

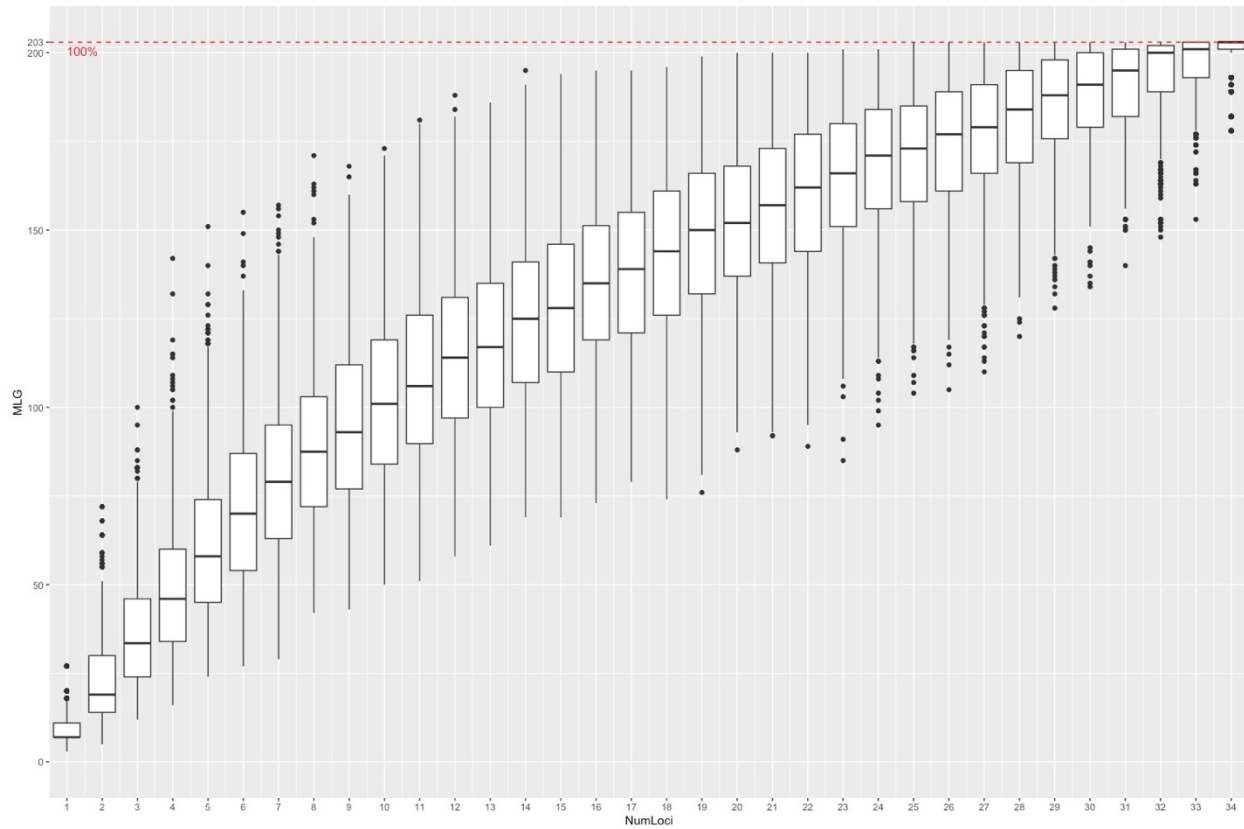
Supplementary Table 1. Clonal assignment by site and by five different genetic distance thresholds, with proportion distinguishable (*PD*) and *R* values calculated.

Site name (site code)	N	G0	G1	G2	G3	G4
<i>French Broad River - Mud Creek, Henderson County, NC</i>						
Ochlawaha (SF14)	5	5	4	4	2	1
		1.00	0.80	0.80	0.40	0.20
		1.00	0.75	0.75	0.25	0.00
Ochlawaha (SF16)	17	13	9	6	5	4
		0.76	0.53	0.35	0.29	0.24
		0.75	0.50	0.31	0.25	0.19
Ochlawaha (SF17)	24	11	4	2	2	1
		0.46	0.17	0.08	0.08	0.04
		0.43	0.13	0.04	0.04	0.00
<i>French Broad River - Bat Fork Creek, Henderson County, NC</i>						
Bat Fork (SF10)	24	11	3	2	1	1
		0.46	0.13	0.08	0.04	0.04
		0.43	0.09	0.04	0.00	0.00
Bat Fork (SF11)	22	21	11	7	4	3
		0.95	0.50	0.32	0.18	0.14
		0.95	0.48	0.29	0.14	0.10
Bat Fork (SF12)	4	4	2	1	1	1
		1.00	0.50	0.25	0.25	0.25
		1.00	0.33	0.00	0.00	0.00
Bat Fork (SF13)	4	3	2	1	1	1
		0.75	0.67	0.50	1.00	1.00
		0.67	0.33	0.00	0.00	0.00
<i>North Enoree River, Greenville County, SC</i>						
Belvue (SF05)	20	16	8	7	3	3
		0.80	0.40	0.35	0.15	0.15
		0.79	0.37	0.32	0.11	0.11
<i>Enoree River - mainstem, Greenville County, SC</i>						
Bunched Arrowhead (SF06)	21	14	6	4	3	2
		0.67	0.29	0.19	0.14	0.10
		0.65	0.25	0.15	0.10	0.05
Bunched Arrowhead (SF07)	24	18	4	3	1	1
		0.75	0.17	0.13	0.04	0.04

