

# **MOLECULAR EPIDEMIOLOGY of TB in RUSSIA**

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# **The main statistical data of TB in Russia, 2007\***

## **Incidence**

**157 000 new cases (110 per 100 000 population)**

**smear positive cases of these**

**68 000 (48 per 100 000 population)**

## **Prevalence**

**164 000 cases (115 per 100 000 population)**

## **Mortality**

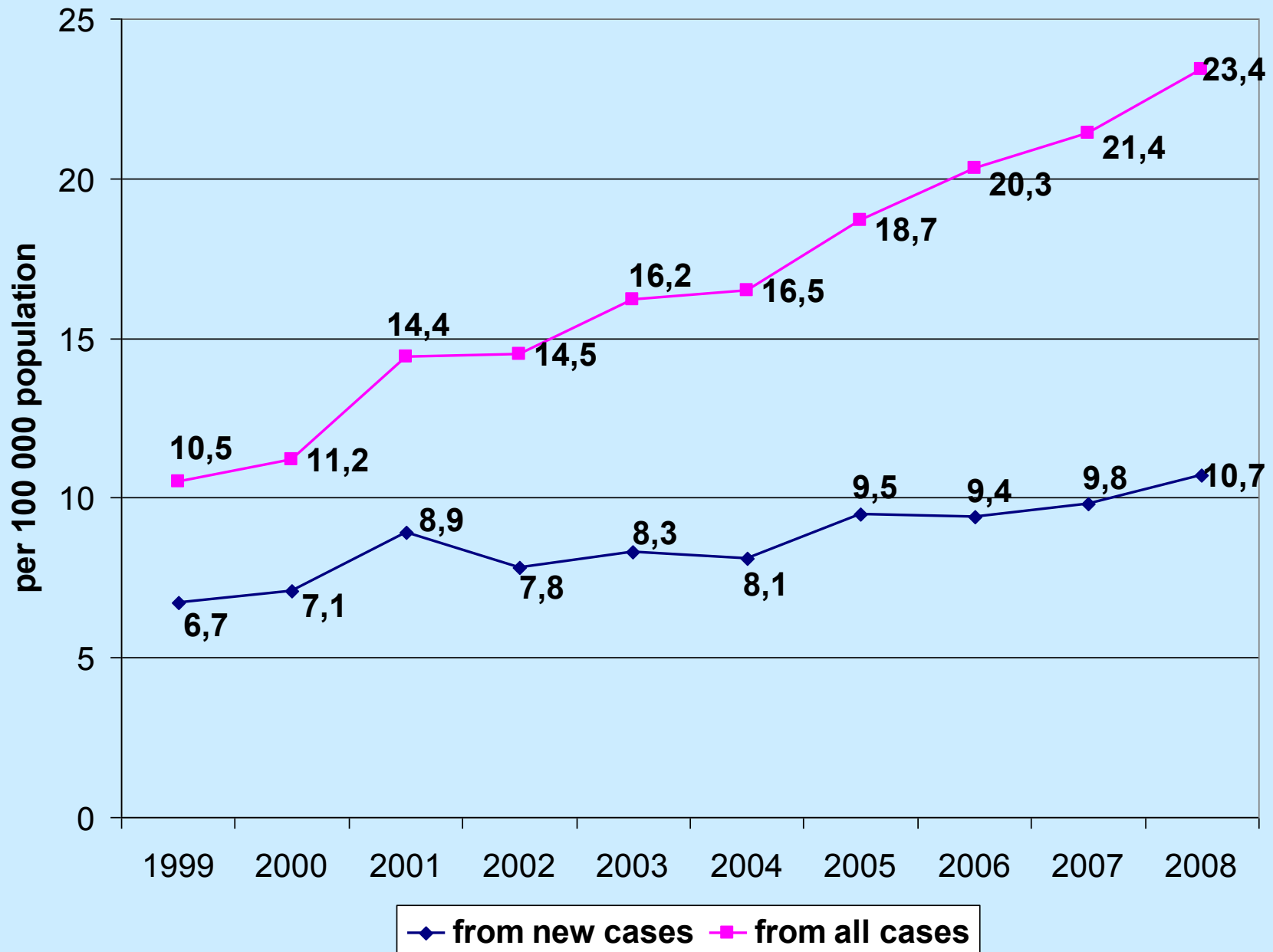
**20 000 HIV-negative people (14 per 100 000 population)**

**5100 among HIV-positive people**

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**\* WHO report 2009. Global tuberculosis Control, Epidemiology, Strategy, Financing**

# MDR TB in Russia



# **Molecular typing provides an important epidemiological tool with which to investigate the transmission of tuberculosis**

- **Molecular typing of *M.tuberculosis* strains**
- **Analysis of genotypes of MDR strains of *M.tuberculosis***

- **It was investigated 1227 M.tuberculosis strains from various regions of Russia (Ivanovo, Vladimir, Nizhnii Novgorod, Samara, Tomsk, Kemerovo, Khabarovsk oblasts, Republics Marii-El and Tuva).**

