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Editorial

Molecular taxonomy of gastric carcinoma

Banushree CS[1]*

[1] *Dept. of Pathology, Indira Gandhi Medical College and Research Institute, Puducherry, India*

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The outcome of gastric carcinoma is dismal and molecular breakthrough is important to extend the lifespan of patients diagnosed with gastric carcinoma.[1] Apart from Lauren's and The World Health Organization's classifications of gastric carcinoma, the classification proposed by The Cancer Genome Atlas (TCGA) and The Asian Cancer Research Group (ACRG) is gaining momentum as it helps in the better management of patients suffering from gastric Carcinoma.[2] TCGA has recognized four molecular subtypes namely, Epstein–Barr virus (EBV)-positive, microsatellite instability (MSI), chromosomal instability (CIN), and genomically stable (GS).[3] The ACRG has also proposed four molecular subtypes: Microsatellite instability-H (MSI-H), Microsatellite stable/Epithelial Mesenchymal Transition (MSS/EMT), Microsatellite stable/TP53 mutant (MSS/TP53+), and Microsatellite stable/TP53 wildtype (MSS/TP53-).[4]

The most common subtype of TCGA is Chromosomal instability and the least common subtype is Epstein-Barr virus subtype positive.[5] The Epstein-Barr virus-associated subtype is more commonly seen in young males and on the upper part of the stomach. Some studies suggest longer recurrence-free survival than the other subtypes.[6,7] There are conflicting studies regarding the prognosis of Microsatellite instability. According to some studies, the MSI subtype has a favorable prognosis and responds to immunotherapy.[8] Gastric Carcinoma with chromosomal instability is the most common subtype and shows various mutations commonly amplification of receptor tyrosine kinase, TP53. It carries an intermediate prognosis. The diffuse type of gastric carcinoma of Lauren classification is placed under the genomically stable subtype. Even though it's genomically stable with low levels of mutation like CDH1 mutation and Claudin 18 rearrangements, it carries the worst prognosis.[9]

The predisposing factors for the development of gastric carcinoma in Asians are different from others. So, The ACRG has come up with different molecular classifications. The MSI-H subtype is similar to the MSI subtype of TCGA.[10] The MSS/EMT subtype is similar to the diffuse type of Lauren classification and carries the worst prognosis.[11] The MSS/TP53 mutant shows a high incidence of EBV association. The MSS/TP53 wildtype shows various genetic mutations including MDM2 amplification, Cyclin D1, and EGFR.[9]

1. Conclusion

The molecular classification is gaining momentum in the management of stomach carcinoma. Gastric carcinoma is heterogeneous at the molecular level and the mutations are different in different parts of the world, especially between Asians and the rest of the world. The molecular analysis aids in the targeted therapy and recurrence-free survival of the patients.

* *Corresponding author*.
E-mail address: drbanushree15@hotmail.com (Banushree CS).

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3. Conflict of Interest

None.

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Author biography

Banushree CS, Professor & Head https://orcid.org/0000-0003-4637-8837

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