

Table S2: Divergence rate (%) of the *wsp* marker between the 14 *Wolbachia* strains and strain variants characterized from *Bicyclus* butterfly species (as characterized in this study and by (Duplouy and Brattstrom 2018)). A-supergroup strains are shown in pink, B-*Wolbachia* in blue. All variants share the same color. Inside cell colors vary and in accordance with degree of similarity (white: less than 75% similarity, gray: between 75 & 97% similarity, dark-gray: more than 97% similarity).

Infected species (N)	id	Divergence (%)												
		13	14	15	3	4	6	16	17	18	19	29	21	22
<i>B. mandanes</i> (1)	12: wBman_A wBcol_A	99,7	99,8	78,0	72,8	72,8	72,8	72,7	72,8	72,6	72,5	72,8	74,4	72,0
<i>B. collinsi</i> (1)		-	99,8	78,0	72,9	72,8	72,9	72,7	72,8	72,7	72,6	72,9	74,7	71,8
<i>B. auricruda</i> (2)	13: wBaur_A wBaur2_A	-	99,8	78,0	72,9	72,8	72,9	72,7	72,8	72,7	72,6	72,9	74,7	71,8
<i>B. xeneas</i> <i>occidentalis</i> (2)		14: wBxen_A wBign_A		-	78,2	73,1	72,9	73,1	72,8	73,0	72,9	72,8	73,1	74,7
<i>B. ignobilis</i> (3)	wBxen2_A													
<i>B. evadne</i> (1)	15: wBeva_A			-	77,0	77,2	77,4	77,2	77,5	77,2	77,2	77,4	76,7	73,8
<i>B. sangmelinae</i>	3: wBsang_B wBeph_B wBfun_B				-	98,3	99,1	99,1	98,9	98,8	98,9	99,1	79,1	81,8
<i>B. funebris</i>														
<i>B. ephorus</i>														
<i>B. pavonis</i>	4: wBpav_B					-	99,2	99,1	99,3	98,9	99,0	98,8	77,9	82,1
<i>B. xeneas xeneas</i>	6: wBxen_B						-	99,6	99,8	99,6	99,8	99,6	78,8	80,8

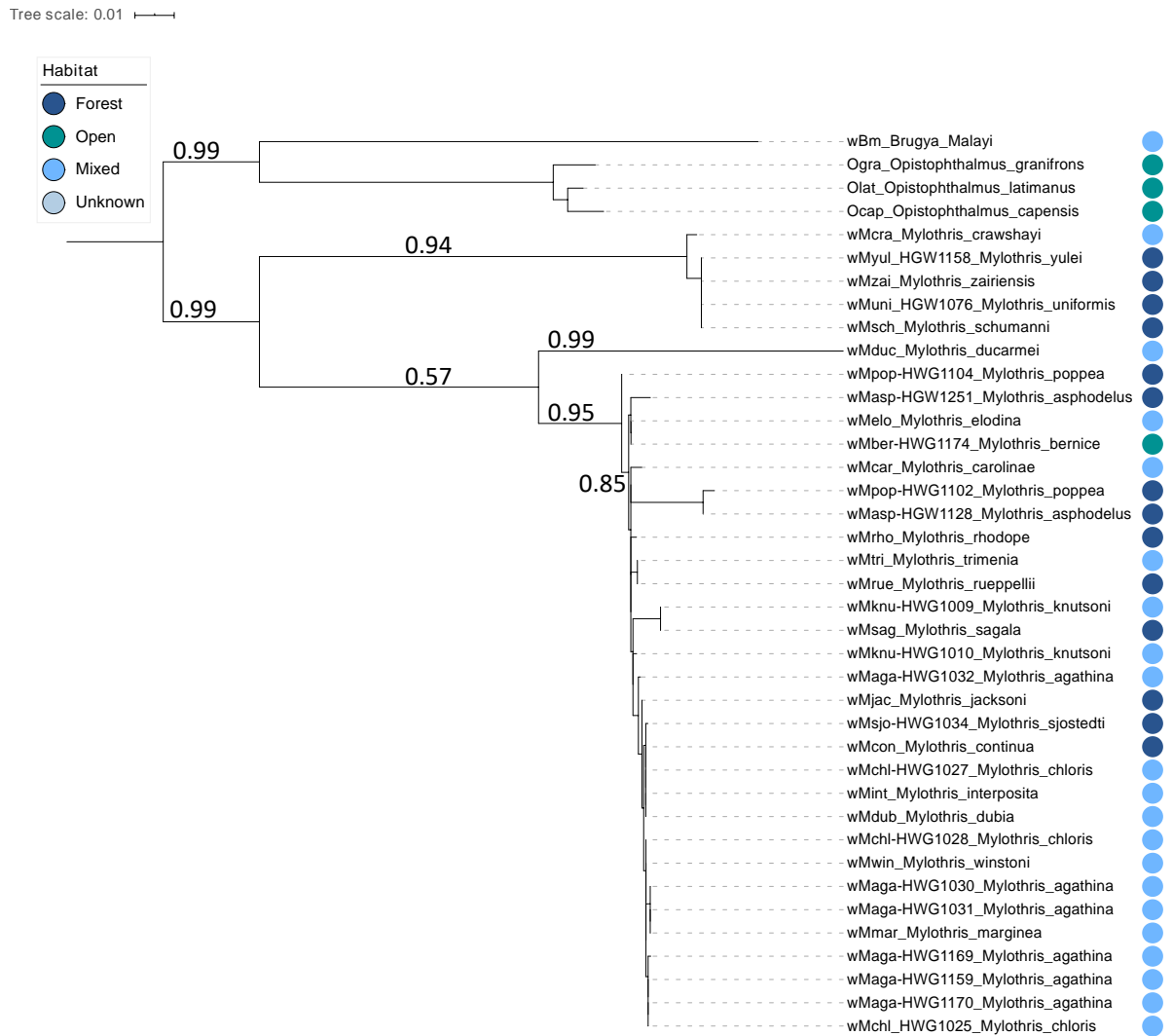
Table S3: Divergence rate (%) between the *Wolbachia* strains and strain variants characterized from the *Mylothris* butterflies and the *Bicyclus* butterflies (as characterized in this study and by (Duplouy and Brattstrom 2018)). Central cells colored in accordance with degree of similarity between strains (white: less than 75% similarity, gray: between 75 and 97% similarity, dark-gray: more than 97% similarity).

