ЗАКЛЮЧЕНИЕ

Эволюция ТП предстает не как линейный процесс, а как результат сложного взаимодействия универсальных молекулярных механизмов и видоспецифичных эволюционных траекторий. Таким образом, наблюдаемые в природе разнообразие и динамика ТП являются продуктом универсальных молекулярных процессов, особенность применения которых определяется специфическим режимом каждого генома — уникальным сочетанием скорости удаления ДНК, уровня точечных мутаций, популяционной истории, исторической активностью МЭ, уровня рекомбинации, возможных эпизодов гибридизации, особенностей мейоза, морфофункциональных ограничений и антропогенных влияний, включая одомашнивание. Понимание этих процессов необходимо для раскрытия роли ТП не только в архитектуре генома, но и в видообразовании и адаптации.

Важно подчеркнуть, что описанная динамика ТП — их амплификация, сокращение и быстрый эволюционный оборот — имеет прямое эволюционное значение. Изменения в их репертуаре могут не только отражать популяционные процессы, что показано, например, для *Tribolium castaneum* (Feliciello et al., 2015), *Drosophila melanogaster* (Wei et al., 2014) и *L. migratoria* (Camacho et al., 2022), но и способствовать геномной дивергенции на популяционном уровне (Feliciello et al., 2015). В макроэволюционном контексте высокая скорость эволюции ТП и их локализация в гетерохроматиновых областях делают их, наряду с другими повторяющимися элементами, ключевым компонентом, определяющим структурное и количественное разнообразие геномов. Будучи «горячими точками» для хромосомных перестроек, они участвуют в формировании архитектуры генома (Adega et al., 2009; Paço et al., 2013; Rojo et al., 2015; Vozdova et al., 2016; Escudeiro et al., 2019), тогда как их амплификация или сокращение могут вносить вклад в вариацию размеров генома (Macas et al,. 2015; Garrido-Ramos et al., 2025).

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