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经作所蔬菜团队在国际学术期刊《International Journal of Molecular Sciences》上发表萝卜资源文章

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近日, 经作所蔬菜团队在国际学术期刊《International Journal of Molecular Sciences》(JCR一区, IF=6.208)在线发表题为“Genetic diversity analysis and core germplasm collection construction of radish cultivars based on structure variation markers”的研究论文。

该研究以蔬菜团队近二十年收集的萝卜种质为基础, 采用结构变异分子标记对217份萝卜种质进行基因分型, 并进行遗传多样性及群体结构分析。研究结果显示已收集的217份萝卜种质可分为三个主要类群, 且不同群体之间存在中等程度以上的遗传分化。此外, 群体的分类与种质的地理分布以及叶表型存在一定的相关性。本研究共筛选出43份核心种质资源, 基于以上核心种质建立了新的萝卜胞质不育系, 并培育出了3个优良的萝卜新品种“楚玉2号”“楚翠2号”“紫美人”。以上结果将对培育高品质萝卜新品种提供材料资源与理论指导。

李道瑶硕士研究生和崔磊副研究员为论文共同第一作者, 邱正明研究员和严承欢副研究员为通讯作者, 省农科院经作所为通讯单位。该论文获国家自然科学基金青年基金项目(31902058), 国家重点研发计划项目(2021YFD1600303), 现代农业技术体系国家大宗蔬菜岗位科学家项目(CARS-23-B06), 省农科院经作所重大培育项目(2022JZKC001)以及省农科院青年拔尖人才培养计划项目的支持。

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Article

Genetic Diversity Analysis and Core Germplasm Collection Construction of Radish Cultivars Based on Structure Variation Markers

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Abstract: Radish is an economically important root vegetable worldwide. In this study, the 217 cultivated radish accessions were collected and genotyped. To detect the genotypes of these accessions, a total of 24 structure variation (SV) markers distributed on nine chromosomes were employed to analyze genetic diversity and construct a core germplasm collection of radish. The results of polymorphism information content (PIC) indicated a good polymorphism of these SV markers. Population structure analysis and principal component analysis (PCA) results showed that the 217 radish accessions fell into three main populations (P1, P2, and P3). Genetic diversity analysis showed that these populations were highly associated with geographical distribution. The values of the fixation index (F_{ST}) indicated a high genetic diversity between P2 and P3, and a moderate genetic diversity between P1 and P2, and P1 and P3. Furthermore, the 43 core germplasm were exploited for creating cytoplasmic male sterility (CMS) lines and cultivating new radish varieties. The high genetic diversity of 217 radish germplasm will not only provide valuable resources for future genetic mapping and functional genomic research, but also facilitate core germplasm utilization and the molecular breeding of radish.

Keywords: radish; genetic diversity; molecular marker; core germplasm collection; structure variation

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