



# FREQUENCY OF KNOCKDOWN RESISTANCE MUTATIONS IN BODY LICE (PHTHIRAPTERA: PEDICULIDAE) FROM RUSSIA

Yuliya V. Lopatina<sup>1,2</sup>, Olga Yu. Eremina<sup>2</sup>, Liudmila S. Karan<sup>3</sup>

<sup>1</sup> Lomonosov Moscow State University, Russia; <sup>2</sup> Scientific Research Institute for Disinfectology, Moscow, Russia; <sup>3</sup> Central Research Institute of Epidemiology, Moscow, Russia  
ylopatina@mail.ru



Published in ICUP 2017 Proceedings, available from QR code & [www.icup.org.uk](http://www.icup.org.uk)



## INTRODUCTION

The human louse, *Pediculus humanus* L., is a prevalent pest of human populations. Over the last few decades of about 300,000 cases of pediculosis were being reported annually in Russia, which is about 250 cases per 100,000 of population. Body lice have an important medical significance as the vectors of three pathogenic bacteria - *Rickettsia prowazekii* (epidemic typhus), *Borrelia recurrentis* (relapsing fever), and *Bartonella quintana* (trench fever). Actual infestation with body lice occurs mainly in homeless and other asocial persons (alcoholics, drug addicts and etc.). The first cases of insufficient efficacy of the permethrin-based anti-lice products have been registered in Russia in 2008. The aim of this study to evaluate the distribution of knockdown-type resistance (*kdr*-type) allele frequency in body louse populations from Russia.

## MATERIALS AND METHODS

The material has been collected from 2009 through 2015 from six locations in Russia (fig. 1) in eight Moscow and other cities' shelters from homeless people. Lice have been studied by real-time PCR to detect the associated with permethrinresistance double *kdr*



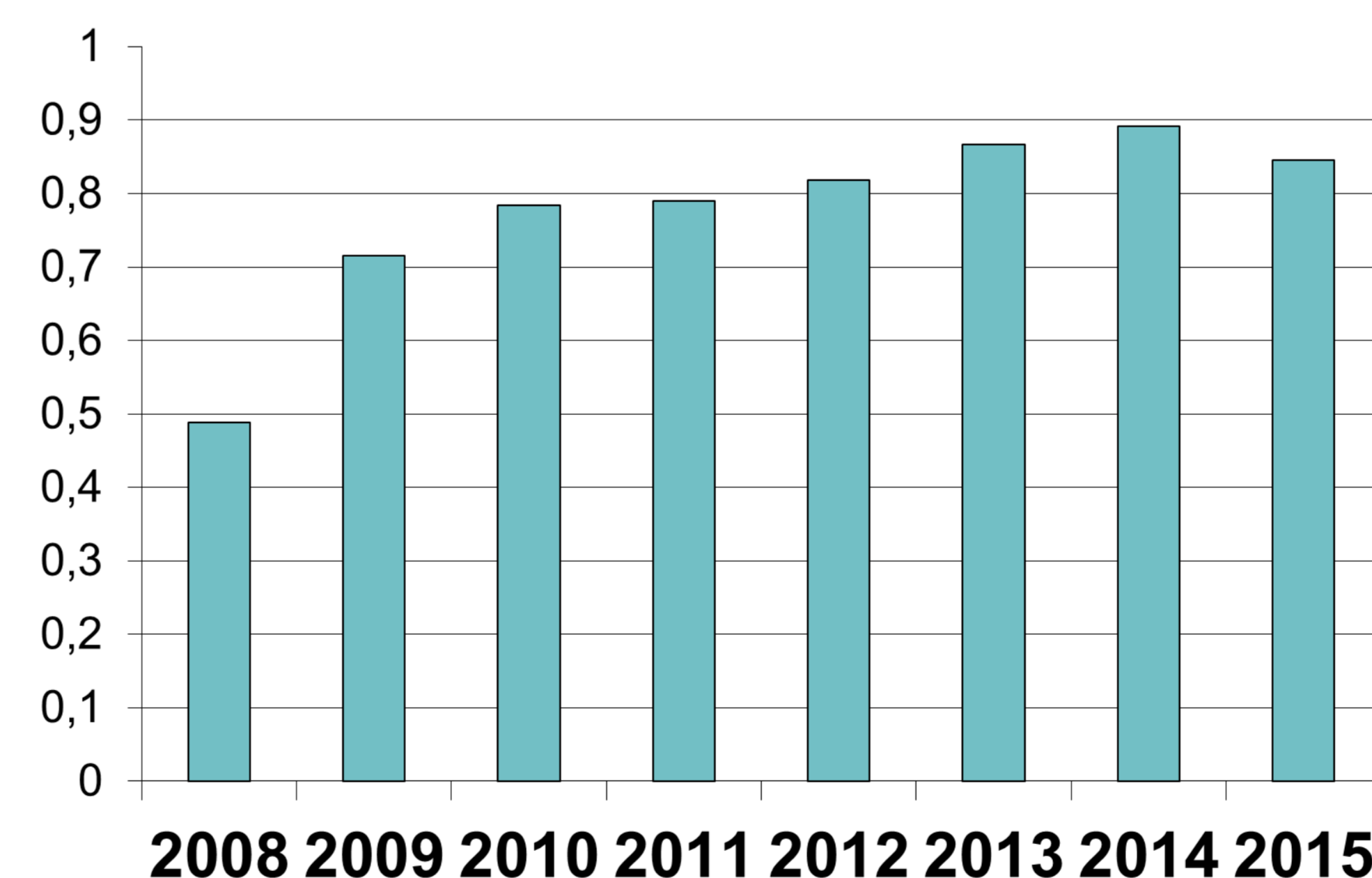
**Fig. 1. *Pediculus humanus humanus* collection sites in Russia (2013-2015) and *kdr* allele frequencies determined by real-time PCR in body louse populations**

