Research Partnerships (RP)

FINAL TECHNICAL REPORT

Team 1		**Team 2** ***(If applicable)***
PI's name:	**Valeriu Crudu**	**PI's name: _____**
Country:	**Moldova**	**Country: _____**
Institution Name:	**Phthisiopneumology Institute**	**Institution Name: _____**
Award number:	**OISE-15-61136-1**	**Award number: _____**

Date submitted: (MM/DD/YYYY)

GENERAL INSTRUCTIONS:

This document contains information and instructions necessary for your research team to complete the final technical report of their CRDF Global award. The final report provide an accurate and comprehensive representation of the research conducted under your CRDF Global award. In the case of a joint-team project, drafting the report should be a collaborative effort undertaken by all Principal Investigators.

The Final Report serves several important functions to CRDF Global and its funders and is used as:

- An essential component of CRDF Global's due diligence activities;
- A metric for gauging the impact of CRDF Global's programs;
- An opportunity for grantees to suggest areas for improvement;
- Publicity and marketing information (with the approval of the Principal Investigators) to advance CRDF Global's mission and activities

In addition to the Final Report template, teams are also asked to provide responses to separate surveys (please see other attachments). Teams should complete these according to instructions contained within the individual documents.

All answers provided in this document should be typed within the **non-shaded** text boxes.

Please note that final reports are due within thirty (30) days of the end date of your CRDF Global award. Failure to provide the required information will delay final payments of your grant and may jeopardize your ability to participate in future CRDF Global funding opportunities. All questions contained within this template must be answered completely and accurately to the best of your knowledge and ability. Incomplete reports will be returned and you will be required to remediate any missing information.

When finished, please submit the completed report electronically to finalreports@crdfglobal.org with subject line: *Project Final Report - Award # [team 1]/ [team 2 – if applicbale].* Technical reports should only be submitted once by one PI and the other PI cc-ed on the email. Additional questions, comments, and supplemental information may also be sent to this address.

SECTION I: CGP PROJECT RESULTS & ACCOMPLISHMENTS

BRIEF STATEMENT OF MAJOR RESEARCH ACCOMPLISHMENTS

Instructions:

In one or two sentences, please state major research accomplishments made possible by receiving your CRDF Global grant. Please indicate how your research results contributed to the advancement of scientific knowledge nationally and internationally.

Major Accomplishments and Results:

In total 157 TB patients (new-64 and retreatment cases-93) were selected; the results of microbiological investigations, the clinical and radiological data of examinations were collected. The majority of selected patients was with MDR TB and XDR TB – 82.8% (65 patients in each group), only 10.2% (n=16) of patients were non-MDR and 7.0% (n=11) were with pre-XDR resistance pattern. All information of selected patients was included in the TB Portal site. For the future WGS examination, 96 M. tuberculosis isolated strains were selected, the DNA extraction was performed and was organized the shipment to Broad Institute, US.

PUBLIC SUMMARY

Instructions:

Please describe your major scientific achievements to a non-scientific community highlighting (in non-scientific language), including major benefits of your research for your home university/institution, industry and the society at large. The public summary should begin by clearly stating the project's goal(s) as originally outlined in the proposal, but without restating the project title. The summary should highlight findings and implications as concisely and informatively as possible, commenting as appropriate on the techniques or approaches used and the significance of your research to the public domain.

Using the template below as guidance, please provide your public summary in the blank text box located at the end of this section. The public summary should **NOT** be in outline format – rather, the outline is to check that you have addressed all relevant topics in your summary.

The summary should be written from the point of view of a completed project, and should be self-contained and intelligible to a layperson. Please do not re-submit the proposal abstract. The public summary should be no more than 300 words in length and should be prepared in both English and the native language of the non-US team.

Note: CRDF Global may use the public summary in publicly-distributed documents and other materials.

Do not include proprietary or business-sensitive information.

RECOMMENDED PUBLIC SUMMARY OUTLINE:

Goals (list up to three):

1.

2.

3.

Research Problem Statement

This should include a brief statement about the research problem you attempted to solve; the importance of this problem to the scientific community; and a description of how the results of your research contributed to solving the problem and/or furthering knowledge in the field.

Summary of Research Findings and Research Impacts

This section should address the following (described in more detail below). When thinking about each issue, we encourage you to consider the kind of impact your research has on local, national, regional, and international levels.