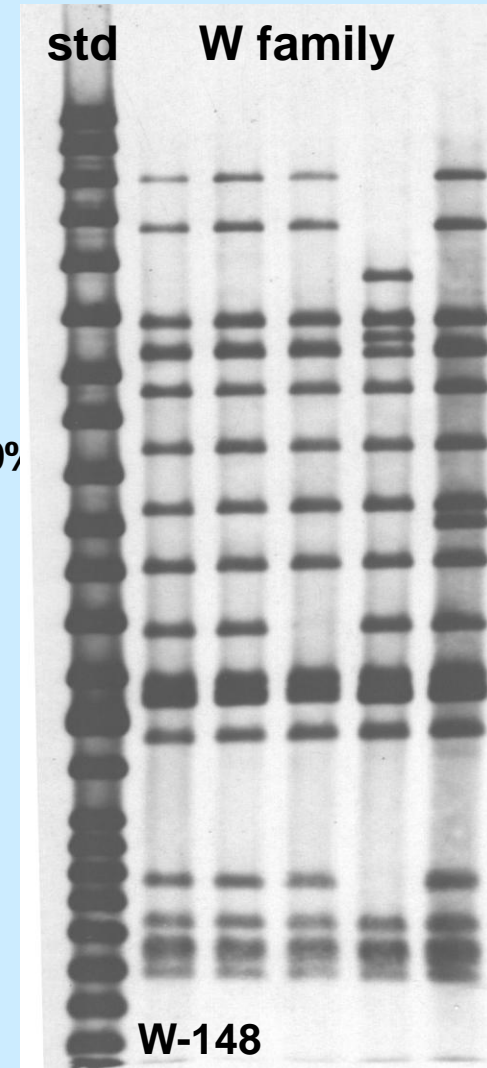
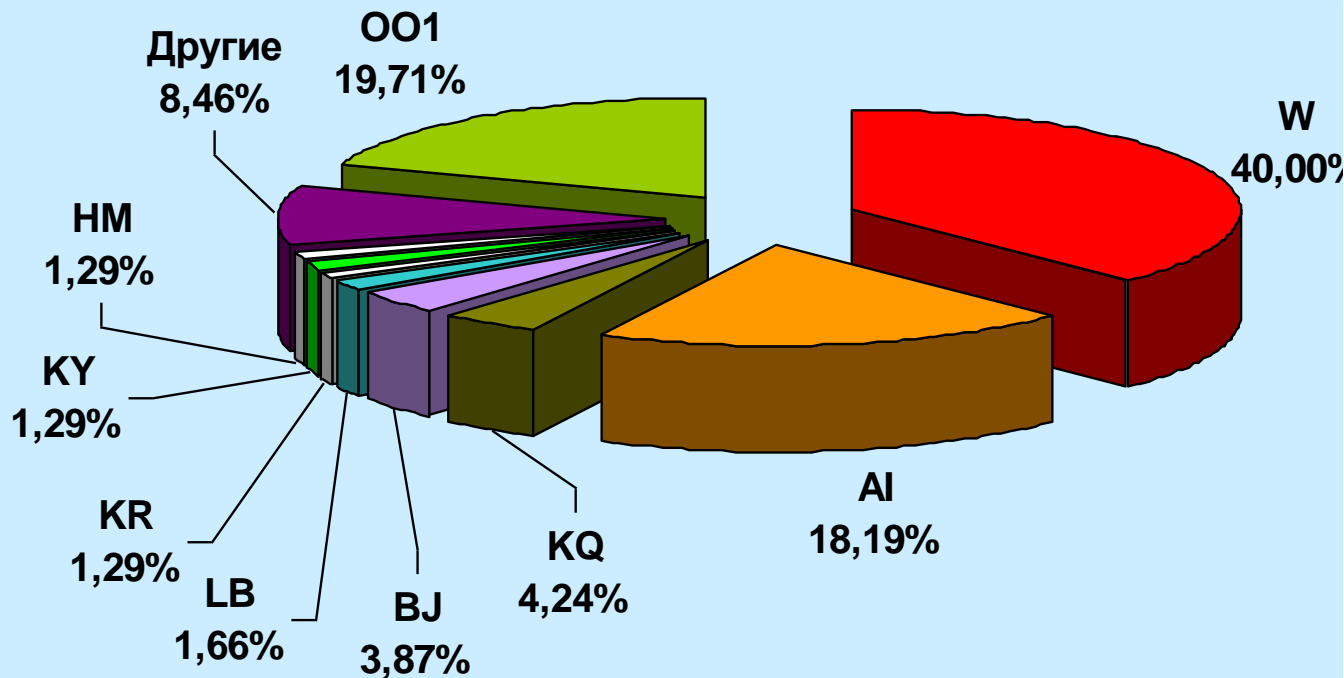
# **We used the following methods of genotyping**

