

Supplementary Materials

Table S1: Reference list of used layers from Copernicus Land Monitoring Service © and maps created in ArcMap to form the landscape models for the analysis of *Bombina variegata* in the northern Weser Hills.

Landscape Category and Type	Source	Land Cover/ Land Use
<i>Forest</i> type, status map 2015, resolution 20x20 m, version 04	URL: https://land.copernicus.eu/pan-european/high-resolution-layers/forests/forest-type-1/status-maps/2015 [Download: 01.06.2020] Tile: E40N30	Forest free areas Broadleaf/ Coniferous forest
<i>Grassland</i> status map 2018, resolution 10x10 m, version 01	URL: https://land.copernicus.eu/pan-european/high-resolution-layers/grassland/status-maps/grassland-2018 [Download: 01.06.2020] Tile: E40N30	Grassland free areas Grassland
<i>Water & Wetness</i> status map 2018, resolution 10x10 m, version 011	URL: https://land.copernicus.eu/pan-european/high-resolution-layers/water-wetness/status-maps/water-wetness-2018 [Download: 01.06.2020] Tile: E40N30	Dry Permanent waterbody Temporary waterbody Permanent wet Temporary wet
<i>Imperviousness</i> density, status map 2018, resolution 10x10 m, version 020	URL: https://land.copernicus.eu/pan-european/high-resolution-layers/imperviousness/status-maps/imperviousness-density-2018 [Download: 01.06.2020] Tile: E40N30	Continuous raster ranging from 0 to 100 % imperviousness
<i>Agricultural Land</i> raster layer, resolution 10x10 m	ArcMap version 10.5.1 by ESRI © Basemap © Google Maps	Agricultural Land No Agricultural Land
<i>Motorway A2 and Underpasses</i> polygon, resolution 10x10 m,	ArcMap version 10.5.1 by ESRI © Basemap © Google Maps	Motorway A2 Underpasses

Table S2: Summary statistics for the used microsatellite markers (loci), averaged across all study sites. Number of detected alleles, expected heterozygosity ("He"), observed heterozygosity ("Ho"), size range of each loci in base pairs, allelic richness of each loci and confidence interval ("CI"). "Tetra" and "di" refers to the number of repeats (tetranucleotide or dinucleotide). 10 loci in 440 *Bombina variegata* individuals analysed.

Loci	n alleles	He	Ho	Size range (bp)	Allelic richness
1A (tetra)	5	0.11	0.12	320 – 360	1.17
F2 (di)	23	0.85	0.19	407 – 527	2.77
5F (tetra)	14	0.56	0.4	88 – 164	2.1
8A (tetra)	13	0.79	0.63	203 – 336	2.46
9H (tetra)	13	0.7	0.58	142 – 206	2.17
10F (tetra)	9	0.69	0.64	181 – 227	2.21
12F (tetra)	9	0.63	0.6	164 – 236	2.13
B14 (di)	11	0.61	0.50	116 – 200	2.09
F22 (di)	9	0.09	0.06	132 – 152	1.19
B13 (di)	17	0.39	0.22	93 – 149	1.83
Mean (95 % CI)	12.3 (0.39 – 0.7)	0.54 (0.26 – 0.53)	0.39	x	2.01 (1.72 – 2.31)

Table S4: Matrix of pairwise genetic (F_{ST} values; lower triangle) and geographic distance (km; upper triangle) among *Bombina variegata* populations in the northern Weser Hills. Divided by clusters. Fuchsloch ("FL"), Edler/Brinkmeyer ("BM"), Bokshorn ("BH"), Wülpker Egge ("WE"), Messingsberg ("MB"), Schlingmühle ("SM"), Bernsen ("BE"), Liekwegen ("LI"), Waldwiese ("WW"), JBF-Wiese ("JW"), Borstel ("BO"), Rohden ("RO"), Nato-Station ("NS"), Segelhorst ("SH") and Pötzen ("PA"). * = $n < 10$. † = reintroduced populations.

