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NATURAL RESOURCES, LOCAL CULTURES AND ICT AS STRATEGIC INPUTS ON EDUCATION DEVELOPMENT

JAMBI - INDONESIA, NOVEMBER 19TH - 20TH 2014

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Dyslexia: Children’ Learning Disability and Experiences
Genetic Analysis of the *Daemonorops draco* (Willd.) Blume (Palmae) among Wild and Cultivated Populations

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ABSTRACT

Genetic analysis among wild and natural populations of *Daemonorops draco* (Willd.) Blume from Central Sumatera, Indonesia was assessed using ISSR analysis. From the screening results of 15 ISSR primers produced 5 primers which showed clear and reproducible bands. The analysis of data by using POPGENE version 3.2 (2012). Our results showed the level of genetic variation of cultivated population *D. draco* (PP = 50.86%, He = 0.219 and I = 0.313) lower than wild population (PP = 70.29%, He = 0.233 and I = 0.353). The genetic drift and apomictic character may be responsible for the low level of genetic variation of cultivated population of *D. draco*.

Keywords: *Daemonorops draco*, ISSR genetic diversity, wild populations, cultivated population,

INTRODUCTION

*Daemonorops* is a genus of Palmae or Arecales. Some species of this genus that can produce red resin, so they called dragon's blood palm. One of this species was *Daemonorops draco* (Willd.) Blume.

*D. draco* resin in the 11th century, is used as a hair dye, and since the 21st century used as ink (Cavallo et al., 2008). In Europe, red resin is used as a cure dysentery, diarrhea and astringent in toothpaste. In Malaysia *D. draco* resin is used for digestive problems, abdominal pain and ulcers. Red resin containing resinitannol 56%, and benzoic acid (Burkill, 1953 in Rustiami et al., 2004). Benzoic acid in the dragon's blood resin acts as an antiseptic (Piozzi et al., 1974). According to the Department of Forestry Jambi (2008), this species is included in the list of rare species. Therefore, plantation of this species must be done. The data of genetic analysis must become a measure to determine the effectiveness of plantation.

ISSR marker was developed from the common simple repeat sequence (microsatellites) (Gupta et al., 1994). ISSR markers could produce more reliable and reproducible bands than than RAPD because of the longer length of their primer and higher annealing temperature (Nagaoka and Oghara, 1997).

In the present study, the ISSR method was conducted to analyze genetic variation among wild and cultivated population of *Daemonorops draco*.

Objective

To quantify the level of genetic analysis among wild and cultivated population of *Daemonorops draco*.

MATERIALS AND METHODS

Plant materials

Five populations of *D. draco* were obtained from central of Sumatera, Indonesia.

Genomic DNA Extraction

All of genomic DNA was extracted with modification protocol by Asra et al. (2013).
PCR (Polymerase Chain Reaction)

The DNA amplification was carried out following ISSR techniques using kits Go Taq® Green Master Mix, Promega Madison WI USA’s product. The primers used in this study were: HB 8, UBC 807, UBC 808, UBC 810 and UBC 834 (Asra et al. 2014).

Data analysis

The results of the binary data matrix were analyzed using the population genetics software POPGENE version 3.2 (Yeh et al., 1997).

RESULTS

The band profiles that were produced from the five primers were used to study the genetic variation between wild and cultivated populations of *D. draco*, the resulting bands were clear, polymorphic, and reproducible (Figure 1).

![ISSR profile from D. draco with UBC 810 primer.](image)

Table 1. The analysis of genetic variation of *Dracon draco* in wild and natural population using ISSR markers

<table>
<thead>
<tr>
<th>Population</th>
<th>Na</th>
<th>Ne</th>
<th>H</th>
<th>I</th>
<th>Pp (%)</th>
<th>N</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild</td>
<td>1.70</td>
<td>1.29</td>
<td>0.23</td>
<td>0.35</td>
<td>0.002</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>0.003</td>
<td></td>
<td></td>
<td></td>
<td>70.2</td>
<td>123</td>
</tr>
<tr>
<td>Cultivated</td>
<td>1.51</td>
<td>1.41</td>
<td>0.22</td>
<td>0.31</td>
<td>0.002</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>0.003</td>
<td></td>
<td></td>
<td></td>
<td>50.8</td>
<td>89</td>
</tr>
</tbody>
</table>

Description:

Pp (%) : Percentage of polymorphic loci
N : Number of polymorphic loci
Na : The average number of alleles observed
Ne : The average number of effective alleles
H : The average heterozygosity / Nei’s genetic variation/diversity
I : Mean Shannon index (Lewontin, 1972)

Based on analysis of Popogene that genetic variation of wild population (H= 0.233) was higher than cultivated population (H = 0.219). This result suggested that farming activities have reduced genetic variation. According to Zohary (2004) that genetic drift was caused by the collection of seeds from a limited number of wild plants, usually found in cultivated populations, causing cultivated populations deviate significantly from the gene pool of parents. These conditions, led to relatively lower genetic variation in cultivated populations.

CONCLUSION

The genetic analysis of wild population was higher than cultivated population. Based on this research we recommended to use wild population to conservation and cultivation.

ACKNOWLEDGEMENTS

We would like to send our grateful thanks to the Bukit Tigapuluh National Park (BTPN), Rengat, for permission and their contributions in helping to use the BTPN’s area as a major base for this research, and to the Frankfurt Zoological Society (FZS), Jambi, for facilitating the research in Tebo’s.
Furthermore, to our field guides in Rengat, Tebo, and Sarolangun.

REFERENCE


