animals

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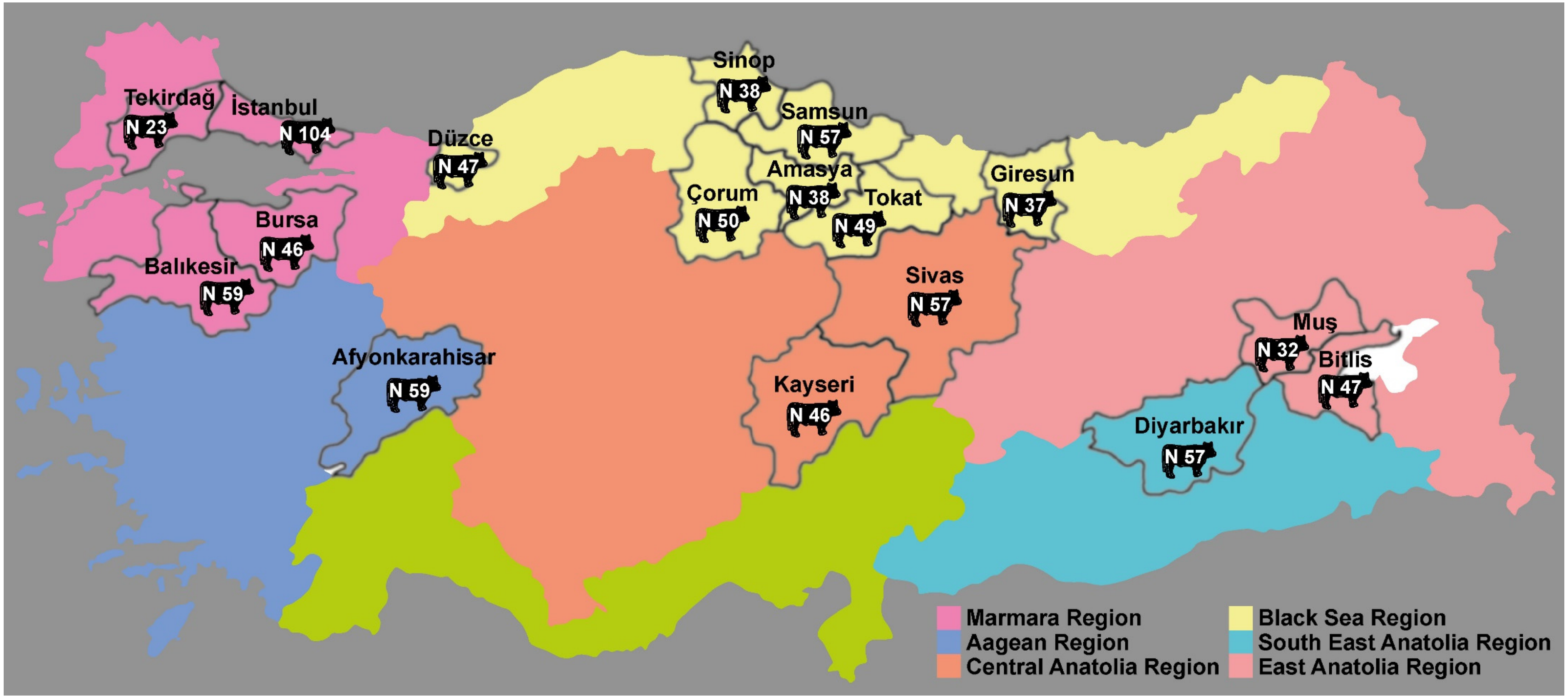

Supplementary Figure S1. Geographic distribution of the 17 Turkish water buffalo populations included in the study. n=number of samples from each province. MRM: Marmara Region, AER: Aagean Region, CAR: Central Anatolia Region, BSR: Black Sea Region, SAR: South East Anatolia Region, EAR: East Anatolia Region.

Supplementary Table S1. Information about the microsatellite loci used for genetic diversity analyses of Turkish water buffalo populations.

