

CORRECTION

Correction: Genetic Analyses of the Internal Transcribed Spacer Sequences Suggest Introgression and Duplication in the Medicinal Mushroom *Agaricus subrufescens*

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[Table 2](#) appears incorrectly in the published article. Please see the correct [Table 2](#) and its caption here.



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Table 2. ITS phenotypes of 94 single spore isolates of strain CA487 and their genotypic interpretation under the hypothesis of two loci *ITSI* and *ITSII*.

Types Of ITS	Phenotypic classes			Genotypic classes among					
	Lengths of DNA fragments ^a after digestion by		N ^b	69 homokaryons ^c			25 heterokaryons ^c		
	enzyme <i>Mbo</i> II	enzyme <i>Fok</i> I		<i>ITSI</i>	<i>ITSII</i>	N ^b	<i>ITSI</i>	<i>ITSII</i>	N ^b
[A]	396 (+377)	773	21	a	n ^d	19	a/a	n/n	2
[B]	772	563 (+209)	23	b	n	20	b/b	n/n	3
[C]	395+264 (+112)	562 (+209)	0			0			0
[A+C]	396+264 (+395+377+112)	773+562 (+209)	21	a	c	19	a/a	c/n or c/c	2
[A+B]	772+396 (+377)	773+563 (+209)	1			0	a/b	n/n	1
[B+C]	772+395+264 (+112)	563 (562+209)	17	b	c	11	b/b	c/n or c/c	6
[A+B+C]	772+396+264 (+395+377+112)	773+563 (562+209)	11			0	a/b	c/n or c/c	11

^a Smallest or redundant uninformative bands in electrophoretic patterns are in parentheses

^b N is the number of single spore isolates among each considered offspring

^c Rates of homokaryotic and heterokaryotic offspring have been determined independently by using other markers

^d Null allele

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