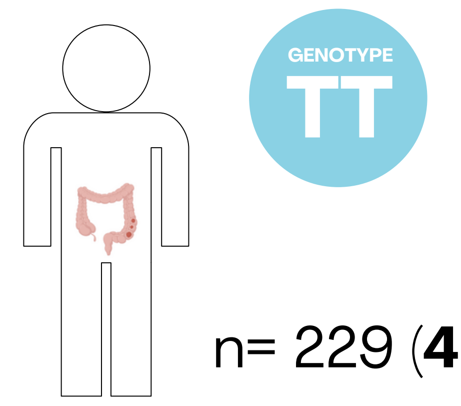
Results

rs2234909 ***(FGFR3)***		**Patient group CRC**		**Reference group**		**OR**	**95% (CI)**	***P*-value**
Model	**Genotype**	**(n=472)**	**%**	**(n=395)**	**%**			
	TT	(243)	51	(224)	21	1.0 (reference)		
	TC	(108)	23	(147)	46	0.50	(0.37-0.67)	**0.001**
	CC	(121)	26	(24)	6	5.34	(3.36-8.47)	**0.001**
Dominant	*TT*	(243)	51	(224)	57	1.0 (reference)		
	TC+CC	(229)	49	(171)	43	1.23	(0.94-1.61)	0.1242
Recessive	*CC*	(121)	26	(24)	6	5.34	(3.36-8.47)	**0.001**
	TT+TC	(351)	74	(371)	94	1.0 (reference)		

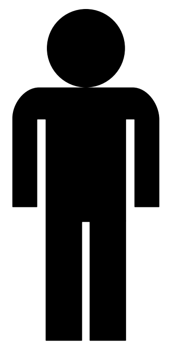
	Patient group CRC		**Reference group**		**OR**	**95%(CI)**	***P*-value**
Allele	**(2n=944)**	**%**	**(2n=790)**	**%**			
A	(594)	63	(595)	73	0.55	(0.45-0.68)	**0.001**
ALTERN ***G***	(350)	37	(195)	27	1.79	(1.46-2.21)	**0.001**

Conclusion

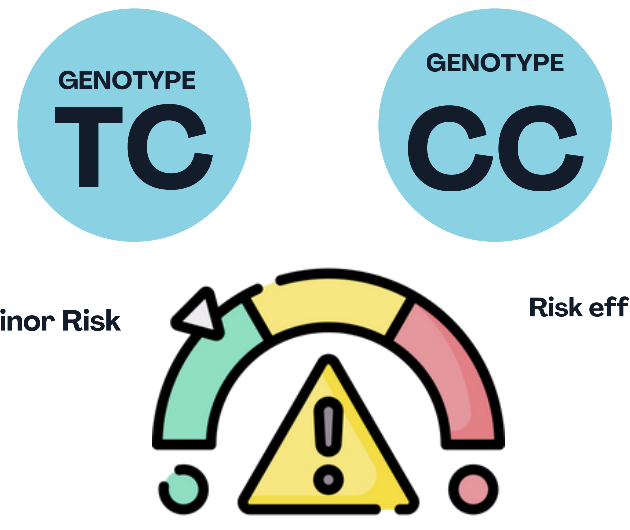
Most frequent



n= 229 (**49%**)



n= 88 (**46%**)



The **rs2234909 variant of *FGFR3*** may serve as a **potential** genetic susceptibility marker for CRC in the Mexican population.

References