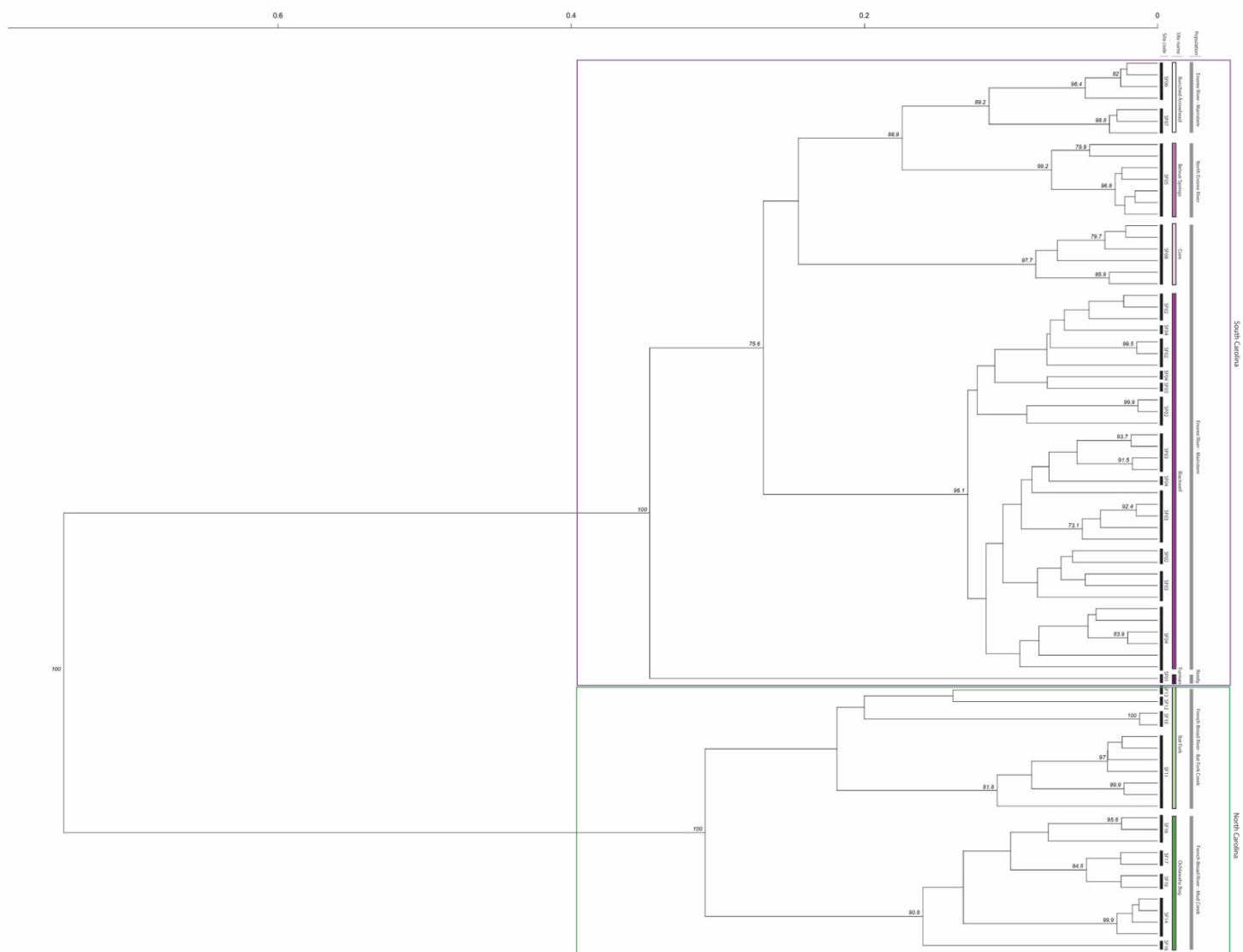
		0.74	0.13	0.09	0.00	0.00
Blackwell (SF03)	20	19	13	13	12	10
		0.95	0.65	0.65	0.60	0.50
		0.95	0.63	0.63	0.58	0.47
Blackwell (SF02)	23	20	12	11	10	8
		0.87	0.52	0.48	0.43	0.35
		0.86	0.50	0.45	0.41	0.32
Blackwell (SF04)	24	19	11	9	8	8
		0.79	0.46	0.38	0.33	0.33
		0.78	0.43	0.35	0.30	0.30
Core (SF08)	25	16	11	6	5	4
		0.64	0.44	0.24	0.20	0.16
		0.63	0.42	0.21	0.17	0.13
<i>Reedy River, Greenville County, SC</i>						
Furman (SF01)	24	13	2	1	1	1
		0.54	0.08	0.04	0.04	0.04
		0.52	0.04	0.00	0.00	0.00

Populations as defined by USFWS (2020) are presented in italics, with site names listed in subsequent rows. Site ID corresponds to unique element occurrences (EOs) with the exception of SF02 and SF03, which combined are recognized as a single EO by SCDNR. Sites are listed in geographic order, roughly north to south.

G0 = number of genets detected using a genetic distance threshold of 0; values for *PD* and *R* are provided below the number of genets for each colony. *G1* through *G4* provide alternative numbers of genets detected using genetic distance thresholds ranging from one to four, each followed by respective *PD* and *R* values.



Supplemental Figure 1. Genotype accumulation curve (GAC) for all individuals and loci sampled in the present study.



Supplemental Figure 2. UPGMA dendrogram of the clone corrected data for all unique genotypes of *Sagittaria fasciculata* genotyped for 35 GBS microsatellite loci. Values at nodes are bootstrap support. Populations are indicated by black lines, and names (as defined by USFWS (2020)) are provided; North ER = North Enoree River. North Carolina populations are labeled as such and indicated with a green line; South Carolina populations are indicated with a purple line.