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PRIMER NOTE

ISOLATION AND CHARACTERIZATION OF MICROSATELLITE LOCI IN Sorbus porrigentiformis and cross-amplification in S. aria and S. rupicola (Rosaceae)¹

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- *Premise of the study:* Southwestern Britain is an emblematic hotspot of polyploid diversity of whitebeams (*Sorbus aria* agg.; Rosaceae) with ca. 30 polyploid endemic species. The tetraploid *S. porrigentiformis* is postulated as one of the parents of most of these endemics, along with the sexual diploid *S. aria* s. str. and the tetraploid *S. rupicola*.
- *Methods and Results:* We isolated 16 nuclear microsatellite loci from *S. porrigentiformis* and characterized them on 45 trees representing the three putative parental species. Eleven loci were polymorphic, and eight of them exhibited species-specific alleles. Allele numbers ranged from one to 11, and observed heterozygosity ranged from 0.40 to 1.00. The intraspecific levels of variation were very low, in agreement with the facultative apomictic reproduction hypothesized for this species.
- *Conclusions:* The species-specific alleles will be useful for tracing the origin of the narrowly distributed *Sorbus* taxa. In addition, the assessment of diversity levels will help design a conservation strategy for the polyploid complex.

Key words: British whitebeams; conservation; nuclear microsatellites; polyploid evolution; Rosaceae; Sorbus porrigentiformis.

British whitebeams (Sorbus aria aggr.; Rosaceae) are an emblematic case study of polyploid evolution in natural tree populations. Southwestern Britain is a "Sorbus hotspot," with ca. 30 polyploid species (3x, 4x, and even 5x), many of them occurring at just a few localities and therefore highly valuable in regard to conservation. Recent studies have provided detailed knowledge of the morphology and ploidy levels in British populations of Sorbus L. (Rich et al., 2010; Pellicer et al., 2012). Despite this effort, some essential questions regarding the evolution of the complex remain unsolved. In addition to the sexual diploid species S. aria (L.) Crantz s. str., current evidence points at the polyploid S. porrigentiformis E. F. Warb., an endemic to the United Kingdom that shows a distribution significantly larger than the other highly endemic polyploids of the complex, as a parental species of many of these polyploid endemics. The apomictic tetraploid S. rupicola (Syme) Hedl., widely distributed in northwestern Europe, including the United Kingdom, may have also been involved. To provide diagnostic alleles for the three species, we isolated and characterized the first set of microsatellites for S. porrigentiformis and tested cross-amplification in S. aria and S. rupicola. Previous studies on Sorbus in southwestern Britain have used two nuclear microsatellites from apple (Malus Mill. sp.)

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and three from *S. torminalis* (L.) Crantz (Robertson et al., 2010; Ludwig et al., 2013).

METHODS AND RESULTS

A DNA library was generated for one sample of S. porrigentiformis and sequenced on a Roche/454 GS FLX platform (454 Life Sciences, a Roche Company, Branford, Connecticut, USA). From the 35,638 reads, 10,872 microsatellite loci were detected. Primer pairs were designed with the software QDD (Meglécz et al., 2010) using default parameters (90-320 bp PCR products, with more than five repeats of 2-6 bp motifs, 18-27 bp primer length, 57-63°C annealing temperature). We tested 20 of the primers on seven geographically separated individuals of S. porrigentiformis (Appendix 1). Fluorescent labeling was performed using three primers per locus: a reverse primer, a forward primer with a universal linker sequence (M13) at the 5' end, and a third primer consisting of the same universal M13 sequence, labeled with 6-FAM or JOE (Schuelke, 2000). We added 7.5 µL of Multiplex Mix (10×), 0.2 µL of bovine serum albumin (BSA), 0.3 µL of each reverse primer (10 µM), 0.15 µL of dye-labeled and forward primers (10 µM), 1 µL of template DNA (ca. 10-50 ng/µL), and H₂O up to a final volume of 15 µL. Amplifications were performed as follows: 94°C (4 min); 25 or 30 cycles of 94°C (30 s), 55°C (45 s), 72°C (1 min); followed by 10 cycles each of 94°C (30 s), 53°C (45 s), 72°C (45 s); and a final extension at 60°C for 30 min. PCR products (0.7 µL) were separated on an ABI 3730 sequencer (Applied Biosystems, Lennik, The Netherlands) with 10 µL of HiDi Formamide and 0.15 µL of GeneScan 500 ROX Size Standard (Applied Biosystems). Sixteen primer combinations exhibiting robust amplification were selected (Table 1). All DNA extractions were performed with the DNeasy Plant Mini Kit (QIAGEN, Valencia, California, USA).

