

GLOBAL RANGE EXPANSION HISTORY OF PEPPER (*CAPSICUM* SPP.) REVEALED BY OVER 10,000 GENE BANK ACCESSIONS

TRIPODI P.*, RABANUS-WALLACE M. T.** , BARCHI L.***, KALE S.****, ESPOSITO S.*,
ACQUADRO A.***, SCHAFLEITNER R.****, VAN ZONNEVELD M.****, PROHENS J.*****, JOSÉ
DIEZ M.*****, BÖRNER A.** , SALINIER J.***** , CAROMEL B.***** , BOVY A.***** ,
BOYACI F.***** , PASEV G.***** , BRANDT R.** , HIMMELBACH A.** , PORTIS E.*** ,
FINKERS R.***** , LANTERI S.*** , PARAN I.***** , LEFEBVRE V.***** , GIULIANO
G.***** , STEIN N.**

*) CREA Research Centre for Vegetable and Ornamental Crops, Pontecagnano (SA), Italy

**) Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Seeland, Germany

***) DISAFA, Department of Agricultural, Forest and Food Sciences, University of Torino, Italy

****) The World Vegetable Centre, Taiwan

*****) Universitat Politècnica de València UPV, Valencia, Spain

*****) INRAE, GAFL, Unité de Génétique et Amélioration des Fruits et Légumes, Montfavet, France

*****) Wageningen University & Research WUR, Wageningen, The Netherlands,

*****) Bati Akdeniz Agricultural Research Institute BATEM, Antalya, Turkey

*****) Maritsa Vegetable Crops Research Institute, Plovdiv, Bulgaria

*****) The Volcani Centre, Bet Dagan, Israel

*****) Agenzia Nazionale per le Nuove Tecnologie, l'Energia e lo Sviluppo Economico Sostenibile (ENEA), Roma, Italy

Genebank, pepper, population genomics, routes of diversification, GWAS

During the early twentieth century, awareness of the increasing loss of genetic diversity in crops first prompted the establishment of genebanks. FAO estimated an overall 7.4 million germplasm accessions to be presently maintained ex-situ in over 1,700 genebanks worldwide. This remarkable volume of preserved genetic material represents an invaluable resource for facing challenges due to climate change and increasing pressure on global food production pathways. Genetic characterization of such collections has the potential to elucidate the genetic histories of important crops, use marker-trait associations to identify loci controlling traits of interest, search for loci undergoing selection, and contribute to genebank management by identifying taxonomic misassignments and duplicates. We conducted a genomic scan with GBS-derived SNPs of 10,038 pepper (*Capsicum* spp.) accessions from worldwide genebanks and investigated the recent history of this iconic staple. Genomic data detected up to 1,618 duplicate accessions within and between genebanks and showed that taxonomic ambiguity and misclassification often involve interspecific hybrids that are difficult to classify morphologically. We deeply interrogated the genetic diversity of the commonly consumed *C. annuum* to investigate its history, finding that the kinds of peppers collected in broad regions across the globe overlap considerably. The novel method ReMIXTURE—using genetic data to quantify the similarity between the complement of peppers from a focal region and those from other regions—was used to supplement traditional population genetic analyses. By tracing back to routes of evolution we provide a

model of *C. annuum* distribution which reflects human trade and historical/cultural influences. Our results highlight west-east routes of expansion shedding light on the links between South and Mesoamerica, Africa and East/South Asia, the latter two constituting important diversification centers of pepper diversity reflecting a vision of pepper as a highly desirable and tradable cultural commodity, spreading rapidly throughout the globe along major maritime and terrestrial trade routes. Genome wide associations and possible selective sweeps affecting traits such as pungency were observed and these traits were shown to be distributed non-uniformly across the globe, suggesting that human preferences exerted a primary influence over domesticated pepper genetic structure. Finally, we outline a roadmap for genebank management and future direction for better exploitation of germplasm resources.