- **RFLP IS6110 (van Embden J.D.A et al., 1993)**
- **Spoligotyping (Kamerbeek J. et al., 1997)**
- **VNTR typing (Frothingham R. et al, 1998)**

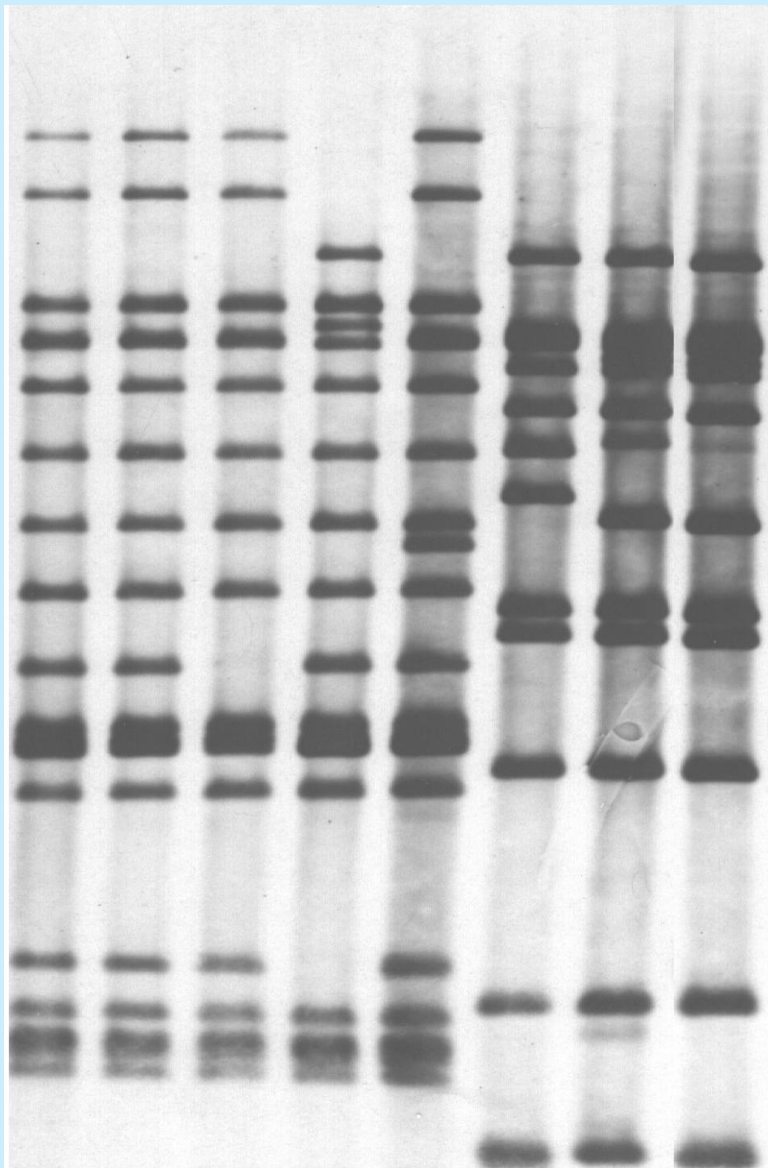
# Drug susceptibility was determined by

- **Methods of absolute concentrations**
- **Microarray technology (“TB-Biochip MDR”) revealing mutations in genes *rpoB*, *katG*, *ahpC*, *inhA***

**RFLP IS6110 typing of 1227 *M.tuberculosis* strains revealed more than 42 clusters.**  
**Strains of W (40%) and AI family (18.2%) were predominated.**