Strain	1: wMuni_A	2: wMcra_A	5: wMsag_B	7: wMtri_B	8: wMcar_B	9: wMrho_B	10: wMaga_B	11: wMduc_B
12: wBman_A	73,1	73,5	70,2	70,2	70,4	70,3	70,5	70,8
13: wBaur_A	73,5	73,9	70,2	70,2	70,4	70,3	70,5	71,0
14: wBxen_A	73,3	73,7	70,4	70,4	70,5	70,5	70,7	71,0
15: wBeva_A	86,3	86,7	76,7	76,7	76,7	77	76,6	74,1
3: wBsang_B	75,6	75,8	99,2	98,9	98,4	98,8	99,6	80,9
4: wBpav_B	75,4	75,6	99,2	99,2	98,8	99,2	98	81,3
6: wBxen_B	74,8	75	99,8	99,8	99,4	99,8	98,6	80,5
16: wBsyl_B	74,5	74,7	99,4	99,4	99	99,4	98,6	80,4
17: wBjac_B	75	75,1	99,6	99,6	99,2	99,6	98,4	80,7

18: wBeva_B	75,4	75,6	99,4	99,4	99,4	99,4	98,2	80,3
19: wBden_B	74,5	74,7	99,6	99,6	99,2	99,6	98,4	80,2
20: wBani_B	74,8	75	99,8	99,4	99	99,4	98,6	80,1
21: wBtri_B	72,9	73,2	80,6	81,2	80,2	80,8	80,8	99,4
22: wBtae_B	73,5	73,7	75,9	75,9	75,7	75,9	76,7	82,0

1 **Figure S1: Rooted phylogenetic relationships of the concatenated MLST and**
 2 ***wsp* genes sequences from the different *Wolbachia* characterized from the**
 3 ***Mylothris* butterflies, with bootstrap values. Additional *Wolbachia* strains**
 4 characterized from *Brugya malayi* (D-supergroup strain) and from
 5 *Opisththalmus* scorpions (F-supergroup strains) were added as outgroup.
 6 Habitat of the host is shown in right-circle.

