

Impact of trehalose transporter knockdown on *Anopheles gambiae* stress adaptation and susceptibility to *Plasmodium falciparum* infection

Kun Liu^{a,1}, Yuemei Dong^a, Yuzheng Huang^b, Jason L. Rasgon^c, and Peter Agre^{a,1}

^aJohns Hopkins Malaria Research Institute, Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, The Johns Hopkins University, Baltimore, MD 21205; ^bKey Laboratory on Technology for Molecular Biology, Prevention and Control of Parasitic Diseases, Ministry of Health, Jiangsu Provincial Key Subject on Parasitic Diseases, Jiangsu Institute of Parasitic Diseases, Wuxi, Jiangsu 214064, China; and ^cDepartment of Entomology, Center for Infectious Disease Dynamics, and the Huck Institutes of The Life Sciences, Pennsylvania State University, University Park, PA 16802

Contributed by Peter Agre, September 4, 2013 (sent for review March 6, 2013)

***Anopheles gambiae* is a major vector mosquito for *Plasmodium falciparum*, the deadly pathogen causing most human malaria in sub-Saharan Africa. Synthesized in the fat body, trehalose is the predominant sugar in mosquito hemolymph. It not only provides energy but also protects the mosquito against desiccation and heat stresses. Trehalose enters the mosquito hemolymph by the trehalose transporter AgTreT1. In adult female *A. gambiae*, AgTreT1 is predominantly expressed in the fat body. We found that AgTreT1 expression is induced by environmental stresses such as low humidity or elevated temperature. AgTreT1 RNA silencing reduces the hemolymph trehalose concentration by 40%, and the mosquitoes succumb sooner after exposure to desiccation or heat. After an infectious blood meal, AgTreT1 RNA silencing reduces the number of *P. falciparum* oocysts in the mosquito midgut by over 70% compared with mock-injected mosquitoes. These data reveal important roles for AgTreT1 in stress adaptation and malaria pathogen development in a major vector mosquito. Thus, AgTreT1 may be a potential target for malaria vector control.**

major hemolymph sugar | sugar transporter | malaria parasite oocysts | malaria control

Critical to the malaria transmission cycle, the mosquito *Anopheles gambiae* is a major vector for *Plasmodium falciparum*, the pathogen responsible for most malignant malaria in sub-Saharan Africa. In malaria endemic regions, vector mosquitoes survive harsh fluctuations of temperature and humidity (1). Mosquitoes adapt to environmental changes by adjusting expression levels of certain genes (2); however, most protective mechanisms apparently remain unknown. Recently, we characterized an aquaporin water channel from *A. gambiae* (AgAQP1) that is important for water homeostasis, because reduced expression protected against dehydration (3). Since water loss has profound effects on mosquito physiology, we investigated other candidate genes that may protect against environmental stress and may affect transmission of *P. falciparum*.

Trehalose is a nonreducing disaccharide of two glucose molecules linked by an α -1,1-glycosidic bond. It is abundant in insects, crustaceans, nematodes, bacteria, fungi, and plants, but not vertebrates. As the major sugar in mosquito hemolymph, trehalose is concentrated more than 10 times higher than glucose or other sugars (4). Trehalose is a versatile molecule, serving as the principal energy storage but also as a stabilizer for dry membranes and proteins due to unique chemical and physical properties—high hydration volume, lack of internal hydrogen bonds, and nonreduction (5–8).

