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Supplementary material

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1 Supplementary material Appendix 1

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Remarkably similar migration patterns between different red-backed shrike
populations suggest that migration rather than breeding area phenology
determines the annual cycle

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7 Geolocator deployment and retrieval

We used light-level geolocators (Mk10s, Mk10 and Mk12 developed by the British Antarctic 8 9 Survey, BAS, weight: 1.1g and P65 from Migrate Technology, weight: 0.75g) to determine geographical locations of staging sites and timing of arrival and departure events of individual red-10 backed shrikes throughout the annual cycle. During eight years (2009 - 2016) a total of 402 11 individual red-backed shrikes were caught at six breeding populations across a wide latitudinal and 12 longitudinal span of the breeding range of red-backed shrikes using spring-traps or mist-nets in 13 14 close proximity to the nesting sites (table 1). 15 A total of 59 birds returned to the breeding site in Gribskov (39, return rate 24%), Spain (11, return 16 rate 18%), the Netherlands (5, return rate 25%) and Greece (4, return rate 22%). These return rates correspond to a control group of red-backed shrikes marked with colour rings at the main study- and 17 breeding site Gribskov in Denmark 2016-2017 (15, return rate 27%). Return rates could not be 18 assessed with any certainty for the Swedish and Russian breeding sites due to inconsistent search 19 efforts between years. As some individuals had lost their geolocator and other loggers had failed, 20 we present a total of 48 tracks of 39 individual red-backed shrikes (table 1). Nine of these are 21 repeated tracks; seven males from the southern Scandinavian breeding population and two males 22 from the Spanish breeding population. 23

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25 Light data analyses

Tracking data from the southern Scandinavian and Spanish breeding populations have been 26 analysed before and published with a different purpose (Tøttrup et al. 2012b, a, 2017, Pedersen et 27 al. 2016, 2018). Data were adjusted for clock drift, and false twilight events caused by shading were 28 29 removed by visual inspection of a plot comparing the specific twilight with the twilight on the previous and following day using the R-package BAStag version 0.1-3 (Wotherspoon et al. 2016). 30 We chose a threshold value of 2 for BAS geolocators and 0.3 for log-transformed data for the 31 32 Intigeo geolocators, corresponding to the sun being well below the horizon, to define twilight occurrences. Between 0 and 50 false twilight events were removed from the data for each track 33 34 (Supplementary material Appendix table A1). The occurrence of false twilights seemed to be roughly evenly distributed across the year. As breeding site habitat varied between populations, we 35 used a Hill-Ekstrom calibration to ensure consistency among tracks (Hill and Braun 2001, Ekstrom 36 37 2004). Sun elevation angles varied from -5.5 - 0 (Supplementary material Appendix table A1). Two daily positions were estimated from day length and local noon and midnight, respectively, using the 38 R-package *GeoLight* version 2.0 (Lisovski and Hahn 2012). During equinoxes, where day length is 39 approximately the same, estimation of latitude becomes unreliable. Thus, we excluded latitudinal 40 data from 14 to 26 days on both sides of equinox for each individual track based on visual 41 42 inspection of a plot of latitude against time (Supplementary material Appendix table A1)

- 44 Summary information on geolocators and data cleaning for each individual using the R package *BAStag* version 0.1-3
- 45 (Wotherspoon et al. 2016). Removed false twilights for each individual were roughly equally distributed throughout the
- 46 annual cycle. Sun elevation angles are based on Hill-Ekström calibration. Tolerance determines the number of days
- 47 excluded during equinox periods (Lisovski and Hahn 2012).

