DEVELOPMENT OF SSR MARKERS FOR *PSAMMOCHLOA VILLOSA* (TRIN.) BOR (POACEAE), A DOMINANT SPECIES IN THE INNER MONGOLIAN PLATEAU

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We developed a set of SSR markers to investigate the genetic diversity and evolutionary history of Psammochloa villosa (Trin.) Bor, a dominant species of the Inner Mongolian Plateau and adjacent regions. We used sequenced transcriptomes of P. villosa to develop primer pairs for 97 SSR markers. Of these, we successfully amplified 46 (47 %) SSRs and found that eleven were polymorphic among individuals. We tested these eleven SSRs in 122 accessions of P. villosa representing ten populations, and determined that the number of alleles per locus ranged from one to seven, with an average of 2.727. The expected and observed heterozygosity per locus varied from 0 to 0.840 (mean: 0.471) and from 0 to 1.000 (mean: 0.679), respectively. The new SSR markers described in this study will be valuable for evaluating the population genetic structure and history of P. villosa throughout its range and may help to develop hypotheses for understanding the history of its divergence from its closest relatives in the genus Stipa L.

Key words: *grass; Illumina; microsatellite marker; orthologous gene; transcriptome.*

РОЗРОБКА SSR МАРКЕРІВ ДЛЯ *PSAMMOCHLOA VILLOSA* (TRIN.) BOR (POACEAE), ДОМІНАНТНОГО ВИДУ НА ПЛАТО ВНУТРІШНЬОЇ МОНГОЛІЇ

Нами було розроблено набір SSR маркерів для вивчення генетичного різноманіття та еволюційної історії *Psammochloa villosa* (Trin.) Bor, домінантного виду на плато Внутрішньої Монголії та в прилеглих регіонах. Секвеновані транскриптоми *P. villosa* було використано для розробки пар праймерів для 97 SSR маркерів. З них ми успішно ампліфікували 46 (47 %) SSR і виявили, що одинадцять були поліморфними в окремих рослинах. Ми перевірили ці одинадцять SSR в 122 зразках *P. villosa*, що представляли десять популяцій, і встановили, що кількість алелів на локус була у межах від одного до семи, при цьому середнє значення становило 2,727. Очікувана і фактична гетерозиготність в одному локусі перебувала у діапазоні від 0 до 0,840 (середнє значення: 0,471) та від 0 до 1,000 (середнє значення: 0,679), відповідно. Нові SSR маркери, описані у цьому дослідженні, будуть корисними для оцінки генетичної структури популяції та історії *P. villosa* у всьому її діапазоні, а також можуть бути використані для висунення гіпотез щодо історії її дивергенції від найближчих родичів з роду *Stipa* L.

Ключові слова: трава; *Illumina*; мікросателітний маркер; ортологічний ген; транскриптом.

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