Trehalose levels rise sharply during several stresses—desiccation (9–12), heat (13), freezing (14, 15), hyperosmolality (16), and oxidation (17). In yeast and plants, trehalose is also a signaling molecule in metabolic pathways affecting growth (18). Evidence is emerging that trehalose protects cultured cells. Increased trehalose in HEK-293 cells expressing *Drosophila* trehalose-phosphate

synthase 1 protects the cells from hypoxic injury (17). Bovine endothelial cell line cultivated with trehalose followed by cryopreservation with trehalose in an optimized solution yielded over 80% viable cells (19). Trehalose levels in anhydrobiotic stage larvae of *Polypedilum vanderplanki* (sleeping chironomid) accumulate rapidly to ~20% of the dry body mass, more than five times higher than that of larvae in fresh water (9, 20). Furthermore, a recent study has shown that injection of D-(+)-trehalose into the hemocoel of head-intact, starved cockroaches lowers the content of short neuropeptide F in hemolymph, suggesting novel roles of trehalose in regulating brain and midgut interplay in insect digestion and nutrition-associated behavior (21).

Synthesized exclusively in the fat body of mosquitoes, trehalose is transported to the circulating hemolymph for delivery to other tissues. This process involves the specific movement of trehalose across cell membranes facilitated by the trehalose transporter, TreT (9, 22). The AgTreT1 cDNA from *A. gambiae* is an ortholog of PvTreT1 from *P. vanderplanki*. Only one TreT gene is present in the *A. gambiae* genome, and its trehalose-transport function was characterized by heterologous expression in *Xenopus* oocytes (22). PvTreT1 was proposed to contribute to the dehydration resistance of *P. vanderplanki* larvae in vivo (9). Nevertheless, no direct evidence has supported this role of AgTreT1 in the whole vector mosquito *A. gambiae*.

Trehalose is a likely energy source for *Plasmodium* pathogens in *A. gambiae* mosquitoes. After ingesting an infected blood meal, *Plasmodium* gametocytes differentiate into male or female gametes and fuse to form ookinetes in the mosquito midgut.

Significance

The trehalose transporter in *Anopheles gambiae* (AgTreT1) is shown here to be important for mosquito adaptation to environmental stresses and malaria infection. As expected since AgTreT1 transports trehalose from site of synthesis in fat body to hemolymph, silencing of AgTreT1 reduces hemolymph trehalose concentration. More importantly, AgTreT1-silenced mosquitoes exhibit shorter survival under desiccation or elevated temperature, and these mosquitoes also harbor fewer parasites after an infectious bloodmeal. We conclude that AgTreT1 is critical to maintain hemolymph trehalose concentration and is a positive mediator for parasite growth. Thus AgTreT1 can be a potential target for interruption of malaria transmission.

Author contributions: K.L., J.L.R., and P.A. designed research; K.L., Y.D., and Y.H. performed research; K.L., J.L.R., and P.A. analyzed data; and K.L., J.L.R., and P.A. wrote the paper.

The authors declare no conflict of interest.

¹To whom correspondence may be addressed. E-mail: kuliu@jhsph.edu or pagre@jhsph.edu.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1316709110/-DCSupplemental.

and transport pathway. We remain mindful that trehalose may not be the only factor in the protection machinery. Other protective agents and their roles in different types of stresses warrant further investigation in vector mosquitoes.

Unlike the closed circulation system of vertebrates, mosquito hemolymph flows in direct contact with internal organs, immersing them in trehalose. Protection against dehydration mediated by a trehalose transporter has been verified by transfection of *PvTreT1* from *P. vanderplanki* larvae, which improved the desiccation tolerance of cultured Chinese hamster ovary cells in the presence of trehalose (28).

Here, we provide evidence for a protective role for *AgTreT1* in whole mosquitoes. Silencing *AgTreT1* expression decreases transport of trehalose from fat body to hemolymph. Trehalose movement from hemolymph to internal organs is likely limited by the trehalose concentration in hemolymph, possibly by the low levels of *AgTreT1* expression in those organs. We observed an up-regulation of *AgTreT1* transcript and increased hemolymph trehalose concentration when mosquitoes were in low relative humidity or high temperature. Similar mRNA induction of the *TreT* ortholog in *P. vanderplanki* was reported during desiccation (9). Thus, multiple lines of research suggest that trehalose transport determines hemolymph trehalose concentration, thereby protecting living organisms in adverse environmental conditions.