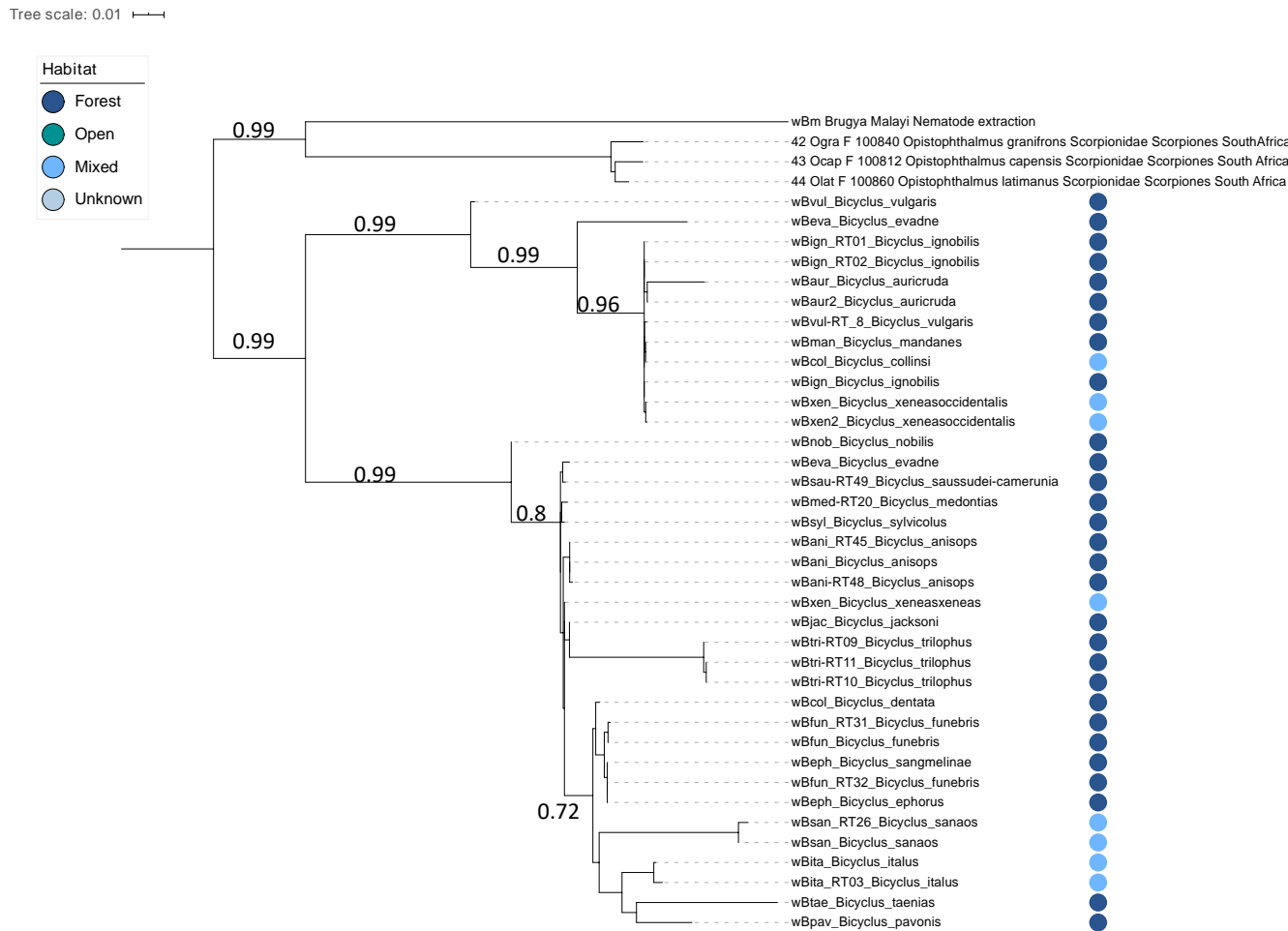
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10 **Figure S2: Rooted phylogenetic relationships of the concatenated MLST and**
 11 ***wsp* genes sequences from the *Bicyclus* butterflies, with bootstrap values.**
 12 Additional *Wolbachia* strains characterized from *Brugya malayi* (D-supergroup
 13 strain) and from *Opisthophthalmus* scorpions (F-supergroup strains) were added
 14 as outgroup. Habitat of the host is shown in right-circle.
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19 **Figure S3: Phylogenetic tree of all available *Wolbachia* strains and strain**
20 **variants characterized from Lepidoptera, Hymenoptera, and all other**
21 **African arthropods.** The tree was built using the concatenated sequences of the
22 *Wolbachia* MLST and *wsp* markers. Colored squares, circles and triangles on the
23 right provide the family, ecoregion and habitat of the hosts, respectively. Dataset
24 includes strains described in the present study, as well as strains from *Bicyclus*
25 butterflies as in [39], from Malagasy *Nanos* dung-beetles as in [11], and all
26 pubMLST-registered strains from Lepidoptera, Hymenoptera and African
27 arthropods [18]. *Wolbachia* strains characterized from *Brugya malayi* nematode
28 (D-supergroup strain) and from *Opisththalmus* scorpions (F-supergroup
29 strains) were used as outgroup.