SS - homozygotes susceptible,  
RS - heterozygotes,  
RR - homozygotes resistant

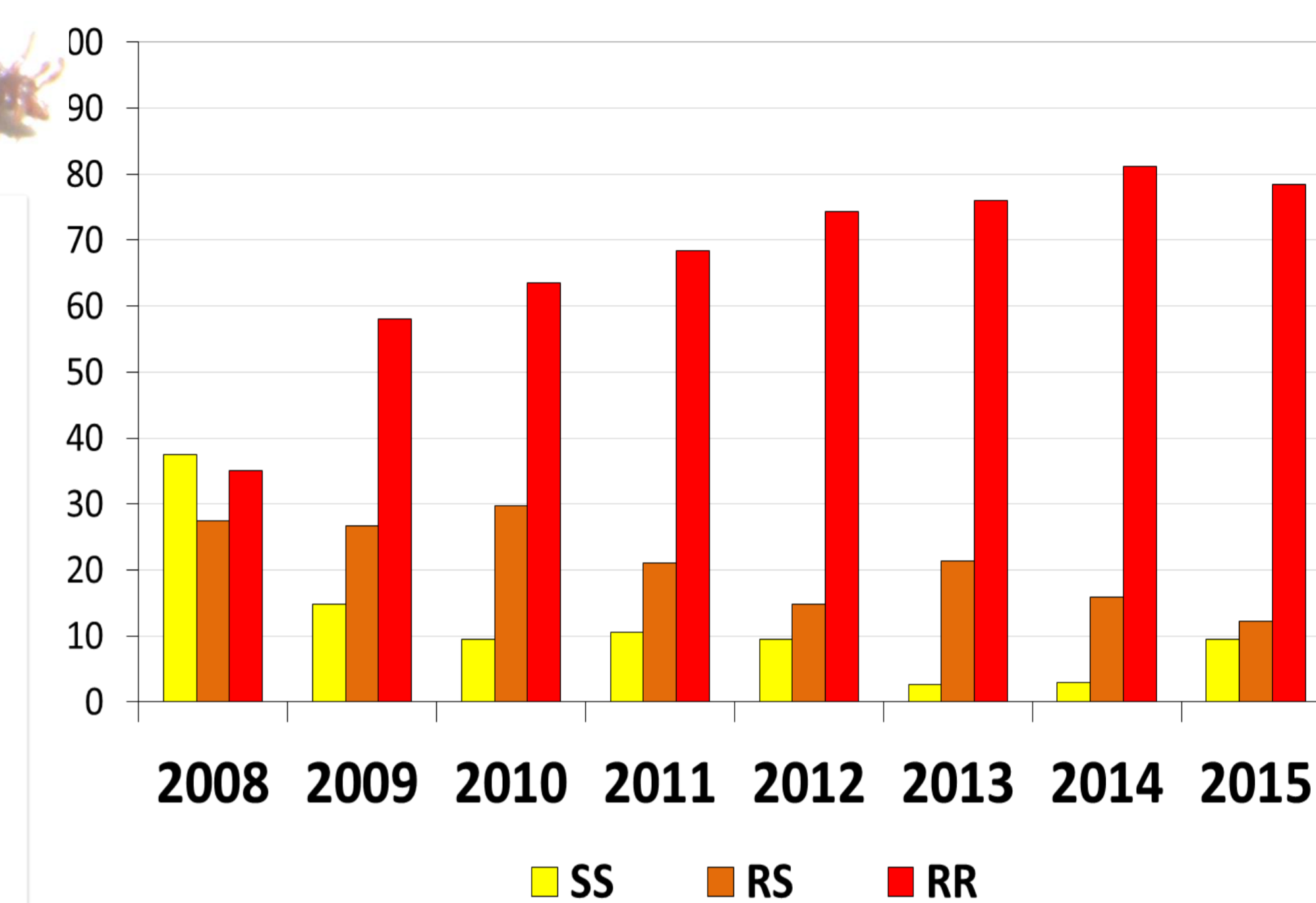
mutations (T917I+L920F) in the *Vssc1* gene, encoding the voltage-sensitive sodium channel protein. The *P. humanus Vssc1* – specific forward and reverse primers were, at 360 nmol/L, Ped-F TGGGTCGAACTGTTGGAGCTT and Ped-R CCATAACGGCAAATATGAATATGAT, respectively. The corresponding dye-labeled probes (final concentration 100 nmol/L) were Ped-S FAM-TGGGTAATTTAACATTCGTCCTTTGCC-BQH1 and Ped-R R6G-TGGGTAATTTAATATTCGTCTTTGCC-BQH1

## RESULTS

The resistant haplotype was found in all lice samples collected in various regions of Russia (fig. 1). The resistant haplotype was found in all of the body lice samples. We produced a *kdr* map based on the resistance allele zygosity data for louse populations from various cities and towns. The resistance monitoring was carried out in Moscow in the 2008-2015. The frequency of the resistant allele was 0.488 in 2008, it increased sharply in 2009 (0.763) and has been gradually growing hereafter with maximum in 2014 (fig. 2). Since 2010, most of insects were the homozygous resistant individuals; the share of susceptible homozygous individuals didn't exceed 10.5% (fig.3).



**Fig. 2. Knockdown resistance alleles (T917I+L920F) frequency in Moscow body louse population**



**Fig 3. Zygosity proportions of body lice collected from Moscow**

*Kdr* mutations associated with permethrin resistance were detected in lice both in big cities and in smaller towns. The frequency of the double mutations T917I-L920F was 0.43-0.89.

## CONCLUSIONS

The resistance of body lice to permethrin is widespread in Russia. Our study suggests that continuous resistance monitoring should be conducted on a regional scale in Russian Federation regularly to identify the efficacy of compounds (pyrethroids and OP) for human lice.

## ACKNOWLEDGEMENTS

This work was in part financially supported by the Russian Foundation for Basic Research (project no. 16-03-01337a).