AgTreT1 Expression and *P. falciparum* Growth. It is believed that *Plasmodium spp.* propagation in mosquitoes consumes nutrients from the vector. Hemolymph sugars, predominantly trehalose, are decreased after *Plasmodium* infection (23). However, molecular understanding of how trehalose is used by the parasite is still not clear. One possibility is that the parasite scavenges and metabolizes trehalose directly whereas another is that trehalose is hydrolyzed to glucose by either the vector or the parasite and the glucose is then taken up by the parasite.

Based on sequence analysis, the enzymes responsible for trehalose metabolism are present in *A. gambiae*—including putative trehalose synthase, trehalase, and the trehalose transporter. So far, orthologs of these genes have not been identified in *Plasmodium spp.* A hexose transporter was cloned from *P. falciparum*, but targeted gene deletion proved lethal during the erythrocytic stages of the parasite (29). Therefore, it is likely that *P. falciparum* propagation during vector stages depletes glucose from the mosquito by scavenging uptake into the parasite cell through membrane transporters. Trehalose, as the energy storage of mosquito, is mobilized to compensate for the glucose depletion. Because trehalose is the major blood sugar in mosquitoes, reductions due to *AgTreT1* silencing would deplete the energy source for parasite growth, resulting in fewer parasite oocysts that eventually survived the energy scavenge.

The interaction between malaria parasites and vector mosquitoes has drawn much attention for possible interventions to prevent transmission of this pathogen (30). Most current studies on vectors are focused on mosquito immune genes. Expression levels of certain genes involved in the mosquito immune response correlate with *Plasmodium spp.* propagation in the vector. For example, targeted silencing of *AgSTAT-A* reduced the number of early oocysts in mosquito midgut, and *TEP1* silencing increased the number of developing parasites (31, 32). In our study, silencing *AgTreT1* expression significantly decreases infection intensity during oocyst stage (Fig. 4) and decreases infection prevalence. This reduction is important for malaria control because, in the field, even a single oocyst probably results in an infective mosquito. The reduction of intensity and prevalence likely occurs by inhibiting *P. falciparum* propagation and limiting the carbon and energy sources for parasite growth. Whether *AgTreT1* or trehalose is directly related to mosquito immunity is unclear. Trehalose concentration in hemolymph may be related to multiple physiological processes in mosquito vectors.

Together, these studies have established that *AgTreT1* is a factor in mosquito adaptation to dehydration and heat. Furthermore, *AgTreT1* is also a positive mediator of *P. falciparum* development as gene silencing reduced parasite load in the mosquito midgut. These findings improve the understanding of malaria parasite development in the mosquito vector and provide a previously undescribed potential target for interrupting malaria transmission.

Materials and Methods

Mosquitoes, Routine Molecular Biology, RNAi, Antibodies, and Western Blot. All experiments used methods and guidelines approved by the Animal Ethical Care Committee of Johns Hopkins University in compliance with US guidelines for the use of animals in research. *AgTreT1* mRNA sequence was obtained from National Center for Biotechnology Information GenBank (XM_315568) and www.VectorBase.org (gene no. AGAP005563). Detailed methods on mosquito (Keele strain) rearing, RNA extraction, reverse transcription, quantitative PCR, relative humidity determination, RNA interference, Western blots, and desiccation assay were described in our previous paper (3). Primers designed for *AgTreT1* cloning, qPCR, and RNAi are listed in Table S3. A rabbit polyclonal antibody was commercially raised against the *AgTreT1* sequence at positions 243–256 (RGRKADVEPELKG) and purified by affinity chromatography (GenScript). Rabbit anti-Actin antibody (Sigma; A2066) was used for loading control.