We set up 12 simplex reactions containing one microsatellite marker and four multiplex reactions containing up to three loci (Table 1). Markers with different amplicon sizes and similar annealing temperature were identified with Multiplex Manager (Holleley and Geerts, 2009) and combined in the same multiplex. Electropherograms were automatically scored with GeneMapper version 3.7 (Applied Biosystems) and manually corrected. Fifteen markers displayed easily interpretable electropherograms with up to two alleles per locus in the diploid

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	Locus ^a		Primer s	squences $(5'-3')$	Fluorescent label ^b	Repeat motif	Min.	Мах.	Α	GenBank accession no.
Multiplex										
PMB	SP22	 Гц	TGATCACTTCTTACCTGCTTGG	R: CGTCATGCAGGCATATCAAT	M13-FAM	$(AC)_{14}$	234	292	11	KX090362
	SP28	 Гч	CCATGTGCTACACCCAATGGA	R: CGCACAGCAGTATAGTATATGTATCA	M13-FAM	(ATGC) ₅	107	118	0	KX090363
	SP38	 Гч	AAGTGAGGCGTTCCTGAGAA	R: AAGTTGAGACGAGAGTGTCGC	M13-FAM	(AG) ₁₁	169	171	0	KX090364
PMA2	SP30	 Гч	TACTGCTCTTCTTCCCGAGC	R: CACGACTTGGTTCCGCTAAG	M13-FAM	$(AAAGAT)_5$	203	214	ŝ	KX090365
	SP37	 Гч	GATGCTCGTTGCACTCTTCA	R: GAGATTCAAGGGACGAGCAG	M13-FAM	(ACCAGC) ₅	131	156	5	KX090366
PMJ2	SP33	 Гч	GCATCTATCCTCCATGCTACC	R: AGAAAGGAGAGTTGCAGATTTGA	M13-FAM	$(AAT)_{13}$	143	163	5	KX090367
	SP39	 Гч	CCGTTATGGGCTATAAGGTCAG	R: TTTCTCCATTCTAGTCTGCCTC	M13-FAM	$(AT)_{13}$	271	283	9	KX090368
PMJ2	SP35	 Гч	GTGCTTCGATAGGCGCGTAGT	R: CCGGTATGAGTAGCGATTCC	M13-FAM	$(ATC)_7$	311	314	0	KX090369
	SP36	 Гч	GTGCCAATAACAACACGCTG	R: GCCTCACTTAACCTCCTGAATG	M13-FAM	(AT) ₉	110	147	٢	KX090370
Simplex	SP29	 Гч	AATCAAGCACACGTCTGTGAG	R: ATGGAGAAGAACTGATATAGATTAGGA	M13-JOE	$(AT)_6$	158	169	ŝ	KX090371
I	SP20	 Гч	TTGGACGATTTCACCCAGAT	R: CTGCTCAATGATTTGTCTGGA	M13-FAM	$(AT)_{10}$	125	170	11	KX090372
	SP21	 Гч	CATCTGCCAATTTCGTCTCCA	R: TAAGGTCTCGTCGGTTAGGG	M13-FAM	(TTC) ₅	175	175	1	KY224065
	SP24	 Гч	CTACTTCGGCCGTAACGATTC	R: TGTCATTGTGTTTCCCTCCC	M13-FAM	$(GGA)_5$	124	124	1	KY224066
	SP25	 Гч	CGGGAACTCTCAACCAGACGA	R: GTTGCAAACAGGAGCTTACG	M13-FAM	$(TCA)_5$	139	139	1	KY224067
	SP26	 Гч	CAAGAAACGGCCTGCATAGAC	R: AGAGAACCCGTTCGTTGTGT	M13-FAM	$(CAG)_6$	239	245	0	KY224068
	SP34	 Гч	CTCCAGAGGAGGAAGTGAAAGA	R: AATTTCAATGGTGTCGGTCC	M13-FAM	(AGC) ₅	189	189	1	KY224069
Note: $A =$: number of	f allel	les; Max. = maximum allele size; N	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1						
^a The ann	ealing temp.	peratu	rre was 55°C for all loci.							
$^{b}M13 = 0$	CACGACG	GTTG	TAAAACGAC (Schuelke, 2000).							

