

研究论文

野生二粒小麦 (*Triticum dicoccoides*) 与普通小麦 (*T. aestivum*) A、B染色体组的同源性分析

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摘要 以普通小麦农家种、野生二粒小麦和野生二粒小麦与节节麦合成的双二倍体为材料, 运用SSR分子标记方法对野生二粒小麦与普通小麦A、B染色体组的同源性进行了研究。结果表明: (1) 野生二粒小麦与普通小麦A、B染色体组的遗传相似系数仅为0.189, 存在较大的差异, 推测野生二粒小麦与普通小麦的A、B染色体组在长期的进化过程中, 形成了各自完整的、平衡的遗传体系; (2) 野生二粒小麦与普通小麦A和B染色体组各自的遗传相似系数分别为0.264、0.125, 结合两个染色体组的聚类结果, 发现A、B染色体组在进化上是不同步的, 且A染色体组比B染色体组更为保守; (3) 通过比较人工合成的双二倍体与普通小麦的遗传结构, 发现双二倍体基因组的简单重复序列发生了明显的变化, 印证了“小麦异源多倍体形成初期就发生了遗传物质变化”的观点。

关键词 [野生二粒小麦](#) [普通小麦](#) [SSR标记](#) [同源性](#)

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Homology Analysis of A and B Genomes between Wild Emmer (*T. dicoccoides*) and Common Wheat(*T. aestivum*)

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Abstract In the history of wheat evolution studies, *T. dicoccoides* has been recognized to be the tetraploid ancestor of *T. aestivum*. To study the homology of genome A and B between *T. dicoccoides* and *T. aestivum*, germplasm resources of 13 accessions from *T. aestivum*, 12 accessions from *T. dicoccoides* and 4 accessions of the allopolyploid synthesized between *T. dicoccoides* and *Ae. tauschii* were analyzed by SSR (simple sequence repeat) markers. The results indicated that: (1) The genetic similarity between *T. dicoccoides* and *T. aestivum* on genomes A and B was 0.189, and the similarities of the accessions within genome A and genome B were 0.264 and 0.125 respectively. Therefore, it could be concluded that a considerable degree of genetic differentiation has occurred within genome A and genome B of the two species, and importantly, these two genomes have formed integrated and balanced genetic systems during the evolution from *T. dicoccoides* to *T. aestivum*; (2) Through comparison of the genetic similarities and dendrograms of genome A and genome B between *T. dicoccoides* and *T. aestivum*, the genetic similarity of these two species on genome A was higher than that on genome B, meaning that genome A and genome B had different evolutionary speeds and genome A was more conservative than genome B during the evolution. The reason of the phenomena might be that genome B of *T. aestivum* had several diploid donors, and thus the genetic background of genome B was more instable and complicated than genome A during the evolution; 3) Obvious changes of simple sequence repeats between the allopolyploid and *T. aestivum* could be applied to support the conclusion that the genetic background had been changed even in the early stage during the formation of allopolyploid plant.

Key words [T. dicoccoides](#) [T. aestivum](#) [SSR marker](#) [Homology](#)

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