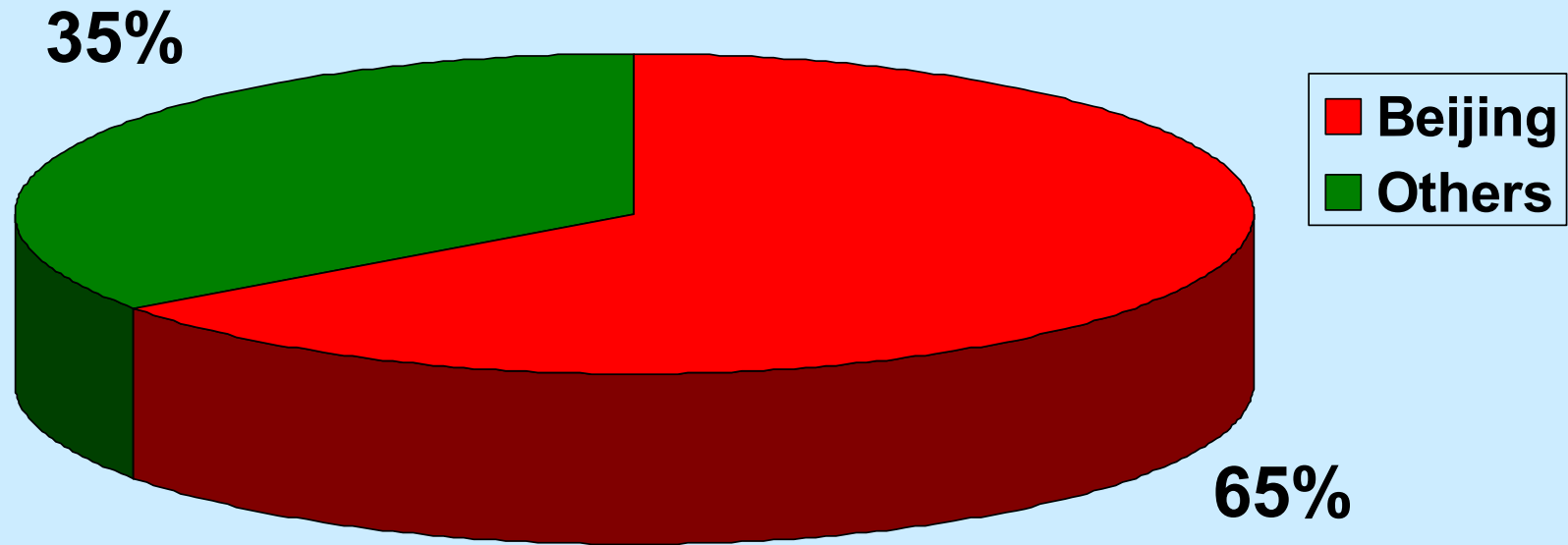




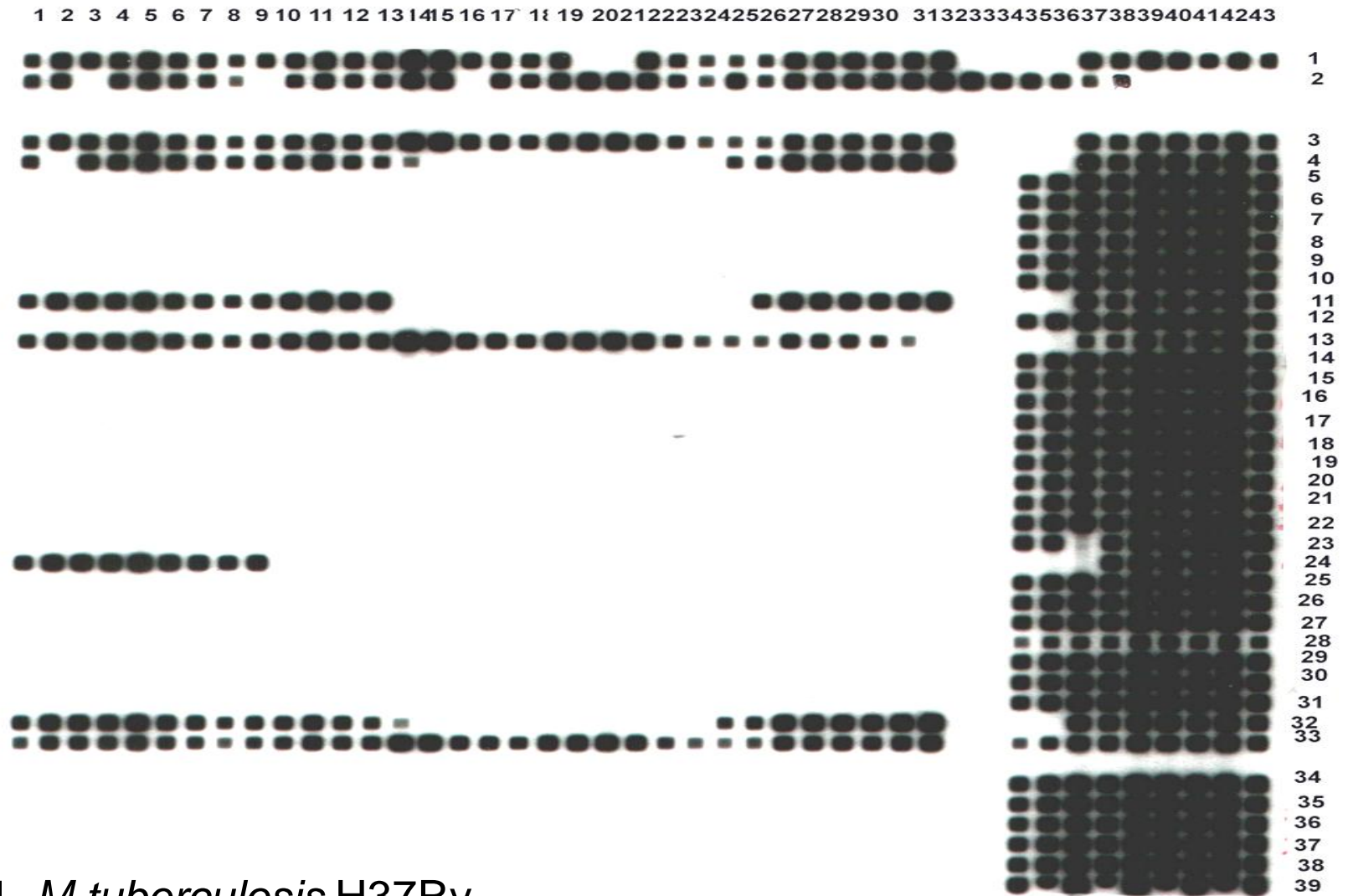
W W W W W AI AI AI

**RFLP IS6110**  
***M.tuberculosis***  
**W and AI family**

**Spoligotyping of 167 *M.tuberculosis* strains  
revealed 11 cluster groups  
The most quantity of strains belonged to  
Beijing spoligotype (65%)**



