



Editorial Note

Tea plants are exposed to various stresses during development, advancement, and postharvest handling, which influences levels of optional metabolites in leaves and impacts tea practical properties and quality. Most examinations on auxiliary digestion in tea have zeroed in on quality, protein, and metabolite levels, though upstream administrative instruments stay muddled. In this survey, we embody DNA methylation and histone acetylation, sum up the significant administrative impacts that epigenetic adjustments have on plant auxiliary digestion, and examine achievable examination methodologies to explain the fundamental explicit epigenetic systems of optional digestion guideline in tea. This data will assist scientists with exploring the epigenetic guideline of optional digestion in tea, giving key epigenetic information that can be utilized for future tea genetic breeding [1].

When compared to diploid progenitors, Raphanobrassica (RrCr, $2n = 4x = 36$) is produced through remote hybridization between the maternal parent *Raphanus sativus* (Rs, $2n = 2x = 18$) and the paternal parent *Brassica oleracea* (C°, $2n = 2x = 18$). However, the hybrid's