Name(s)	Chromosome[1]	Primer sequence (5' → 3') Forward / Reverse	Annealing Temperature (°C)	GenBank (Accession Number) or citation	Allele range (bp)	Multiplex Group (Dye)	Repetitive sequence	Allele range (bp)
CSSM061	8	AGGCCATATAGGAGGCAAGCTTAC TTCAGAAGAGGGCAGAGAATACAC	60	Barker et al.. 1997	100-126	1 (HEX)	-	99-125
CSSM033	17 (17)	CACTGTGAATGCATGTGTGTGAGC CCCATGATAAGAGTGCAGATGACT	65	U03805	154-175	1(FAM)	$(GT)_n$	151-171
ILSTS005	11 (10)	GGAAGCAATGAAATCTATAGCC TGTTCTGTGAGTTTGTAAGC	55	L23481	173-186	1(HEX)	$(TG)_n$	173-189
CSSM022	4q (5)	TCTCTCTAATGGAGTTGGTTTTTG ATATCCCACTGAGGATAAGAATTC	55-60	U03806	203-213	1(FAM)	$(CA)_n$	245-267
CSRM060	11 (10)	AAGATGTGATCCAAGAGAGAGGCA AGGACCAGATCGTGAAAGGCATAG	60	AF232758	95-135	2 (FAM)	$(AC)_n$	91-133
BRN	11 (10)	CCTCCACACAGGCTTCTCTGACTT CCTAACTTGCTTGAGTTATTGCCC	60	X59767	121-147	2 (HEX)	$(AC)_n$	121-147
ILSTS033	13 (12)	TATTAGAGTGGCTCAGTGCC ATGCAGACAGTTTTAGAGGG	55	L37213	126-138	2 (TAMRA)	$(AC)_{11}$	137-157
CSSM032	1q (1)	TTATTTTCAGTGTTTCTAGAAAAC TATAATATTGCTATCTGGAAATCC	55	U03811	208-224	2(FAM)	$(CA)_n$	235-265
CSSM045	2q (2)	TAGAGGCACAAGCAAACCTAACAC TTGGAAAGATGCAGTAGAACTCAT	60	U03830	102-122	3(HEX)	(CA)n	99-125
CSSM062	9	GTTTAAACCCCAGATTCTCCCTTG AGATGTAACAGCATCATGACTGAA	55	(Barker et al. 1997)	124-136	3(FAM)	-	113-131
ILSTS030	2q (2)	CTGCAGTTCTGCATATGTGG CTTAGACAACAGGGGTTTGG	55	L37212	146-158	3(HEX)	$(GT)_n$	153-169
BMC1013	3p (19)	AAAAATGATGCCAACCAAATT TAGGTAGTGTTCCTTATTTCTCTGG	54	G18560	217-239	3(FAM)	$(CA)_n$	292-314
CSSM057	9 (7)	GTCGCTGGATAAACAATTTAAAGT TGTGGTGTTTAACCCTTGTAATCT	60	U03840	102-130	4(FAM)	$(TG)_n$	106-128
CSSME070	3p (19)	TTCTAACAGCTGTCACTCAGGC ATACAGATTAAATACCCACCTG	50-55	AF303223	119-139	4(TAMRA)	$(AC)_n$	100-134
CSSM036	1p (27)	GGATAACTCAACCACACGTCTCTG AAGAAGTACTGGTTGCCAATCGTG	55	U03827	162-176	4(FAM)	$(TG)_n$	149-179
CSSM043	1p (27)	AAAACTCTGGGAACTTGAAAACTA GTTACAAATTTAAGAGACAGAGTT	55	U03824	222-258	4(HEX)	$(CA)_n(TC)_n$	173-215
ETH003	3p (19)	GAACCTGCCTCTCCTGCATTGG ACTCTGCCTGTGGCCAAGTAGG	65	Z22744	96-192	5(FAM)	$(GT)_n$ AC $(GT)_6$	105-169
CSSM047	3q (8)	TCTCTGTCTCTATCACTATATGGC CTGGGCACCTGAAACTATCATCAT	55	U03821	127-162	5(TAMRA)	$(TG)_n$	115-169
CSSM029	9 (7)	GCTCCATTATGCACATGCCATGCT CGTGAGAACCGAAAGTCACACATTC	55	U03807	174-196	5(FAM)	$(AC)_n$	161-185
ETH121	2q (2)	CCAACTCCTTACAGGAAATGTC ATTTAGAGCTGGCTGGTAAGTG	59	Z14037	182-198	5(HEX)	$(TG)_n$	181-209

[1] Cattle chromosome assignments in parentheses.