# Patterns of spoligotypes



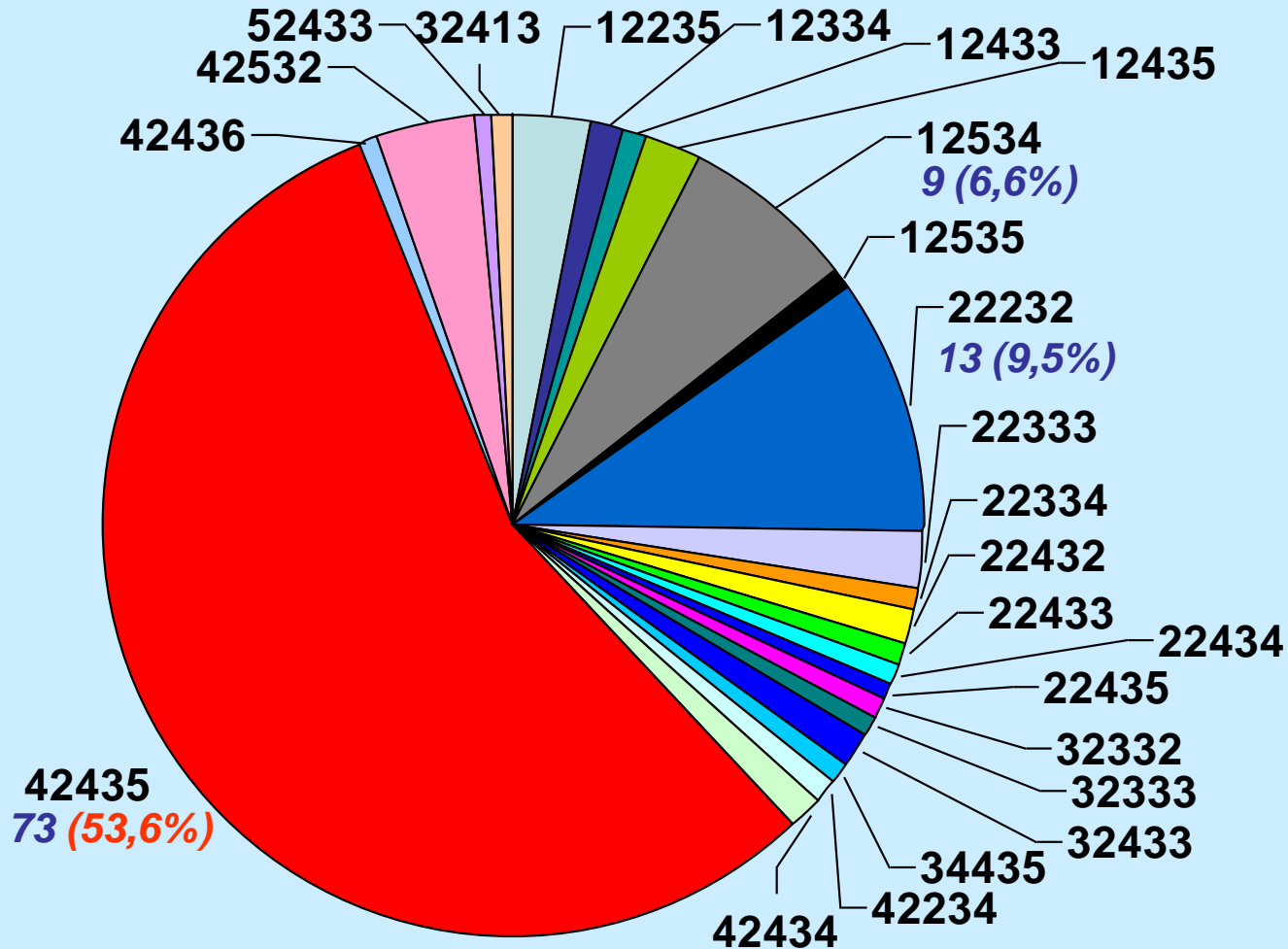
track 1 *M.tuberculosis* H37Rv

track 2 *M.bovis* BCG

tracks 5–10, 12, 14–22, 25–31, 34–39 - *M.tuberculosis* Beijing cluster

# VNTR typing of 136 *M.tuberculosis* strains

**42435 cluster are predominated**



