Abstract: The Study Of STR In E- Cadherin Gene: A New Era Of Breast Cancer Research

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Method: After designing primers, Genomic DNA was extracted from the blood of 100 patients and 100 control, then desired fragments were amplified by PCR technique. The PCR products were analyzed by polyacrylamide gel.

Results: So far we have observed alleles with different number of CTTT repeats.

Conclusion: Characterizing the number of CTTT repeats in intron 2 of CDH1 and finding its relationship with breast cancer can help us in diagnosing people susceptible to breast cancer and also can have therapeutic purposes.