TABLE 2. Genetic diversity of the 11 newly developed polymorphic microsatellites in three populations of *Sorbus porrigentiformis* and cross-amplification in *S. aria* and *S. rupicola*. All populations are located in southwestern Britain.

			S.	porrige	ntiformi	s (4x, 3x)	(N = 25)															
				Bri	istol (N =	= 5)	Som	erset (N	= 9)	Wal	les $(N =$	11)		S. 1	rupicola	t(4x)(N=10)		S	. aria (2x	(N = 1)	(0	
	Locus	Private	A_{p}	H_{0}	$H_{\rm e}$	$H_{\rm e-d}$	H_{0}	$H_{\rm e}$	$H_{\rm e-d}$	H_0	$H_{\rm e}$	$H_{\rm e-d}$	Min.	Max.	Α	Private	$A_{\rm p}$	Min.	Мах.	Α	Private	$A_{\rm p}$
Multiplex PMB	SP22	245, 255, 257, 263, 270, 284, 292	Г	I	I	I	I	I	I	I	I	I	234	276	5	249, 264, 276	б	234	268	4	256	-
	SP28			1.00	0.56	0.55	1.00	0.53	0.53	0.91	0.52	0.51	107	118	0			107	118	7		
	SP38	171	1	1.00	0.56	0.51	0.78	0.53	0.48	0.91	0.52	0.51	165	165	-			165	169	3	166	-
PMA2	SP30			0.40	0.48	0.62	0.89	0.63	0.60	1.00	0.57	0.54	208	214	6			203	214	3		
	SP37	131	1	1.00	0.71	0.75	1.00	0.74	0.73	1.00	0.69	0.69	137	150	6			137	156	4		
PMJ2	SP33	156	1	1.00	0.56	0.79	1.00	0.78	0.72	1.00	0.57	0.55	143	150	0			140	163	9	140, 160	0
	SP39	277, 283	0	1.00	0.79	0.79	1.00	0.80	0.80	1.00	0.77	0.77	271	285	4	285	1	271	310	ŝ	292, 310	0
PMJ2	SP35			1.00	0.56	0.55	1.00	0.53	0.53	0.91	0.52	0.51	311	314	0			311	311	1		
	SP36	132, 138, 140	ю	1.00	0.75	0.86	1.00	0.83	0.81	1.00	0.71	0.70	143	157	9	150, 152, 154, 157	4	110	147	5	143	-
Simplex																						
	SP29	166	1	1.00	0.56	0.68	0.88	0.63	0.50	0.90	0.53	0.51	154	158	б	156	1	154	169	3	169	-
	SP20	125, 132, 149, 152, 154, 156	9	1.00	0.82	0.83	1.00	0.82	0.78	1.00	0.74	0.73	140	174	5	140, 172, 174	3	123	170	5	123	-
Note: A maximum	4 = numt	per of alleles; $A_{\rm p}$ = number of I ze; Min. = minimum allele size	private $N = N$	e allele numbe	s; $H_e =$	= expect lividual	ed hete s sampl	rozygo ed: Pri	sity; H	$e_{-d} = ex$	pected	heteroz alleles.	zygosity	v corre	cted b	y allele dosages;	$H_0 = 0$	observe	d heter	ozygo	sity; Max	

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TABLE 1.

Description of 16 newly developed microsatellite loci in Sorbus porrigentiformis in four multiplex and seven simplex reactions.

individuals and up to four alleles in the tetraploid individuals. Locus SP22 exhibited up to four peaks in diploids and up to six in tetraploids. Two different size ranges with different amplification intensities and up to two peaks per individual each could be distinguished in *S. aria* and *S. rupicola*, but not in *S. porrigentiformis*. Therefore, locus SP22 was analyzed as a dominant marker.