Logger ID	Population	Sex	Logger type	Storing time (mins)	Threshold	False sunrises	False sunsets	Total false twilights removed	Sun elevation angle	Tolerance
48.1	southern Scandinavia	male	BAS mk10, no stalk, 1.1g	2	2	14	20	34	-3.5	0.1
48.2	southern Scandinavia	male	BAS mk10, no stalk, 1.1g	2	2	. 6	3	9	-3.5	0.13
28	southern Scandinavia	male	BAS mk10, no stalk, 1.1g	2	2	25	21	46	-1	0.1
20156	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	2 7	10	17	-	-
20157	southern Scandinavia	female	BAS mk10s, stalk, 1.1g	10	2	5	8	13	-5	0.1
20200	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	5	6	11	-5	0.1
20216	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	12	21	33	-4.5	0.11
20204	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	4	15	19	-5	0.11
20268	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	6	4	10	-5	0.17
20263	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	32	18	50	-5	0.11
20231	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	-	-	-	-	-
13802	southern Scandinavia	male	BAS mk12, 8 mm stalk, 1.1g	2	2	9	11	20	-3.5	0.13
20264	southern Scandinavia	female	BAS mk10s, stalk, 1.1g	10	2	11	16	27	-5	0.12
20252	southern Scandinavia	female	BAS mk10s, stalk, 1.1g	10	2	30	13	43	-5.5	0.14
20257	southern Scandinavia	male	BAS mk10s, stalk, 1.1g	10	2	12	11	23	-5	0.12
13813	southern Scandinavia	male	BAS mk12, 8 mm stalk, 1.1g	2	2	13	11	24	-1.5	0.14
229	southern Scandinavia	female	BAS mk12, 8 mm stalk, 1.1g	2	2	11	2	13	-2	0.13
212	southern Scandinavia	male	BAS mk12, 8 mm stalk, 1.1g	2	2	! 10	7	17	-2	0.13
211	southern Scandinavia	female	BAS mk12, 8 mm stalk, 1.1g	2	2	2 7	12	19	-3	0.12
70	southern Scandinavia	female	BAS mk10, stalk, 1.1g	5	2	15	18	33	-2.5	0.1
19	southern Scandinavia	male	BAS mk10, stalk, 1.1g	5	2	21	18	39	-2.5	0.13
14	southern Scandinavia	male	BAS mk10, stalk, 1.1g	5	2	20	19	39	-2	0.11
504	southern Scandinavia	male	BAS mk10, no stalk, 1.1g	2	2	. 8	5	13	-1	0.12
35	southern Scandinavia	male	BAS mk10, no stalk, 1.1g	2	2	13	21	34	-1	0.12
F121	southern Scandinavia	male	Intigeo P65, no stalk, 0.75g	5	0.3	0	4	4	-2	0.13
F123	southern Scandinavia	female	Intigeo P65, no stalk, 0.75g	5	0.3	1	5	6	-3	0.13
F941	southern Scandinavia	female	Intigeo P65, no stalk, 0.75g	5	0.3	4	8	12	-1	0.1
M014	southern Scandinavia	male	Intigeo P65, no stalk, 0.75g	5	0.3	2	6	8	-4	0.12
M034	southern Scandinavia	male	Intigeo P65, no stalk, 0.75g	5	0.3	3	12	15	-4.5	0.15
M021.1	southern Scandinavia	male	Intigeo P65, no stalk, 0.75g	5	0.3	2	1	3	-5	0.13
M021.2	southern Scandinavia	male	Intigeo P65, no stalk, 0.75g	5	0.3	0	0	0	-5	0.13
38	Spain	male	BAS mk10, stalk, 1.1g	5	2	22	27	49	-2.5	0.1
45	Spain	male	BAS mk10, stalk, 1.1g	5	2	9	18	27	-3.5	0.1
59	Spain	male	BAS mk10, no stalk, 1.1g	2	2	20	36	56	-1.5	0.11
47.1	Spain	male	BAS mk10, stalk, 1.1g	5	2	13	20	33	-3	0.11
47.2	Spain	male	BAS mk10, stalk, 1.1g	5	2	! 10	8	18	-1.5	0.1
F139	Spain	female	Intigeo P65, no stalk, 0.75g	5	0.3	9	10	19	-4	0.13
F647	Spain	female	Intigeo P65, no stalk, 0.75g	5	0.3	4	7	11	-4	0.13
F649	Spain	male	Intigeo P65, no stalk, 0.75g	5	0.3	2	4	6	-3.5	0.15
Mk5520_3	Netherlands	male	BAS mk10s, stalk, 1.1g	2	2	2 12	11	23	-2	0.1
MK5520_5	Netherlands	female	BAS mk10s, stalk, 1.1g	2	2	22	35	57	0	0.1
Mk10_21670	Netherlands	female	BAS mk10, no stalk, 1.0g	5	2	16	6	22	-3	0.1
F126	Greece	male	Intigeo P65, no stalk, 0.75g	5	0.3	12	4	16	-4	0.13
F146	Greece	female	Intigeo P65, no stalk, 0.75q	5	0.3	9	13	22	-1	0.15
F152	Greece	male	Intigeo P65, no stalk, 0.75q	5	0.3	16	14	30	-1	0.12
F953	mid Scandinavia	male	Intigeo P65, no stalk, 0.75g	5	0.3	11	14	25	-2.5	0.1
F955	mid Scandinavia	male	Intigeo P65, no stalk, 0.75g	5	0.3	11	5	16	-3	0.13
BA128	Russia	male	Intigeo P65, no stalk, 0.75g	5	0.3	10	9	19	-3	0.13