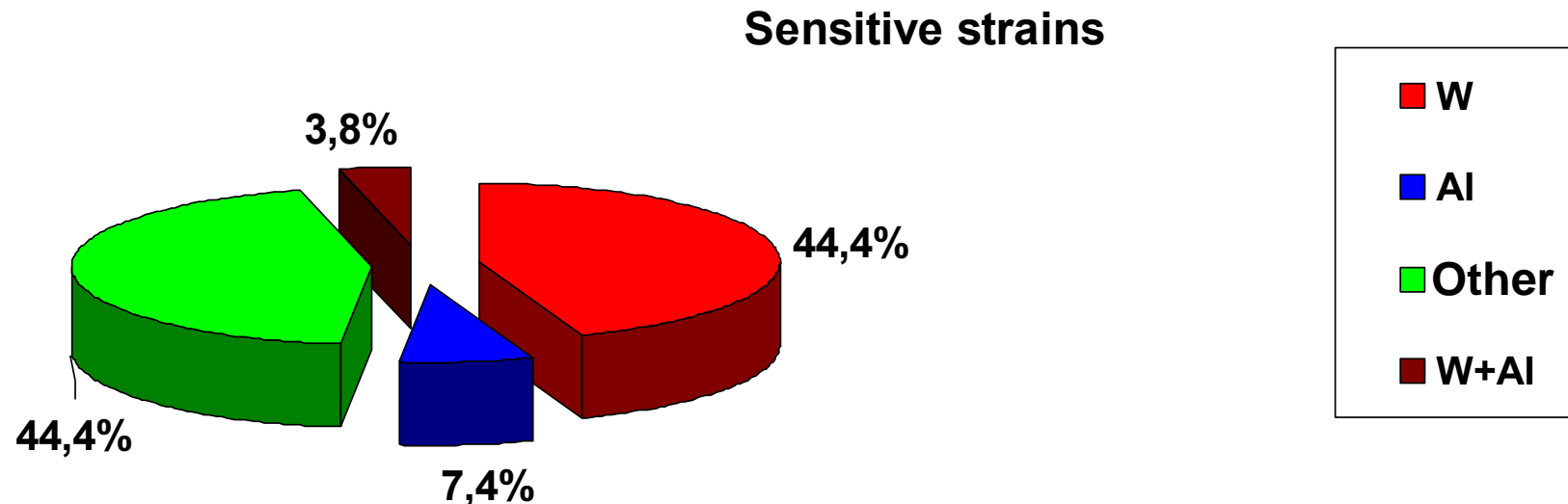
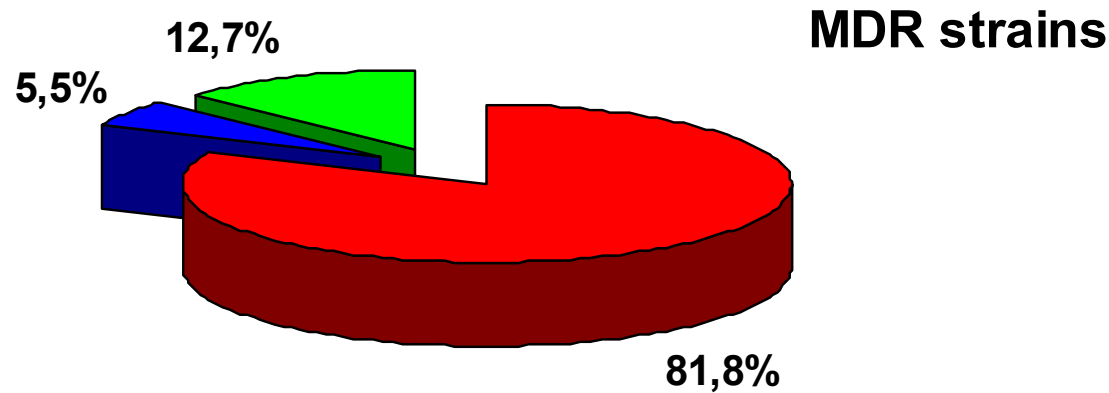
**Analysis of genotyping of each strain by  
three methods  
(RFLP IS6110, spoligotyping, VNTR)  
showed that *M.tuberculosis* strains with the  
same genetic characteristic prevailed**