- Benefit to Institution
- Furthering Knowledge in the Research Field
- Potential Applications (Solving societal problems and/or providing basis for commercial applications)
- Follow-On Activities/Next Steps

Benefit to Institute:

This should state briefly how your research findings benefited your home institution. Please state briefly the research problem you attempted to solve and the importance of this problem to the scientific community and how the results of your research contributed to solving the problem and/or furthering knowledge in the field.

Furthering Knowledge in the Field:

This paragraph should explain how your specific research project will contribute to expanding general knowledge in your scientific discipline.

Potential Applications:

This paragraph should highlight how the results of your research address significant societal problems and/or will contribute to the development of commercial materials.

Public Summary (English):

Goals:

- Reveal phylogenetic / phylogeographer peculiarities of M. tuberculosis strains in Moldova; study the local characteristics of causative agent circulation throughout the country.
- Establish the profiles of M. tuberculosis isolates genotypes and the importance of these in transmission of infection; investigate the differences between genomes of TB strains with varied drugs resistance and clinical manifestation of disease;
- Collect the clinical metadata that describes patients' history will allow for the selection of strains from hundreds of samples, providing a unique opportunity to study the variability and dynamics of TB genome mutations

For project implementation were selected 157 TB patients, new (64) and retreatment cases (93), with culture positive results, from 32 administrative territories of Moldova, who became ill in period from March 2015 up to February 2016. All patients were investigated microbiologically: sputum smear microscopy, GeneXpert MBT/RIF, culture and drug susceptibility testing. M.tuberculosis strains were isolated using solid (Lowenstein-Jensen) and liquid (BACTEC MGIT960) methods. The clinical and radiological metadata that describes the diseases history and treatment outcomes of selected patients, were collected using the special questionnaire. Most of selected patients were aged between 25 and 54 years – 77.1% (n=121). From these male was 77.1% (n=121) and male 22.9% (n=36) patients. TB New cases was 64 (47 males and 17 female) and 93 (74 males and 19 females) patients. The majority of selected patients was with MDRTB and XDRTB – 82.8% (65 patients in each group), only 10.2% (n=16) of patients were non-MDR and 7.0% (n=11) was with pre-XDR resistance pattern. HIV infected were 11 (8 males and 3 female) patients; from these five with MDR, one with pre-XDR and five with XDRTB. 55% (n=6) of patients with TB/HIV co-infection died during first year of treatment. In total from cohort of patients with pre- and XDRTB (n=76) in the first year of treatment 33% (n=25) died. All information of selected patients was included in the TB Portal site. The DNA extraction was performed from 96 M. tuberculosis strains for future WGS examination. The WGS results will promote the possibilities to perform comparative analysis of all existing TB genomes, find SNPs and find correlations of genome variations with patients' medical history, and resistance of corresponding bacteria to known drugs. Will be possible to look for variants with high association to the MDR and XDR phenotypes, as well as resistance to specific drugs using the clinical and in vitro data available for these samples.

Public Summary (Non-U.S. Team Native Language – please copy if both teams are non-U.S. teams with different native languages):

For project implementation were selected 157 TB patients, new (64) and retreatment cases (93), with culture positive results, from 32 administrative territories of Moldova, who became ill in period from March 2015 up to February 2016. All patients were investigated microbiologically: sputum smear microscopy (SSM), GeneXpert MBT/RIF, culture and drug susceptibility testing (DST). M.tuberculosis strains were isolated using solid (Lowenstein-Jensen) and liquid (BACTEC MGIT960) methods. The clinical and radiological metadata that describes the diseases history and treatment outcomes of selected patients, were collected using the special questionnaire. Most of selected patients were aged between 25 and 54 years – 77.1% (n=121). From these male was 77.1% (n=121) and male 22.9% (n=36) patients. TB New cases was 64 (47 males and 17 female) and 93 (74 males and 19 females) patients. The majority of selected patients was with MDRTB and XDRTB – 82.8% (65 patients in each group), only 10.2% (n=16) of patients were non-MDR and 7.0% (n=11) was with pre-XDR resistance pattern. HIV infected were 11 (8 males and 3 female) patients; from these five with MDR, one with pre-XDR and five with XDRTB. 55% (n=6) of patients with TB/HIV co-infection died during first year of treatment. In total from cohort of patients with pre- and XDRTB (n=76) in the first year of treatment 33% (n=25) died. All information of selected patients was included in the TB Portal site. The DNA extraction was performed from 96 M.tuberculosis strains for future WGS examination. The WGS results will promote the possibilities to perform comparative analysis of all existing TB genomes, find SNPs and find correlations of genome variations with patients' medical history, and resistance of corresponding bacteria to known drugs. Will be possible to look for variants with high association to the MDR and XDR phenotypes, as well as resistance to specific drugs using the clinical and in vitro data available for these samples.