50 Model specification of each of the four models applied. For definitions of event, site and segment, please see Table A3.

Model no	Model specification
Model 1	Migratory schedule ~ population + event + (population x event) + (11id) + (11year)
Model 2	Longitude \sim population + site + (population x site) + (11id) + (11year)
Model 3	Latitude \sim population + site + (population x site) + (11id) + (11year)
Model 4	log(travel speed) ~ population + segment + (population x segment) + (11id) + (11year)

52 Table A3

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53 Number of tracks and individuals (n) available at each event, site (longitude/latitude) and segment of migration for the

54 southern Scandinavian and Spanish population, respectively.

	No of tracks / (n) sScand Spain		
Event			
Breeding area departure	31 (24)	8 (6)	
Mediterranean arrival	31 (24)	8 (6)	
Mediterranean departure	29 (23)	8 (6)	
Sahel arrival	29 (23)	8 (6)	
Sahel departure	30 (24)	8 (6)	
Southern Africa arrival	30 (24)	8 (6)	
Southern Africa departure	30 (24)	8 (6)	
Eastern Africa arrival	28 (23)	8 (6)	
Eastern Africa departure	28 (23)	8 (6)	
Breeding site arrival	23 (21)	7 (6)	
Longitude			
Mediterranean	29 (22)	8 (6)	
Sahel	28 (22)	8 (6)	
Southern Africa	28 (22)	8 (6)	
Eastern Africa	27 (22)	8 (6)	
Latitude			
Mediterranean	28 (22)	8 (6)	
Sahel	27 (21)	8 (6)	
Southern Africa	28 (22)	8 (6)	
Eastern Africa	26 (21)	8 (6)	
Segment			
Breeding area - Mediterranean	28 (22)	8 (6)	
Mediterranean - Sahel	26 (21)	8 (6)	
Sahel - southern Africa	27 (21)	8 (6)	
Southern Africa - eastern Africa	26 (21)	8 (6)	
Eastern Africa - breeding area	20 (18)	6 (5)	

56 Model-based estimates of expected migration schedules (days since 1 July) of the southern Scandinavian and Spanish

57 population and the event-wise differences between populations (timing of Spanish population subtracted from timing of

58 the southern Scandinavian population) with corresponding standard errors (SE)^{*}. P-values are for the tests comparing

59 the expected timing of the two populations at each event throughout the annual cycle.

Event	sScand	Spain	sScand - Spain	P _{adj}
	Estimate (SE = 2.8)	Estimate (SE = 4.3)	Difference (SE = 4.3)	
Autumn migration				
Breeding area departure	38.5	38.1	0.4	1
Southern Europe arrival	47.2	50.1	-2.9	1
Southern Europe departure	63.9	63.5	0.4	1
Sahel arrival	72.5	72.1	0.4	1
Sahel departure	126.0	117.7	8.2	0.6
Southern Africa arrival	143.2	144.9	-1.7	1
Spring migration				
Southern Africa departure	267.0	272.5	-5.4	1
Eastern Africa arrival	286.3	290.1	-3.9	1
Eastern Africa departure	297.4	298.9	-1.5	1
Breeding area arrival	327.3	329.7	-2.4	1

60 *Estimated standard deviations of the random intercepts in the model were 6.81 for id and 5.25 for year, while residual standard

deviation was 5.91.