Cluster	G1						G2						G3			G4
Population	FL	MB	SM	WW	BO	NS	WE†	BE†	LI	JW*	RO**	SH**	BM	BH*	PA	
G1	FL	-	20.1	29.2	24.2	23.7	28.8	20.7	21.9	24.3	24.1	27.6	31.2	8.1	10.5	38
	MB	0.09	-	18.3	7.3	4.5	10.5	20.3	1.8	8.7	6.3	7.5	11.1	12.8	11.4	18.2
	SM	0.14	0.07	-	11.5	15.2	12.2	12.4	18.2	9.9	12.9	18.8	19.8	25.9	26.1	26.7
	WW	0.09	0.08	0.09	-	3.7	4.7	17	6.8	1.7	1.4	8	10.2	18.3	17.5	18
	BO	0.12	0.1	0.02	0.07	-	6	19.8	3.4	5.4	2.3	5.1	8.1	17	15.7	15.9
	NS	0.09	0.07	0.06	0.05	0.04	-	20.5	9.3	5.2	4.7	7.1	7.6	22.6	21.5	14.8
G2	WE†	0.19	0.12	0.05	0.12	0.05	0.06	-	21.3	15.7	18.2	24.8	27.2	20.9	22.2	35
	BE†	0.14	0.09	0.02	0.11	0.06	0.04	0.06	-	8.4	5.6	5.7	9.3	14.6	13	16.4
	LI	0.07	0.07	0.03	0.05	0.02	0.03	0.04	0.03	-	3.1	9.6	11.6	18.9	18.3	19.3
	JW*	0.20	0.13	0.07	0.09	0.06	0.05	0.03	0.05	0.03	-	6.7	9.2	17.9	16.9	17
	RO**	0.19	0.14	0.04	0.1	0.03	0.03	0.01	0.04	0.01	0.01	-	3.6	20.2	18.5	10.9
	SH**	0.22	0.19	0.08	0.12	0.04	0.1	0.08	0.07	0.03	0.05	0.03	-	23.8	22	7.8
G3	BM	0.21	0.17	0.13	0.12	0.07	0.09	0.04	0.14	0.09	0.09	0.07	0.1	-	2.5	30.2
	BH*	0.32	0.2	0.17	0.15	0.16	0.1	0.08	0.15	0.13	0.13	0.17	0.22	0.08	-	28.2
G4	PA	0.27	0.18	0.23	0.22	0.19	0.19	0.19	0.23	0.17	0.23	0.22	0.26	0.18	0.22	-

Table S5: Mean migration rate (“ $m[i,j]$ ”), the fraction of individuals in population “ i ” that are migrants derived from population “ j ” (per generation) conducted with BayesAss3. Self-migration is marked grey, the 5 % highest migration rates are in green, the lowest 5 % in pink (self-migration was excluded). Fuchsloch (“FL”), Edler/Brinkmeyer (“BM”), Bokshorn (“BH”), Wülpker Egge (“WE”), Messingsberg (“MB”), Schlingmühle (“SM”), Bernsen (“BE”), Liekwegen (“LI”), Waldwiese (“WW”), JBF-Wiese (“JW”), Borstel (“BO”), Rohden (“RO”), Nato-Station (“NS”), Segelhorst (“SH”) and Pötzen (“PA”). * = $n < 10$. † = reintroduced populations.

Populations [i]	Populations [j]															
	FL	BM	BH*	WE†	MB	SM	BE†	LI	WW	JW*	BO	RO*†	NS	SH*†	PA	
FL	0.679	0.012	0.013	0.013	0.054	0.012	0.013	0.014	0.012	0.012	0.113	0.012	0.016	0.013	0.014	
BM	0.003	0.947	0.003	0.003	0.004	0.003	0.003	0.006	0.003	0.004	0.005	0.003	0.005	0.003	0.004	
BH*	0.018	0.066	0.684	0.018	0.017	0.018	0.017	0.02	0.017	0.018	0.018	0.017	0.036	0.018	0.018	
WE†	0.012	0.07	0.012	0.678	0.014	0.012	0.012	0.084	0.012	0.012	0.031	0.012	0.018	0.012	0.012	
MB	0.005	0.007	0.005	0.006	0.904	0.005	0.005	0.01	0.005	0.005	0.015	0.006	0.009	0.005	0.006	
SM	0.013	0.014	0.014	0.013	0.04	0.68	0.014	0.053	0.013	0.014	0.073	0.013	0.02	0.013	0.014	
BE†	0.007	0.01	0.007	0.007	0.013	0.007	0.677	0.153	0.007	0.007	0.014	0.007	0.068	0.007	0.007	
LI	0.003	0.009	0.009	0.003	0.076	0.003	0.003	0.842	0.003	0.003	0.013	0.003	0.033	0.003	0.003	
WW	0.012	0.033	0.012	0.012	0.016	0.012	0.012	0.014	0.679	0.012	0.056	0.012	0.092	0.012	0.012	
JW*	0.015	0.016	0.015	0.015	0.019	0.015	0.015	0.06	0.015	0.682	0.016	0.015	0.071	0.015	0.015	
BO	0.01	0.032	0.01	0.011	0.017	0.01	0.01	0.057	0.01	0.01	0.717	0.01	0.074	0.011	0.011	
RO**†	0.019	0.021	0.02	0.02	0.02	0.019	0.02	0.048	0.02	0.02	0.021	0.686	0.029	0.02	0.019	
NS	0.008	0.033	0.009	0.009	0.015	0.009	0.008	0.024	0.008	0.009	0.037	0.009	0.805	0.008	0.009	
SH**†	0.016	0.018	0.016	0.016	0.016	0.016	0.016	0.104	0.016	0.016	0.016	0.016	0.021	0.683	0.016	
PA	0.005	0.005	0.004	0.004	0.005	0.005	0.004	0.005	0.004	0.004	0.005	0.004	0.005	0.004	0.937	