Hemolymph Extraction, Osmolality, and Trehalose Measurements. Seven days after dsRNA injection, mosquitoes were anesthetized on ice, and 1–1.5 μ L of PBS was injected into the thorax using a fine glass needle. The needle was then withdrawn from the thorax and inserted into the abdomen to harvest perfused hemolymph. Approximately 10–15 μ L of hemolymph from 10 mosquitoes injected with *AgTreT1* or GFP dsRNA were pooled for each measurement. Osmolality was measured with a VAPRO pressure osmometer 5520 (Wesco Inc.) with the manufacturer's guidance.

In the trehalose measurement, extracted hemolymph was aliquoted into three parts. The first aliquot was used to measure total glucose after trehalase treatment. To hydrolyze hemolymph trehalose into glucose, a 40- μ L reaction containing 0.2 μ L of hemolymph and 10 mU of porcine trehalase (Sigma; T8778) in 50 mM Mes (2-[*N*-morpholino] ethanesulfonic acid) at pH 6.7 was incubated at 37 $^{\circ}$ C for 1 h. The second aliquot was used to measure the glucose concentration without trehalase treatment. The reaction system was the same as the first part except that trehalase was omitted. Then, the glucose concentrations of these two aliquots were determined with the Glucose HK Kit (Sigma; GAHK-20). In each 55- μ L glucose test, 5 μ L of the trehalase treatment product was used. The readouts at OD_{340nm} were within linear range. Trehalose concentrations were calculated by the following equation:

$$C_{\text{trehalose}} = \frac{C_{\text{glucose, treated}} - C_{\text{glucose, untreated}}}{2}$$

where $C_{\text{glucose, untreated}}$ is the basal glucose concentration, $C_{\text{glucose, treated}}$ is the total glucose concentration treated by trehalase, and $C_{\text{trehalose}}$ is the trehalose concentration in the hemolymph. D-(+)-trehalose dihydrate (Sigma; T3663) and D-(+)-Glucose (Sigma; G8270) were positive controls. Experiments were repeated four times. The third aliquot was used to determine the relative level of genomic DNA in *AgTreT1*-silenced extract compared with control extract. The measured trehalose concentrations in *AgTreT1* RNAi mosquitoes or controls were normalized to the amount of genomic DNA extracted with the DNeasy Blood and Tissue Kit (Qiagen; 69504). qPCR was performed to measure the relative level of ribosomal gene *S7* in hemolymph extracts. To verify the specificity, melting curves of qPCR were examined, and the correct sizes of amplicons were confirmed by electrophoresis. Normalized trehalose concentrations of *AgTreT1*-silenced and control hemolymph were subject to the Mann–Whitney *U* test with software GRAPHPAD PRISM 5.

Desiccation and Heat Assays. Four hundred nanograms of dsRNA was injected into the thorax of mosquitoes, and the mosquitoes were cultivated at 17 $^{\circ}$ C and 80% relative humidity to recover until the desiccation assay as described (3) or the heat assay in this paragraph. Both assays were repeated three times with similar results. The median survival is 6–8.5 h in the presence of desiccant and ~17 h in the absence of desiccant (3). In the heat assay, ~20 mosquitoes injected with *AgTreT1* or GFP dsRNA were put in cardboard cups and cultivated at 17 $^{\circ}$ C for optimal recovery. On day 6 after dsRNA injection, the cups were transferred to 27 $^{\circ}$ C and incubated for 16 h for

acclimation. The heat assays were carried out on day 7 after dsRNA injection. Mosquitoes were placed in a Forma Environmental Chamber (Model 3851; Thermo Electron Corp.) at 39 °C and 80% relative humidity. Mosquito viability was monitored every 1–1.5 h. Survival analyses and log-rank tests were performed as described (3).

***P. falciparum* Infection and Oocyst Determination.** Five-day-old *A. gambiae* female adults were infected with a *P. falciparum* GFP-3D7 strain (33) by membrane feeding. The gametocytemia in each independent infection experiment was 0.2–0.3%. On day 1 after infected-blood feeding, fully-engorged females were anesthetized on ice, separated from the unfed mosquitoes, and used for dsRNA injection. Mosquito viability was monitored after injection with no significant difference between the AgTreT1 or GFP dsRNA injected groups. Eight days after blood feeding, mosquito midguts were dissected, and GFP-3D7 oocysts were counted under a fluorescence microscope (Leica DM 2500). At least 30 mosquitoes were used in experimental or control group in

each experiment. The assay was repeated three times. The Mann–Whitney *U* test was performed with software GRAPHPAD PRISM 5.

