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Whole-genome sequencing of cultivated and wild peppers provides insights into *Capsicum* domestication and specialization

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As an economic crop, pepper satisfies people's spicy taste and has medicinal uses worldwide. To gain a better understanding of Capsicum evolution, domestication, and specialization, the genome sequence of the cultivated pepper Zunla-1 (*C. annuum* L.) and its wild progenitor Chiltepin (*C. annuum* var. *glabriusculum*). It is estimated that the pepper genome expanded ~0.3 Mya (with respect to the genome of other Solanaceae) by a rapid amplification of retrotransposons elements, resulting in a genome comprised of ~81% repetitive sequences. Approximately 79% of 3.48-Gb scaffolds containing 34,476 protein-coding genes were anchored to chromosomes by a high-density genetic map. Comparison of cultivated and wild pepper genomes with 20 resequencing accessions revealed molecular footprints of artificial selection, providing us with a list of candidate domestication genes. It was also found that dosage compensation effect of tandem duplication genes probably contributed to the pungent diversification in pepper. The *Capsicum* reference genome provides crucial information for the study of not only the evolution of the pepper genome but also, the Solanaceae family, and it will facilitate the establishment of more effective pepper breeding programs.

Biography

Cheng Qin has completed his PhD at the age of 30 years from Sichuan Agricultural University and postdoctoral studies from South China Agricultural University in China. He is the director of Pepper Institute, Zunyi Academy of Agricultural Sciences in China, the only international, non-profit organization devoted to education and research related to Capsicum or peppers. He has published papers in PNAS, BMC genomics, etc.

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Comparative analysis of adoption level of sugarcane in Cauvery, Tunga and Ghata prabha areas of Karnataka

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The present study was conducted in 18 villages of Cauvery, Tunga and Ghata prabha command areas of Karnataka state during 2009 to measure the adoption level of sugar cane growers revealed that, 36.67 per cent of the respondents were in medium adoption level in Tunga command area (Shimoga district) 26.67 per cent respondents were in medium adoption level in Cauvery command area (Mandya district) and 48.33 per cent of respondents were in high Adoption level in Ghata prabha command area (Belgaum district). Education, mass media participation, extension participation, credit borrowing pattern, risk orientation, scientific orientation, economic motivation, self reliance and extension agency contact of sugarcane growers had a positive and significant relationship with the adoption level. All the 20 variables selected contributed to a tune of 72 per cent in the adoption level of the sugarcane growers as indicated by R^2 value adoption level of respondents in all the three areas differed significantly as indicated by χ^2 tests.

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