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TTI GG 150 Tomato Genome ReSequencing project



An international consortium, led by Wageningen UR, with partners from industry, government and science, have started to sequence the DNA of 150 tomato plants. The aim of the so-called 150 Tomato Genome Sequencing project is to reveal and explore the genetic diversity available in tomato. The project will unlock important traits that are lost during domestication of the ancestors, for example resistance against pathogens, taste and health improving compounds. The project will thus help to make food production more sustainable. It will also help to reduce the time needed to develop new tomato lines

Tomato is economically one of the most important crop species for the Dutch breeding industry, and is one the most important vegetables globally. The seed companies involved in this project cover 30 % of the global seed market for tomato. Seed companies need to continuously develop new tomato lines to match the changing preferences of consumers or to combat new tomato pathogens.

The pool of modern tomato lines contains only a small percentage of the genetic diversity of tomato available in nature, because breeding and selection in the past 100 years was targeted at a limited number of desirable traits, such as yield. Potentially interesting genetic variation may have been lost during this process. This loss may include genes for good taste, genes for health beneficial compounds, resistance against pests and diseases, and genes for adaptation to harsh climatic conditions.

To develop new commercial breeding lines, it is necessary to explore unused genetic diversity from tomato and its close relatives. This new project will use so-called whole-genome resequencing as a strategy to develop a high-resolution catalogue containing genetic diversity from 84 tomato types. These 84 tomato types have been selected to represent the maximum range of expected genetic diversity. The genetic diversity catalogue will be constructed using resequencing data from 10 old tomato varieties, 44 tomato land races and 30 close relatives of tomato. The 10 old tomato varieties date back to the fifties and sixties of the last century and represent the ancestors of modern tomato breeding lines. The 44 tomato land races have been obtained from collections worldwide and include plants adapted to local environments, plants stored in gene banks since the beginning of the last century, and very old accessions which have been maintained by enthusiasts. The 30 close relatives of tomato are naturally occurring in the wild and include varieties that grow in harsh environments such as very dry (desert), very humid (forest areas), or very cold (high mountains). Genetic diversity from these tomato relatives can be valuable for breeding tomato lines for marginal regions, and thus contributing to global food security. In addition to the 84 tomato types, 60 plants of a breeding population will be sequenced at "low depth". These plants will be used to study aspects of the breeding process in detail. The interest for sequencing these plants is to develop strategies on how to efficiently breed new lines using the genetic diversity identified in the 84 tomato types.

The value of the tomato genome-sequencing project is that it will unlock traits that are lost during domestication of the ancestors, for example resistance genes against pathogens, or taste and health improving compounds. It will also reveal how traits are transferred from parents to offspring, and this will help to reduce the time needed to develop novel tomato lines.

The 150 Tomato Genome Sequencing project is a Sino-Dutch collaboration of which the Chinese part is funded and executed by the Beijing Genomics Institute (BGI Shenzhen). The Dutch part is funded by the Technological Top institute Green Genetics (TTI-GG), international breeding industry, and the Dutch Ministry of Economic Affairs, Agriculture and Innovation.

website: <http://www.tomatogenome.net/index.html>

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