

Conservation of rabbitear iris (*Iris laevigata*) community in the Kozutsumi Nishi Pond

– Restore genetic diversity by seed propagation –

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Introduction

Kozutsumi Nishi Pond is a state's natural monument in Kariya City

Population of flowers is decreasing



WHY?

Vegetative propagation irises were mainly conserved before

Conservation of seed propagation irises and ones with rare genes

Make proposal to Kariya City

Fig 1. Propagation types of the irises

Seed propagation (Sexual reproduction)	Vegetative propagation (Asexual reproduction)
	
Seed	Underground stem
Sparse	Concentric circle
Each iris has DIFFERENT genetic trait	SAME genetic trait
Genetic diversity 14.6%	4.3%

(Aichi University of Education)

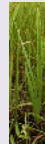
Methods

We have done in July.

- Find young seed propagation irises (under 30cm) and pick their leaves.
- Analyse the leaves and calculate the frequency of the alleles and genetic diversity using allozyme polymorphism analysis.
- Looking at the result (Table 1), we focus on one allele and compare the frequency at each spots.

Allozyme polymorphism analysis: the way in which we electrophoresis extract using polyacrylamide vertical electrophoresis

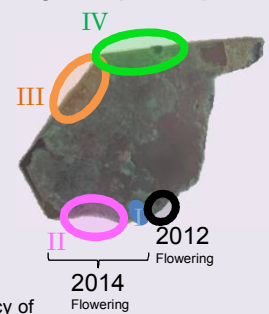
Fig 2. Young iris



Characteristics of the 4 spots

- I Especially many seeds in small area
- II Large area
- III IV Large area with many vegetative propagation irises, few first-year-old irises

Fig 3. Map of the pond



How to calculate frequency

GOT-1	
aa	18
ab	4
ac	16
bb	6
bc	2
cc	14

Ex.
GOT-1 allele "a"
 $\frac{(18 \times 2) + (4 \times 1) + (1 \times 1)}{2 \times (18 + 4 + 16 + 6 + 2 + 14)}$
 $\approx 0.466 \dots$
 ≈ 0.47

Genetic diversity (Heterozygosity)

$$1 - \sum_{i=1}^k p_i^2$$

(p_i : frequency of the i th of k alleles)

Results and Discussion

Table 1. Results of allozyme polymorphism analysis

Number shows frequency of each allele (indicates only with variation)

Enzyme	Allele	2014 I	2014 II	2014 III	2014 IV	2014 Flowering I, II	2012 Flowering East I
		First-year-old	First-year-old	First-year-old	First-year-old		
		60 (Samples)	38	6	9	15	8
GOT-1	a	0.47	0.26	0.50	0.61	0.40	0.69
	b	0.15	0.18	0.17	0.17	0.27	0.13
	c	0.38	0.55	0.33	0.22	0.33	0.19
LAP-2	a	0.98	1	1	1	1	0.75
	b	0.02	0	0	0	0	0.25
PGM-3	a	0.10	0.50	0.17	0.11	0	0.06
	b	0.44	0.50	0.83	0.89	0.13	0.31
	c	0.41	0	0	0	0.87	0.56
	d	0.05	0	0	0	0	0.06
DIA-2	a	0	0	0.08	0.11	0	0
	b	1	1	0.83	0.89	1	1
	c	0	0	0.08	0	0	0
SKD	a	0.21	0.21	0.08	0.17	0.27	0.31
	b	0.76	0.76	0.67	0.67	0.60	0.50
	c	0.03	0.03	0.25	0.17	0.13	0.19
PGI	a	1	1	0.92	0.89	1	1
	b	0	0	0.08	0.11	0	0

Table 2. Genetic diversities

at spots I, II

Spot	%
I	11.1
II	9.8

For spots III and IV, we were unable to verify genetic diversities due to lack of data.



Only spots:

- I PGM-3 allele "d" (also found near I from previous study)
- III IV New allele DIA-2 "a" and PGI "b"

Spots I, III, IV are especially necessary to be conserved

Further Prospects

- Collect more samples.
- Identify the parent iris, and check the change of genetic diversity.
- Research on how genetic diversity will change as they grow.

Acknowledgements

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Bibliography

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