Supplementary Table S2. Genetic polymorphism parameters estimated for 20 microsatellite markers over all Turkish water buffalo populations.

Loci	TNA	N_a	Ne	Rs	PIC	I	N_m^*	F_{IS}^a	F_{ST}^a	F_{IT}^a	H_O	H_E	H_T	H_S	D_{ST}	G_{ST}	HWE	$F_{(null)}$	SR
CSSM061	9	7.71	5.23	7.73	0.787	1.86	7.23	0.028	0.023	0.050	0.77	0.81	0.81	0.79	0.018	0.023	***	0.101	109-125
CSSM033	7	4.88	1.80	4.35	0.412	0.91	6.88	0.129	0.028	0.154	0.38	0.44	0.44	0.43	0.010	0.023	***	0.075	151-171
ILSTS005	6	4.29	2.30	3.99	0.471	0.98	7.02	-0.089	0.023	-0.064	0.50	0.57	0.56	0.55	0.014	0.025	***	0.029	173-189
CSSM022	8	6.71	3.03	6.15	0.628	1.41	9.26	0.116	0.015	0.130	0.58	0.67	0.67	0.66	0.010	0.015	***	0.059	245-267
CSRM060	10	7.71	3.65	7.38	0.697	1.64	6.26	0.013	0.028	0.042	0.70	0.73	0.73	0.71	0.020	0.028	**	0.017	91-133
BRN	9	6.59	2.49	5.80	0.561	1.27	8.45	0.151	0.017	0.165	0.50	0.60	0.60	0.59	0.010	0.017	***	0.041	121-147
ILSTS033	7	5.94	2.84	5.31	0.612	1.33	9.38	0.089	0.015	0.103	0.59	0.65	0.66	0.65	0.010	0.015	***	0.075	137-157
CSSM032	8	6.18	1.80	5.64	0.429	1.02	4.18	0.249	0.048	0.286	0.33	0.45	0.46	0.44	0.020	0.044	***	0.151	235-265
CSSM045	13	10.88	8.41	11.44	0.869	2.32	4.68	0.221	0.045	0.257	0.67	0.88	0.88	0.85	0.034	0.038	***	0.099	99-125
CSSM062	10	7.77	5.66	7.53	0.800	1.88	5.55	0.178	0.037	0.209	0.66	0.82	0.82	0.79	0.025	0.031	***	0.091	113-131
ILSTS030	7	5.41	2.55	4.76	0.532	1.14	7.25	0.093	0.019	0.111	0.55	0.61	0.62	0.60	0.014	0.022	***	0.044	153-169
BMC1013	9	7.94	4.51	7.36	0.747	1.73	4.00	0.159	0.047	0.199	0.61	0.78	0.77	0.74	0.036	0.047	***	0.241	292-314
CSSM057	8	6.24	4.44	5.93	0.737	1.60	9.29	0.049	0.016	0.064	0.73	0.78	0.77	0.76	0.012	0.015	*	0.032	106-128
CSSME070	10	7.12	6.12	7.84	0.815	1.94	2.05	0.086	0.104	0.181	0.69	0.84	0.84	0.76	0.083	0.098	***	0.191	100-134
CSSM036	10	6.77	2.91	6.01	0.594	1.34	6.99	-0.085	0.024	-0.059	0.70	0.66	0.65	0.64	0.016	0.025	***	0.017	149-179
CSSM043	8	5.53	2.57	5.25	0.570	1.25	3.31	0.074	0.060	0.129	0.55	0.61	0.62	0.58	0.037	0.060	***	0.067	173-215
ETH003	17	12.59	5.13	12.08	0.789	2.17	8.07	0.217	0.019	0.231	0.61	0.81	0.80	0.79	0.014	0.017	***	0.089	105-169
CSSM047	14	11.18	7.74	10.88	0.859	2.26	7.87	0.091	0.021	0.110	0.78	0.87	0.87	0.86	0.017	0.020	***	0.077	115-169
CSSM029	10	5.82	2.17	4.52	0.461	1.01	26.87	-0.042	0.023	0.050	0.56	0.54	0.54	0.54	-0.001	-0.001	***	0.030	161-185
ETH121	10	8.29	4.16	7.54	0.731	1.72	8.48	0.042	0.020	0.061	0.72	0.76	0.76	0.75	0.014	0.018	***	0.027	181-209
Mean		7.28	3.98	6.87	0.655	1.54	5.85	0.091	0.031	0.119	0.61	0.69	0.69	0.67	0.021	0.030	-	-	-