ACKNOWLEDGMENTS. We thank Dr. Marcelo Jacobs-Lorena for critically reading the manuscript. We appreciate Drs. Takashi Okuda and Takahiro Kikawada from the National Institute of Agrobiological Sciences in Japan for providing PvTret1 antibody and helpful discussions. We are also grateful to the Insectary, Parasitology, and Gene Array Core Facilities at the Johns Hopkins Malaria Research Institute (JHMRI) for help in data collection and supply of materials. Lastly, the Keele strain of *A. gambiae* mosquitoes used in this study is established by Drs. Hilary Hurd and Paul Eggleston from Keele University. This study was supported by National Institutes of Health Grants R01 HL48268 and U19 AI089680, a pilot grant from JHMRI and the Bloomberg Philanthropies (to P.A. and K.L.), the Jiangsu Health International Exchange Program in China, National Natural Science Foundation of China Grant 31201893, National Science Foundation of Jiangsu Province Grant BK2011164, and Jiangsu Health Science Projects X201110 and X200736.

- Bernstein AS, Myers SS (2011) Climate change and children's health. *Curr Opin Pediatr* 23(2):221–226.
- Zhang Q, Denlinger DL (2011) Elevated couch potato transcripts associated with adult diapause in the mosquito *Culex pipiens*. *J Insect Physiol* 57(5):620–627.
- Liu K, Tsujimoto H, Cha SJ, Agre P, Rasgon JL (2011) Aquaporin water channel AgAQP1 in the malaria vector mosquito *Anopheles gambiae* during blood feeding and humidity adaptation. *Proc Natl Acad Sci USA* 108(15):6062–6066.
- Becker A, Schlöder P, Steele JE, Wegener G (1996) The regulation of trehalose metabolism in insects. *Experientia* 52(5):433–439.
- Jain NK, Roy I (2010) Trehalose and protein stability. *Curr Protoc Protein Sci* Chap 4, Unit 4.9. 10.1002/0471140864.ps0409s59.
- Crowe JH (2007) Trehalose as a "chemical chaperone": Fact and fantasy. *Adv Exp Med Biol* 594:143–158.
- Crowe JH, Hoekstra FA, Crowe LM (1992) Anhydrobiosis. *Annu Rev Physiol* 54: 579–599.
- Kaushik JK, Bhat R (2003) Why is trehalose an exceptional protein stabilizer? An analysis of the thermal stability of proteins in the presence of the compatible osmolyte trehalose. *J Biol Chem* 278(29):26458–26465.
- Kikawada T, et al. (2007) Trehalose transporter 1, a facilitated and high-capacity trehalose transporter, allows exogenous trehalose uptake into cells. *Proc Natl Acad Sci USA* 104(28):11585–11590.
- Benoit JB, et al. (2007) Mechanisms to reduce dehydration stress in larvae of the Antarctic midge, *Belgica antarctica*. *J Insect Physiol* 53(7):656–667.
- Browne JA, et al. (2004) Dehydration-specific induction of hydrophilic protein genes in the anhydrobiotic nematode *Aphelenchus avenae*. *Eukaryot Cell* 3(4):966–975.
- Crowe LM, Crowe JH (1992) Anhydrobiosis: A strategy for survival. *Adv Space Res* 12(4):239–247.
- Singer MA, Lindquist S (1998) Thermotolerance in *Saccharomyces cerevisiae*: The Yin and Yang of trehalose. *Trends Biotechnol* 16(11):460–468.
- Aguilera J, Randez-Gil F, Prieto JA (2007) Cold response in *Saccharomyces cerevisiae*: New functions for old mechanisms. *FEMS Microbiol Rev* 31(3):327–341.