**W-Beijing-VNTR 42435**

# **Genotyping of MDR and sensitive *M.tuberculosis* strains showed**

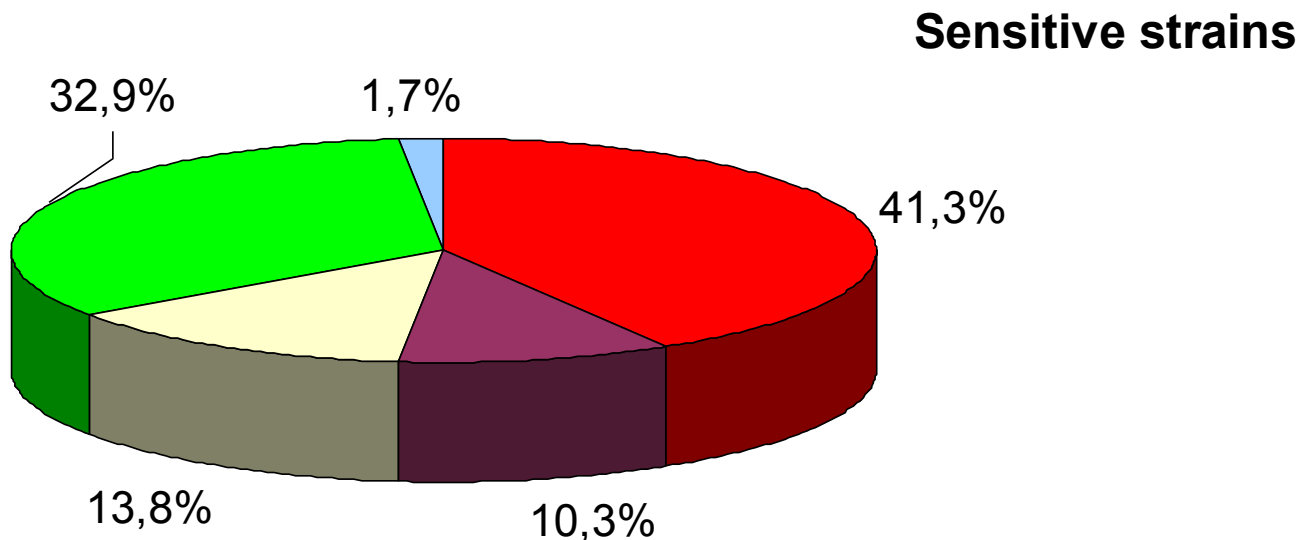
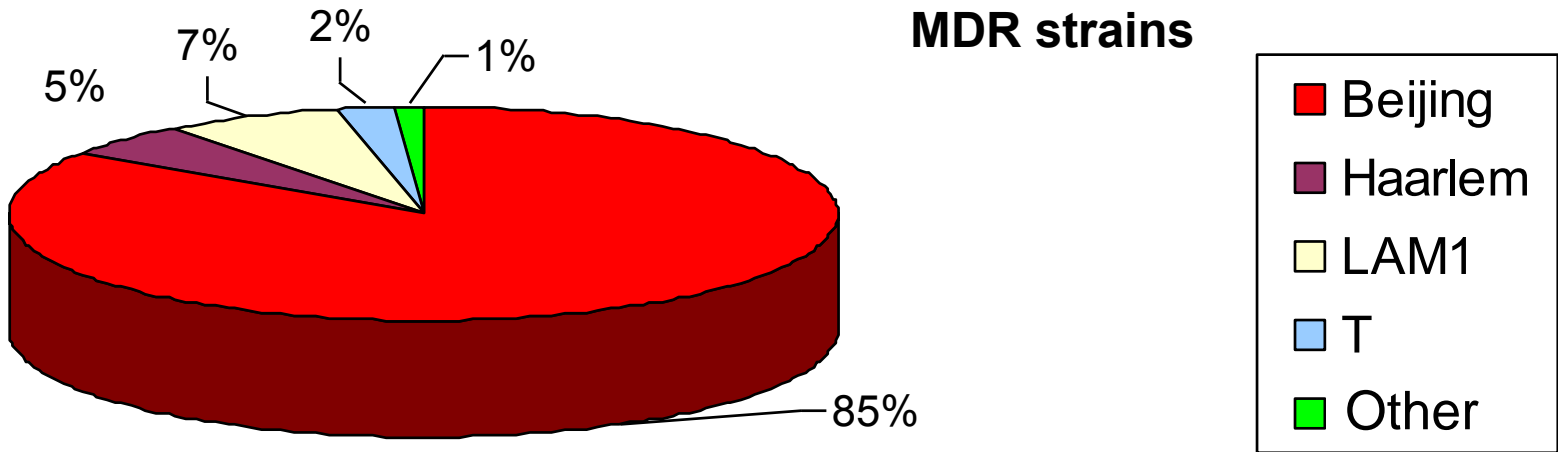
- **Strains belonged to the same cluster groups were found as among MDR so as among sensitive strains**
- **MDR strains had more clusterization than sensitive strains**

**81.8% of MDR strains belonged to W family**  
**In contrast among sensitive strains only**  
**44.4% belonged to W family**