63 Model-based estimates of expected longitude and latitude of the southern Scandinavian and Spanish population at each

64 staging site throughout the annual cycle and site-wise differences between the populations (longitude/latitude of

65 Spanish population subtracted from longitude/latitude of the southern Scandinavian population) with corresponding

standard errors (SE)*. P-values are for the tests comparing the expected timing of the two populations at each site

67 throughout the annual cycle.

Site	sScand	Spain	sScand - Spain	P adj.
	Estimate (SE = 0.6)	Estimate (SE = 1.1)	Difference (SE = 1.3)	
Longitude				
Mediterranean	22.48	21.43	1.1	0.6
Sahel	26.84	25.49	1.4	0.6
Southern Africa	20.60	32.39	-11.8	<0.001
Eastern Africa	39.82	41.67	-1.8	0.4
	Estimate (SE = 0.9)	Estimate (SE = 1.7)	Difference (SE = 2.0)	
Latitude				
Mediterranean	44.19	41.35	2.8	0.3
Sahel	9.42	7.69	1.7	0.4
Southern Africa	-21.53	-15.44	-6.1	0.01
Eastern Africa	-1.51	2.44	-3.9	0.1
* Estimated standard	deviations of the random	intercepts in the model for	r longitude were 7.02 for id a	and 3.40 fc

69 standard deviation was 3.01. In the model for latitude they were 6.62 for id and 0.33 for year, while residual standard deviation was

70 4.82.

68

Model-based estimates of expected travel log-speed (natural logarithm; km d⁻¹) of the southern Scandinavian and Spanish population and segment-wise differences between populations (log-speed of Spanish population subtracted from log-speed of the southern Scandinavian population) with corresponding standard error (SE)^{*}. P-values are for tests comparing the expected speed at each migratory segment throughout the annual cycle.

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Segment	sScand	Spain	sScand - Spain	P _{adj.}
	Estimate (SE = 0.1)	Estimate (SE = 0.2)	Difference (SE = 0.2)	
Autumn migration				
Breeding area – Mediterranean	5.3	5.3	0	1
Mediterranean - Sahel	6.2	6.1	0.1	1
Sahel – southern Africa	5.4	4.7	0.7	< 0.001
Spring migration				
Southern Africa – eastern Africa	5.1	5.0	0.1	1
eastern Africa - Breeding area	5.5	5.5	-0.1	1

*Estimated standard deviation of the random intercept for year was 0.08, while residual standard deviation was 0.43. As the standard deviation of the random intercept of individual was estimated to 0, the model was refitted without this random intercept.



Figure A1

Seasonal development of NDVI at the local breeding sites averaged over a 15-year period (2001-2015). Annual variation is shown as 95 percent confidence intervals at each time stamp. Colours depict different breeding populations (dark blue: Denmark, orange: Spain, khaki: The Netherlands, red: Greece, green: mid Scandinavia and light blue: Russia).



Figure A2

Mean longitude of the main non-breeding area in southern Africa in response to breeding area latitude. Colours depict different breeding populations (dark blue: southern Scandinavia, orange: Spain, khaki: The Netherlands, red: Greece, green: mid Scandinavia and light blue: Russia).



Figure A3

Distance (A) and duration (B) of main travel segments throughout the annual cycle. Colours depict different breeding populations (dark blue: southern Scandinavia, orange: Spain, khaki: The Netherlands, red: Greece, green: mid Scandinavia and light blue: Russia). Boxes indicate median values with 25 and 75 percentiles. Whiskers represent 5 and 95 percentiles while dots indicate extreme values.