TNA-Total number of alleles; Na-Mean number of alleles; Ne-Effective number of alleles; PIC-Polymorphic information content for each locus; F statistics (F_{IS}, F_{ST}, F_{IT}); H_O-Observed heterozygosity; H_E-Expected heterozygosity; H_T-Nei's gene diversity; Hs-Diversity within breeds; D_{ST}-diversity between breeds; G_{ST}-coefficient of gene differentiation; HWE-test for significant deviation from Hardy-Weinberg equilibrium with the hypothesis of the heterozygote excess; SR-Size range of the observed allele in bp. a Wright's statistics according to Weir and Cockerham (1984). $^*P < 0.05$; $^{**}P<0.01$, $^{***}p<0.001$, Nm* gene flow estimated from $Nm=0.25 (1-F_{ST}) / F_{ST}$ (Nei, 1987).

Supplementary Table S3. D_{AS} genetic distance

	IST	TEK	BAL	BUR	AFY	DUZ	GIR	AMS	TOK	COR	SIN	SAM	DYB	MUS	BIT	KAY	SVS
IST	0.0000																
TEK	0.0320	0.0000															
BAL	0.0406	0.0157	0.0000														
BUR	0.0899	0.0711	0.0520	0.0000													
AFY	0.0567	0.0424	0.0469	0.1095	0.0000												
DUZ	0.0257	0.0165	0.0478	0.1007	0.0584	0.0000											
GIR	0.1144	0.0686	0.0629	0.1256	0.0652	0.1058	0.0000										
AMS	0.1228	0.0896	0.0972	0.1505	0.0671	0.1184	0.0483	0.0000									
TOK	0.1242	0.0708	0.0997	0.1642	0.1038	0.1225	0.0776	0.0616	0.0000								
COR	0.1294	0.0956	0.1102	0.1650	0.0959	0.1352	0.0820	0.0594	0.0299	0.0000							
SIN	0.1118	0.0993	0.1022	0.1483	0.0849	0.1233	0.0713	0.0651	0.0520	0.0189	0.0000						
SAM	0.0618	0.0322	0.0594	0.0828	0.0588	0.0546	0.0813	0.0808	0.0648	0.0701	0.0611	0.0000					
DYB	0.0433	0.0165	0.0370	0.0880	0.0369	0.0387	0.0854	0.0904	0.0751	0.0738	0.0793	0.0179	0.0000				
MUS	0.0479	0.0233	0.0350	0.1122	0.0465	0.0497	0.0898	0.0891	0.0761	0.0893	0.1069	0.0474	0.0073	0.0000			
BIT	0.0464	0.0221	0.0474	0.1100	0.0550	0.0515	0.0898	0.0858	0.0777	0.0951	0.0944	0.0197	-0.00003	-0.0008	0.0000		
KAY	0.0526	0.0290	0.0586	0.0933	0.0582	0.0545	0.1061	0.1053	0.0951	0.1111	0.1099	0.0221	0.0041	0.0135	-0.0035	0.0000	
SVS	0.0463	0.0394	0.0509	0.0829	0.0725	0.0546	0.1133	0.1259	0.1073	0.1188	0.1229	0.0285	0.0159	0.0229	0.0126	-0.0021	0.0000

Supplementary Table S4. Reynold's genetic distance values.