- Wharton DA (2011) Cold tolerance of New Zealand alpine insects. *J Insect Physiol* 57(8):1090–1095.
- Wood JM, et al. (2001) Osmosensing and osmoregulatory compatible solute accumulation by bacteria. *Comp Biochem Physiol A Mol Integr Physiol* 130(3):437–460.
- Chen Q, Behar KL, Xu T, Fan C, Haddad GG (2003) Expression of *Drosophila* trehalose-phosphate synthase in HEK-293 cells increases hypoxia tolerance. *J Biol Chem* 278(49): 49113–49118.
- Elbein AD, Pan YT, Pastuszak I, Carroll D (2003) New insights on trehalose: A multifunctional molecule. *Glycobiology* 13(4):17R–27R.
- Campbell LH, Brockbank KG (2012) Culturing with trehalose produces viable endothelial cells after cryopreservation. *Cryobiology* 64(3):240–244.
- Kikawada T, Minakawa N, Watanabe M, Okuda T (2005) Factors Inducing Successful Anhydrobiosis in the African Chironomid *Polypedium vanderplanki*: Significance of the Larval Tubular Nest. *Integr Comp Biol* 45(5):710–714.
- Mikani A, Wang QS, Takeda M (2012) Brain-midgut short neuropeptide F mechanism that inhibits digestive activity of the American cockroach, *Periplaneta americana* upon starvation. *Peptides* 34(1):135–144.
- Kanamori Y, et al. (2010) The trehalose transporter 1 gene sequence is conserved in insects and encodes proteins with different kinetic properties involved in trehalose import into peripheral tissues. *Insect Biochem Mol Biol* 40(1):30–37.
- Mack SR, Samuels S, Vanderberg JP (1979) Hemolymph of *Anopheles stephensi* from noninfected and *Plasmodium berghei*-infected mosquitoes. 3. Carbohydrates. *J Parasitol* 65(2):217–221.
- Zancan P, Sola-Penna M (2005) Trehalose and glycerol stabilize and renature yeast inorganic pyrophosphatase inactivated by very high temperatures. *Arch Biochem Biophys* 444(1):52–60.
- Jain NK, Roy I (2009) Effect of trehalose on protein structure. *Protein Sci* 18(1):24–36.
- Laksanalamai P, Robb FT (2004) Small heat shock proteins from extremophiles: A review. *Extremophiles* 8(1):1–11.
- Al-Nabulsi AA, et al. (2011) Impact of environmental stress desiccation, acidity, alkalinity, heat or cold on antibiotic susceptibility of *Cronobacter sakazakii*. *Int J Food Microbiol* 146(2):137–143.
- Chakraborty N, et al. (2012) Trehalose transporter from African chironomid larvae improves desiccation tolerance of Chinese hamster ovary cells. *Cryobiology* 64(2): 91–96.
- Slavic K, et al. (2010) Life cycle studies of the hexose transporter of *Plasmodium* species and genetic validation of their essentiality. *Mol Microbiol* 75(6):1402–1413.
- Karunamoorthi K (2011) Vector control: A cornerstone in the malaria elimination campaign. *Clin Microbiol Infect* 17(11):1608–1616.
- Gupta L, et al. (2009) The STAT pathway mediates late-phase immunity against *Plasmodium* in the mosquito *Anopheles gambiae*. *Cell Host Microbe* 5(5):498–507.
- Blandin S, et al. (2004) Complement-like protein TEP1 is a determinant of vectorial capacity in the malaria vector *Anopheles gambiae*. *Cell* 116(5):661–670.
- Talman AM, Blagborough AM, Sinden RE (2010) A *Plasmodium falciparum* strain expressing GFP throughout the parasite's life-cycle. *PLoS ONE* 5(2):e9156.