

## Supplementary File 1:

**Table S1:** The accessions number of sequences of *An. stephensi* that are currently available in the GenBank and were included in the analysis and comparing of our sequences.

### India:

DQ154166.1	AY729980.1	DQ310143.1	DQ310148.1	DQ317594.1	MG571266.1
MH512893.1	MH538702.1	MH538703.1	MH538704.1	MH538705.1	MK265738.1
MK265740.1	MK265741.1	MK265742.1	MK265743.1	MK265744.1	MK704465.1
MK726121.1	LR736010.1	LR736014.1	LR736013.1	LR736015.1	MN329060.1
MN660044.1	MT899149.1	MW549046.1			

### Pakistan:

KF406680.1	KF406682.1	KF406683.1	KF406684.1	KF406685.1	KF406686.1
KF406687.1	KF406688.1	KF406689.1	KF406690.1	KF406691.1	KF406692.1
KF406693.1	KF406694.1	KF406695.1	KF406696.1	KF406697.1	KF406698.1
KF406699.1	KF406700.1	KF406701.1	KF406702.1	KF406703.1	KF406704.1
KF406705.1	KF406706.1	KF406707.1	KF406708.1	KJ528895.1	

### Sri Lanka:

MF124608.1	MF124609.1	MF124610.1	MF124611.1	MF975722.1	MF975723.1
MF975724.1	MF975725.1	MF975726.1	MF975727.1	MF975728.1	MF975729.1
MF975730.1	MF975731.1	MG970564.1	MG970566.1	MG970565.1	MG970567.1

### Saudi Arabia:

KJ528887.1	KJ528888.1	KJ528889.1	KJ528890.1	KJ528891.1	KJ528892.1
KJ528893.1	KJ528894.1				

### Sudan:

MW197099.1	MW197100.1	MW197101.1
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### Iran:

FJ210893.1	FJ210894.1
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### Djibouti:

KF933378.1
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### Ethiopia:

MH651000.1
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### United Arab Emirates:

MK170098.1
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**Supplementary File 2.**

**Table S2:** P values of the pairwise Fst test was computed to estimate the degree of gene flow among the different populations.

	<b>North Darfur</b>	<b>River Nile</b>	<b>Khartoum</b>	<b>Red Sea</b>	<b>Kassala</b>	<b>Al Gedarif</b>	<b>India</b>	<b>Iran</b>	<b>Pakistan</b>	<b>Saudi Arabia</b>	<b>Sri Lanka</b>
<b>River Nile</b>	0.008	-	-	-	-	-	-	-	-	-	-
<b>Khartoum</b>	0.007	0.006	-	-	-	-	-	-	-	-	-
<b>Red_Sea</b>	0.010	0.006	0.007	-	-	-	-	-	-	-	-
<b>Kassala</b>	0.010	0.006	0.007	0.003	-	-	-	-	-	-	-
<b>Al Gedarif</b>	0.011	0.007	0.008	0.004	0.005	-	-	-	-	-	-
<b>India</b>	0.010	0.005	0.007	0.002	0.002	0.004	-	-	-	-	-
<b>Iran</b>	0.012	0.007	0.009	0.004	0.005	0.006	0.003	-	-	-	-
<b>Pakistan</b>	0.009	0.005	0.007	0.002	0.002	0.003	0.001	0.003	-	-	-
<b>Saudi Arabia</b>	0.016	0.013	0.013	0.012	0.011	0.010	0.012	0.015	0.012	-	-
<b>Sri Lanka</b>	0.010	0.005	0.007	0.002	0.003	0.004	0.001	0.004	0.001	0.013	-
<b>Sudan</b>	0.009	0.005	0.005	0.003	0.003	0.004	0.002	0.005	0.002	0.011	0.003

**Supplementary File 3:****Table S3:** Pairwise fixation index (Fst values) between *An. stephensi* populations calculated from the nucleotide data set of the mitochondrial cytochrome c oxidase subunit 1 (cox1) gene.

<b>Populations*</b>	<b>India</b>	<b>Iran</b>	<b>Pakistan</b>	<b>Saudi Arabia</b>	<b>Sri Lanka</b>
<b>Iran</b>	0.876	-	-	-	-
<b>Pakistan</b>	0.023	0.906	-	-	-
<b>Saudi Arabia</b>	0.879	0.927	0.885	-	-
<b>Sri Lanka</b>	0.126	0.824	0.224	0.863	-
<b>Sudan</b>	0.067	0.593	0.071	0.729	0.104

\*All sequences representing Sudan were included in Sudan population. Populations consisted of one sequence were not included in the comparison.

**Supplementary File 4:**

**Table S4:** The distribution of the detected haplotypes among the different study sites compared to the previously published *An. stephensi* cytochrome c oxidase 1 (CO1) sequences.

Populations	Hap 01	Hap 02	Hap 03	Hap 04	Hap 05	Hap 06	Hap 07	Hap 08	Hap 09	Hap 10	Hap 11	Hap 12	Hap 13	Hap 14	Hap 15	Hap 16	Hap 17	Hap 18	Hap 19
North Darfur	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0
River Nile	3	0	0	3	0	0	0	0	0	0	0	1	2	0	0	0	1	1	0
Khartoum	1	0	0	1	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0
Red Sea	124	24	7	10	5	5	8	1	1	1	1	0	0	0	0	0	0	0	0
Kassala	60	8	6	6	4	2	3	1	1	2	1	0	0	0	0	0	0	0	0
Gezira	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gedarif	56	6	12	2	3	4	2	3	3	2	3	0	0	0	0	0	0	0	0
Pakistan	26	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Djibouti	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sri Lanka	12	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
India	23	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sudan*	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UAE	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ethiopia	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saudi Arabia	0	0	5	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0
Iran	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0

**Hap:** haplotype, **UAE:** United Arab Emirates. **Sudan\*:** indicates previously published sequences from Sudan.