To characterize the 16 microsatellite loci, 45 individuals were genotyped (Appendix 1): 25 S. porrigentiformis from three different populations in southwestern Britain (3x and 4x), 10 S. aria (2x), and 10 S. rupicola (4x). Sorbus porrigentiformis is endemic to southwestern Britain and individuals occur scattered in the field, which explains the limited sample sizes in this study. However, given that reproduction is mostly clonal, our sampling strategy is representative of the real genetic variation of the species. Ploidy levels of all samples were known from a previous flow cytometry study (Pellicer et al., 2012). Five markers were monomorphic across all 45 samples studied (Table 1). Locus SP26 was biallelic, whereas SP21, SP24, SP25, and SP34 were monoallelic. The remaining 11 microsatellite markers were polymorphic across the three congeners (Tables 1, 2), eight of them exhibited species-specific alleles. Twenty-two private alleles were identified for S. porrigentiformis. Locus SP28, although monomorphic in terms of allele counts, exhibited species-specific differences in allele dosage between S. porrigentiformis and S. rupicola that could be clearly detected, with a ratio of peak areas of 0.45 and 1.34, respectively (Esselink et al., 2004).

For the 11 polymorphic loci, one to 11, one to six, and one to six alleles per locus were retrieved for *S. porrigentiformis, S. aria*, and *S. rupicola*, respectively (Tables 1, 2). Allele sizes, number of alleles, and number of private alleles were calculated for each polymorphic locus and species using SPAGeDi (Hardy and Vekemans, 2002). *Sorbus porrigentiformis* genotypes were further evaluated with GENODIVE (Meirmans and Van Tienderen, 2004) by estimating the expected and observed heterozygosity, with and without correction of allele dosages for polyploids using a maximum likelihood method. Within *S. porrigentiformis*, populations for most loci exhibited fixed alleles. The observed heterozygosity varied between 0.40 and 1.00. *Sorbus porrigentiformis* exhibited low genetic variation at the intraspecific level, but it was not completely clonal, fitting the expectations for a facultative apomict.

CONCLUSIONS

The newly developed nuclear microsatellite loci allow discrimination between the species *S. porrigentiformis*, *S. aria*, and *S. rupicola*. These markers will be an important tool to trace the origin of polyploid endemic species of the *S. aria* agg. in southwestern Britain, and to understand the relative contribution of *S. aria*, *S. rupicola*, and *S. porrigentiformis* as parents of these local polyploids. The resulting genetic information will be relevant for choosing the best approach for the conservation of the polyploid complex *S. aria* agg. in southwestern Britain either by focusing on the conservation of the local endemic taxa or by focusing on the preservation of the polyploidization process (Ennos et al., 2012) by protecting the parental species, even if they are not local endemics themselves.