	IST	TEK	BAL	BUR	AFY	DUZ	GIR	AMS	TOK	COR	SIN	SAM	DYB	MUS	BIT	KAY	SVS
IST	0																
TEK	0.0179	0															
BAL	0.0229	0.0085	0														
BUR	0.0565	0.0387	0.0295	0													
AFY	0.0331	0.0249	0.0255	0.0698	0												
DUZ	0.0133	0.0124	0.0291	0.0622	0.0318	0											
GIR	0.0609	0.0359	0.0317	0.0780	0.0378	0.0606	0										
AMS	0.0754	0.0508	0.0593	0.1021	0.0404	0.0713	0.0263	0									
TOK	0.0704	0.0422	0.0582	0.1096	0.0600	0.0707	0.0428	0.0312	0								
COR	0.0748	0.0557	0.0646	0.1108	0.0575	0.0790	0.0461	0.0320	0.0160	0							
SIN	0.0653	0.0599	0.0616	0.1022	0.0506	0.0728	0.0408	0.0365	0.0303	0.0115	0						
SAM	0.0318	0.0180	0.0328	0.0502	0.0333	0.0298	0.0450	0.0412	0.0397	0.0404	0.0380	0					
DYB	0.0166	0.0070	0.0156	0.0438	0.0168	0.0169	0.0386	0.0410	0.0370	0.0364	0.0390	0.0086	0				
MUS	0.0182	0.0090	0.0144	0.0575	0.0196	0.0218	0.0386	0.0383	0.0325	0.0412	0.0504	0.0215	0.0033	0			
BIT	0.0176	0.0102	0.0227	0.0556	0.0254	0.0220	0.0426	0.0382	0.0371	0.0475	0.0472	0.0093	0.0017	0.0015	0		
KAY	0.0208	0.0129	0.0269	0.0448	0.0258	0.0228	0.0497	0.0472	0.0453	0.0549	0.0540	0.0075	0.0024	0.0073	0.0006	0	
SVS	0.0177	0.0175	0.0225	0.0405	0.0326	0.0226	0.0526	0.0601	0.0536	0.0585	0.0610	0.0112	0.0063	0.0101	0.0065	-0.0001	0

Supplementary Table S5. The pairwise FST distance values between the studied 17 Turkish water buffalo populations

	IST	TEK	BAL	BUR	AFY	DUZ	GIR	AMS	TOK	COR	SIN	SAM	DYB	MUS	BIT	KAY	SVS
IST	-																
TEK	0.01567***	-															
BAL	0.01903***	0.00722^{NS}	-														
BUR	0.04832***	0.03866***	0.02857***	-													
AFY	0.02820***	0.02135***	0.02257***	0.06031***	-												
DUZ	0.01137***	0.00934^{NS}	0.02362***	0.05454***	0.02629***	-											
GIR	0.05215***	0.03183***	0.02779***	0.06735***	0.03243***	0.04934***	-										
AMS	0.05550***	0.03935***	0.04380***	0.07604***	0.03223***	0.05187***	0.02184***	-									
TOK	0.05801***	0.03411***	0.04633***	0.08589***	0.05134***	0.05583***	0.03766***	0.02761***	-								
COR	0.05830***	0.04485***	0.05080***	0.08662***	0.04793***	0.06096***	0.04148***	0.02836***	0.01366 ***	-							
SIN	0.05115***	0.04804***	0.04764***	0.07936***	0.04213***	0.05567***	0.03665***	0.03151***	0.02625***	0.00885^{NS}	-						
SAM	0.02667***	0.01608***	0.02715***	0.04232***	0.02870***	0.02409***	0.04132***	0.03730***	0.03525***	0.03549***	0.03240***	-					
DYB	0.01439***	0.00550^{NS}	0.01379***	0.04181***	0.01498***	0.01357***	0.03498***	0.03452***	0.03215***	0.03129***	0.03267***	0.00750^{NS}	-				
MUS	0.01661***	0.00737^{NS}	0.01300***	0.05452***	0.01709***	0.01781***	0.03471***	0.03129***	0.02729***	0.03467***	0.04227***	0.01899 ***	0.00212 ^{NS}	-			
BIT	0.01601***	0.00791^{NS}	0.01887***	0.05125***	0.02301***	0.01838***	0.03803***	0.03317***	0.03282***	0.04176***	0.04146***	0.00915 ^{NS}	0.00067^{NS}	0.00017^{NS}	-		
KAY	0.01798***	0.01087^{NS}	0.02300***	0.04317***	0.02297***	0.01903***	0.04413***	0.04001***	0.03942***	0.04739***	0.04670***	0.00736 ^{NS}	0.00130 ^{NS}	0.00585^{NS}	0.00036^{NS}	-	
SVS	0.01509***	0.01559***	0.01880***	0.03869***	0.02973***	0.01956***	0.04668***	0.04911***	0.04543***	0.04957***	0.05156***	0.01030***	0.00537 ^{NS}	0.00912^{NS}	0.0053^{NS}	0.00080^{NS}	-

*** Significant at $P < 0.001$.