

## 琉球大学学術リポジトリ

Cytological diversity of the genus *Hydrangea* (Saxifragaceae) in the Ryukyu Archipelago of Japan - On the origin of tetraploid *Hydrangea liukiensis* endemic to Okinawajima Island -

メタデータ	言語: 出版者: 琉球大学21世紀COEプログラム 公開日: 2009-01-07 キーワード (Ja): キーワード (En): 作成者: Denda, Tetsuo メールアドレス: 所属:
URL	<a href="http://hdl.handle.net/20.500.12000/8751">http://hdl.handle.net/20.500.12000/8751</a>

(12%–37%). The population differentiation measure, the  $F_{st}$  value, was highly significant ( $P < 0.001$ ) and ranged from 0.1235 (*Jt. magnifica*) to 0.3277 (*Jt. altifrons*) indicating that there is gene flow between populations of each species. AMOVA results were corroborated by Bayesian analysis with significant  $F_{st}$  values for all species. The best model selected was  $f = 0$  ( $f$  being the inbreeding coefficient), suggesting all congeners are outcrossing species. Results from Mantel test demonstrated there is a significant correlation between geographical and genetic distance in *Jt. altifrons* but insignificant for the others.

Oral -22

**Cytological diversity of the genus *Hydrangea* (Saxifragaceae)  
in the Ryukyu Archipelago of Japan  
- On the origin of tetraploid *Hydrangea liukiuensis* endemic to Okinawajima  
Island –**

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Despite corresponding to roughly 1 % of the area of Japan, the Ryukyu Archipelago support more than 1600 seed plant species. This marvelous plant diversity in the current Ryukyu Archipelago must have been established due to the influence of the paleogeographical dynamics of this area. In addition, such speciation processes as interspecific hybridization and polyploidization appear to play an important role in creating plant diversity in the Ryukyus. Some examples of the intraspecific polyploidy have been reported from the *Hydrangea chinensis*-complex that comprises five species distributed in the Ryukyu - Taiwan region. Of the five species, *H. chinensis*, *H. grosseserrata* and *H. kawagoeana* are diploid ( $2n=36$ ), while *H. liukiuensis* has diploid ( $2n=36$ ) and tetraploid ( $2n=72$ ) cytotypes, and *H. yayeyamensis* has octoploid ( $2n=144$ ) and decaploid ( $2n=180$ ) cytotypes. In this workshop, I will focus on the origin of tetraploid *H. liukiuensis* inferred from chloroplast and nuclear DNA sequences.

*Hydrangea liukiuensis* is a small shrub endemic to Okinawa-jima Island of the central Ryukyus. In a preliminary cytogeographical survey of this species, only diploids were found in 15 of 18 populations investigated, whereas tetraploids occurred at remaining three populations (Mt. Nekumachiji, Taiho Riv., Mt. Yae). Intra-population variation in the ploidy level was observed in Taiho Riv., in which diploids were dominant and only four tetraploids grew next to each other. Ten diploids and six tetraploids of *H. liukiuensis*, together with *H. chinensis* (Taiwan), *H. grosseserrata* (Yaku-shima Isl.) and *H. yayeyamensis* (Ishigaki-jima and Iriomote-jima Isls.) were used for molecular analysis. *Cardiandra alternifolia* (Hyogo Pref.) was also used as an out-group. The *trnS/trnG* intergenic spacer region (*trnS*-*G* region) of the chloroplast DNA and the internal transcribed spacer region (ITS) of nuclear ribosomal DNA were PCR amplified and sequenced. Most parsimonious (MP) and maximum likelihood (ML) trees were then constructed based on the nucleotide sequence of each region. On the MP and ML trees of *trnS*-*G* region, *H. liukiuensis* was monophyletic with high bootstrap values (97% and 95%, respectively) and this clade was sister to one composed of remaining three *Hydrangea* species. On the other hand, tetraploids of *H. liukiuensis* were nested with *H. chinensis*, *H. grosseserrata* and *H. yayeyamensis* to construct a monophyletic clade on the MP and ML trees of ITS region (bootstrap values of 60% and 55%, respectively). This clade was sister to a monophyletic clade composed of all diploids of *H. liukiuensis*. This incongruence between chloroplast and nuclear DNA phylogenies of *H. liukiuensis* seem to suggest an allopolyploid origin of tetraploid *H. liukiuensis*. However, no other *Hydrangea* species except *H. liukiuensis* are distributed on Okinawa-jima Island. Past interspecific hybridization event(s) between diploid *H. liukiuensis* and an extinct parent may have caused the origin of tetraploid *H. liukiuensis*.