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PPENDI	PPENDIX 1. Voucher information for Sorbus populations characterized in this study. All collections are located in southwestern Britain. Herbarium vouchers are deposited in the Welsh Nation	Herbarium (NMW).
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L139	Species	Ploidy level	Collection locality	Collection date ^a	Collector	Latitude (°N)	Longitude (°E)
	S. aria	2x	Burrington Combe	15/08/11	L. Houston	51.32	-2.74
L106	S. aria	2x	Cheddar Gorge S side	09/08/11	L. Houston	51.29	-2.75
FC066	S. aria	2x	East Wood, Portishead	11/07/11	L. Houston, M. Fay, J. P. Moscardo, S. Clermont, T. Rich	51.49	-2.77
FC067	S. aria	2x	East Wood, Portishead	11/07/11	L. Houston, M. Fay, J. P. Moscardo, S. Clermont, T. Rich	51.49	-2.77
FC353	S. aria	2x	Gorrashill Wood	11/08/11	T. Rich	51.64	-2.71
FC018	S. aria	2x	Leigh Woods, Quarry 4	04/07/11	T. C. G. Rich, L. Houston, S. Ludwig, I. Trotman	51.46	-2.63
FC156	S. aria	2x	Offa's Dyke, Tidenham Chase	12/07/11	M. Fay, J. P. Moscardo, S. Clermont, T. Rich	51.68	-2.66
FC109	S. aria	2x	Seven Sisters	12/07/11	M. Fay, J. P. Moscardo, S. Clermont, T. Rich	51.83	-2.66
L130	S. aria	2x	Weston Big Wood: Valley Road	15/08/11	L. Houston	51.47	-2.79
FC056	S. aria	2x	Worlebury Hill, west end	11/07/11	L. Houston, M. Fay, J. P. Moscardo, S. Clermont, T. Rich	51.36	-2.99
FC168	S. rupicola	4x	Craig y Cilau NNR	18/07/11	T. C. G. Rich	51.83	-3.17
FC173	S. rupicola	4x	Craig y Cilau NNR	18/07/11	T. C. G. Rich	51.83	-3.18
FC174	S. rupicola	4_X	Craig y Cilau NNR	18/07/11	T. C. G. Rich	51.83	-3.18
FC315	S. rupicola	4_X	Neck Wood, Trentishoe	10/08/11	T. Rich & S. Whild	51.22	-3.96
FC320	S. rupicola	4_X	Neck Wood, Trentishoe	10/08/11	T. Rich & S. Whild	51.22	-3.96
FC197	S. rupicola	4_X	Penmoelallt	18/07/11	T. C. G. Rich	51.77	-3.43
FC203	S. rupicola	4x	Penmoelallt	18/07/11	T. C. G. Rich	51.77	-3.43
FC205	S. rupicola	4x	Penmoelallt	18/07/11	T. C. G. Rich	51.77	-3.43
FC102	S. rupicola	4x	Seven Sisters	12/07/11	M. Fav. J. P. Moscardo. S. Clermont. T. Rich	51.83	-2.66
FC106	S. rupicola	4_X	Seven Sisters	12/07/11	M. Fay, J. P. Moscardo, S. Clermont, T. Rich	51.83	-2.66
FC306	S. porrigentiformis s. str.	4 <i>x</i>	Bristol	28/08/11	T. C. G. Rich		
L039	S. porrigentiformis s. str.	4x	Bristol	23/07/11	L. Houston	51.47	-2.64
L041	S. porrigentiformis s. str.	4x	Bristol	23/07/11	L. Houston	51.47	-2.64
L044	S. porrigentiformis s. str.	4x	Bristol	23/07/11	L. Houston	51.46	-2.63
L124	S. porrigentiformis agg.	4 <i>x</i>	Bristol	15/08/11	L. Houston	51.50	-2.64
L046	S. porrigentiformis s. str.	4 <i>x</i>	Somerset	25/07/11	L. Houston	51.28	-2.77
L050	S. porrigentiformis s. str.	4x	Somerset	25/07/11	L. Houston	51.28	-2.77
L069	S. porrigentiformis s. str.	4x	Somerset	25/07/11	L. Houston	51.28	-2.76
L074	S. porrigentiformis s. str.	4 <i>x</i>	Somerset	25/07/11	L. Houston	51.28	-2.76
L077	S. porrigentiformis s. str.	4 <i>x</i>	Somerset	25/07/11	L. Houston	51.28	-2.76
L089	S. porrigentiformis s. str.	4 <i>x</i>	Somerset	07/08/11	L. Houston	51.20	-2.42
L115	S. porrigentiformis agg.	3x	Somerset	10/08/11	L. Houston	51.28	-2.76
L136	S. porrigentiformis agg.	3x	Somerset	15/08/11	L. Houston	51.32	-2.74
L138	S. porrigentiformis agg.	3x	Somerset	15/08/11	L. Houston	51.32	-2.74
FC164	S. porrigentiformis s. str.	4 <i>x</i>	Wales	18/07/11	T. C. G. Rich	51.84	-3.21
FC171	S. porrigentiformis s. str.	4 <i>x</i>	Wales	18/07/11	T. C. G. Rich	51.83	-3.17
FC176	S. porrigentiformis s. str.	4 <i>x</i>	Wales	18/07/11	T. C. G. Rich	51.84	-3.18
FC185	S. porrigentiformis s. str.	4 <i>x</i>	Wales	18/07/11	T. C. G. Rich	51.84	-3.18
FC188	S. porrigentiformis s. str.	4 <i>x</i>	Wales	18/07/11	T. C. G. Rich	51.84	-3.18
FC191	S. porrigentiformis s. str.	4 <i>x</i>	Wales	18/07/11	T. C. G. Rich	51.84	-3.18
FC192	S. porrigentiformis s. str.	4x	Wales	18/07/11	T. C. G. Rich	51.84	-3.18
FC194	S. porrigentiformis s. str.	4x	Wales	18/07/11	T. C. G. Rich	51.84	-3.19
FC207	S. porrigentiformis s. str.	4x	Wales	18/07/11	T. C. G. Rich	51.54	-3.26
FC212	S. porrigentiformis s. str.	4_X	Wales	18/07/11	T. C. G. Rich	51.80	-3.08
FC301	S. porrigentiformis s. str.	4x	Wales	28/08/11	T. C. G. Rich	51.83	-3.17

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