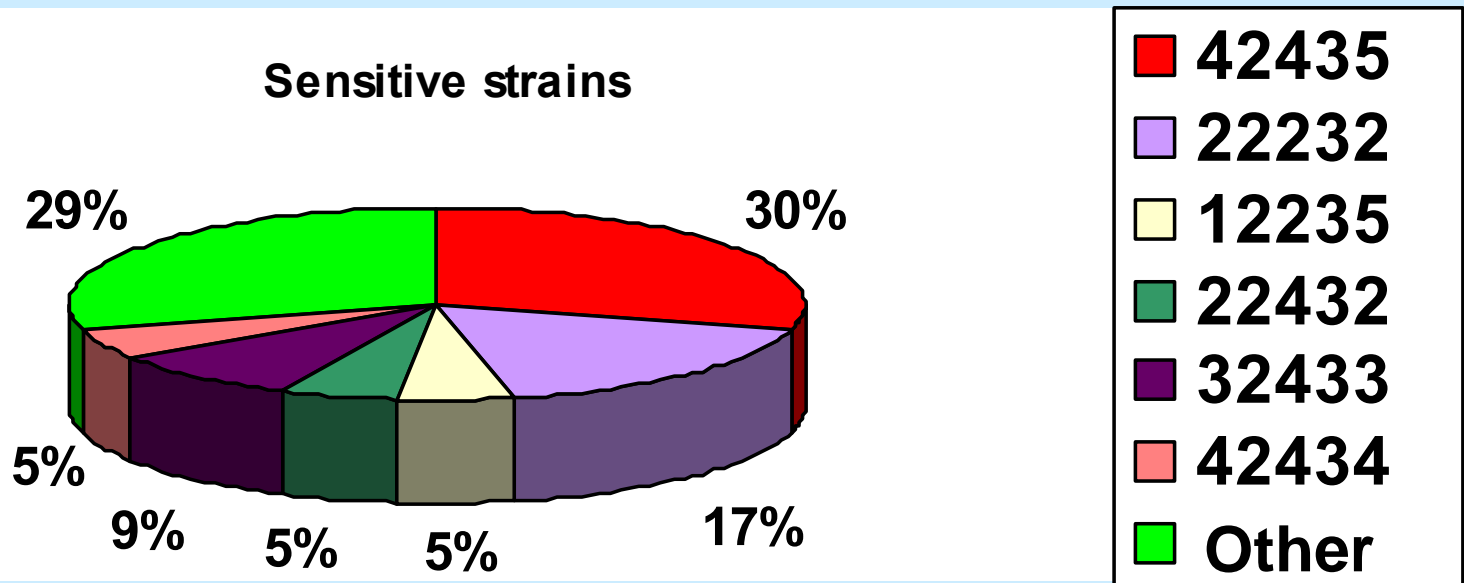
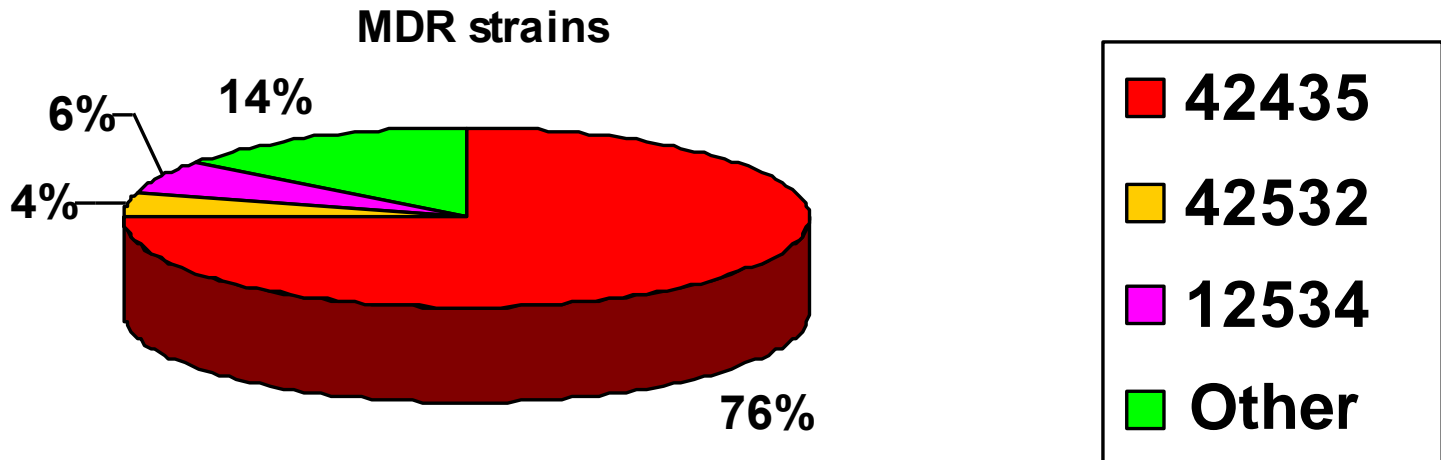
# 85% of MDR strains had Beijing spoligotype

## Among sensitive strains 41.3% belonged to Beijing spoligotype





**76% of MDR strains belonged to 42435 VNTR cluster  
but among sensitive strains only 30% belonged to  
42435 VNTR cluster**



**Complex analysis of *M.tuberculosis* strains showed that about 70% of MDR strains had the same genetic characteristics:**

**W – Beijing - VNTR 42435**

**Our results testify about the  
threat of spread of MDR  
tuberculosis in Russia**

***THANK YOU!***