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学 位 （ 博 士 ） 論 文 要 旨
(Doctoral thesis abstract)

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論文題目 Title	AAL 毒素感受性を決定する Asc1 遺伝子の多様性解析に基づくトマト栽培化・進化に関する研究 Study on tomato domestication and evolution based on diversity analysis of *Asc1* gene determining AAL-toxin susceptibility				

論文要旨 (和文要旨(2000 字程度)または英文要旨(500words))
※欧文・和文どちらでもよい。但し、和文の場合は英訳を付すこと。
Write a summary in Japanese (2000 characters) or in English (500words).
If the abstract is written in Japanese, needed to translate into English.

Modern plant breeding has enhanced the selection of genes determining favorable phenotypes within a diverse gene pool, which has led to a reduction in genetic diversity among agricultural plants.

Tomato (*Solanum lycopersicum* L., formerly *Lycopersicon esculentum* Mill; *SLL*) is the most abundantly produced vegetable in the world. *SLL* originated from *S. pimpinellifolium* L. (*SP*) in the Andean region, and sustain wild tomato species, including not only *SP* but *S. lycopersicum* var. *cerasiforme* (Dunal) A.Gray (*SLC*), an apparent intermediate hybrid between *SP* and *SLL*, is currently found as a native-grown tomato in Mexico and several Central and South American countries. Traditional *SLL* cultivars, considered to be the archetype of modern *SLL* cultivars, have been handed down by generations of peasants in mountain villages in Mexico and designated "jitomate criollo" in Spanish (*SLJ*).

Tomato susceptibility/resistance to stem canker disease caused by *Alternaria alternata* tomato pathotype (*Aat*) and its pathogenic susceptibility/resistance factor AAL-toxin is determined by the presence of the *Asc1* gene that encodes an enzyme in the ceramide biosynthesis pathway, thereby protecting tomato tissues from the AAL-toxin. Several cultivars of commercial tomato (*Solanum lycopersicum* var. *lycopersicum*, *SLL*)

and two wild tomato species (*S. cheesmaniae* (*SC*) and *S. galapagense* (*SG*)) are reported to have mutations in *Asc1*, resulting in their susceptibility to stem canker disease and AAL-toxin.

I hypothesized that there would be some diversity among *Asc1* sequences in ancestral species of tomato. To test this hypothesis, 115 wild and transition tomato accessions including *SP*, *SLC* and *SLJ* were evaluated in the AAL-toxin susceptibility assay and their *Asc1* genes were sequenced.

Three accessions, *SP* PER018805 from Peru, *SLC* PER018894 from Peru, and *SLJ* M5-3 from Mexico, were susceptible to AAL-toxin. *SLC* PER018894 and *SLJ* M5-3 had a two- nucleotide deletion (nt 854_855del) in *Asc1* that was identical to that found in susceptible commercial *SLL*. Another mutation (nt 931_932insT) that may confer AAL-toxin susceptibility was identified in *SP* PER018805. A phylogenetic tree based on the 18 COSII sequences formed three clades, S1, S2 and S3. Clade S1 is composed of *SC* and *SG*. Clade S2 is composed of *SLL*, *SLJ* and *SLC*. Clade S3 is composed of *SLC* and *SP* from Peru and Ecuador. All the tested *SP* accessions, including the AAL-toxin susceptible accession PER018805, were in Clade S3. Two AAL-toxin susceptible accessions, *SLC* PER018894 and *SLJ* M5-3, were in Clade S2 with *SLL* susceptible commercial tomato. As *SLC* is thought to be the ancestor of *SLL*, and *SLJ* is an intermediate tomato between *SLC* and *SLL*, *Asc1* genes containing a two-nucleotide deletion (nt 854_855del) and those without the mutation seem to have been inherited throughout the history of tomato domestication and breeding.

Since plant breeding is usually carried out by crossing with wild species, conserving the rich genetic resources of wild species is an important issue. Rich genetic resources of wild tomato will continue to play an important role in the future breeding of this globally important crop.

(英訳) ※和文要旨の場合(300 words)
If the abstract is written in Japanese, needed to translate into English.(300 words)