SECTION II: TECHNICAL REPORT

Instructions:

The technical report should be **no more than five (5) pages in length with one-inch margins on all sides and a font no larger than Arial 10pt (or equivalent).** The technical report should outline the goals of the original research project and provide a technical description of how these goals were or were not met, highlighting specific achievements.

Note: Please do not re-submit the project narrative from the original proposal.

Note: From time to time, CRDF Global conducts a review of completed grant projects for possible inclusion in publicity materials, for presentations at symposia, etc. In connection with this, CRDF Global occasionally asks expert reviewers from the original grant selection panels to review the final technical reports to assist staff in selecting projects for possible feature in such activities. CRDF Global does not use specific information (except as otherwise indicated in these Final Project Report instructions) about individual projects in publicity activities without the permission of both Principal Investigators.

Technical Report:

Tuberculosis (TB) now kills more people than any other infectious disease. Of the 9 million individuals the World Health Organization (WHO) estimated in 2014 to have newly acquired TB, around 1.5 million died. From these approximately 480,000 had multidrug resistant tuberculosis (MDR-TB) and estimated 40% of those patients died within one year, accounting for almost 13% of total TB deaths in this year.

Patients with drug resistant TB (DR-TB) have a much greater risk of dying than those with drug susceptible TB. Resistance to second-line anti-TB drugs can increase this risk more than fourfold with treatment success rates as low as 30%. The rise of multidrug resistant tuberculosis and extremely drug resistant tuberculosis (XDR-TB) is a severe threat to effective TB control as well as to successful treatment of individual patients. The concern that these strains could spread around the world further stresses the need for additional control measures, such as new diagnostic methods, better drugs for treatment. Patients harboring MDR strains of Mycobacterium tuberculosis need to be entered into alternative treatment regimens involving second-line drugs that are more costly, more toxic, and less effective. XDR-TB now constitutes an emerging threat for the control of the disease and the further spread of drug resistance, especially in HIV-infected patients [6, 7].

The highest incidence of MDR-TB (about 20% of new and 60% of re-treatment cases) is reported in Eastern Europe for some of the countries of the former Soviet Union. To date there are no studies that have examined the genomic composition of M. tuberculosis isolates from the former Soviet Union.

The Republic of Moldova is high burden TB and MDRTB country. In 2014 WHO estimated the TB prevalence at 229/100000 populations and TB incidence was 153/100 000 population, which is the highest in the European Region of the WHO. The prevalence of MDR-TB in the Republic of Moldova was 22,6% in new cases and 63.4% among re-treatment cases in 2014 (Diagram 1, D2).

Diagram 1. TB Prevalence and Incidence in Europe, 2014

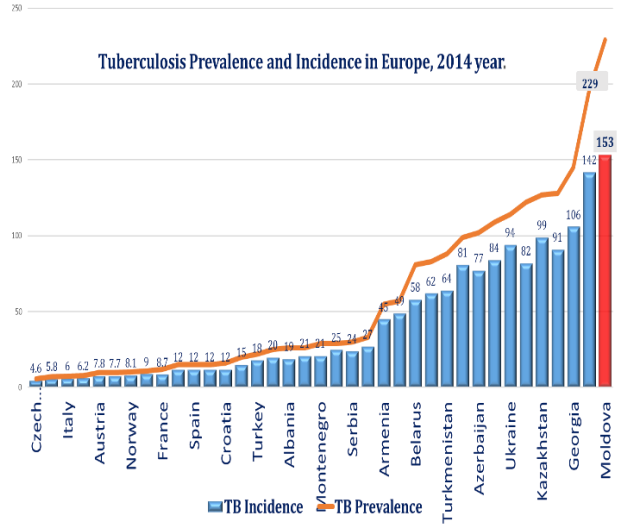
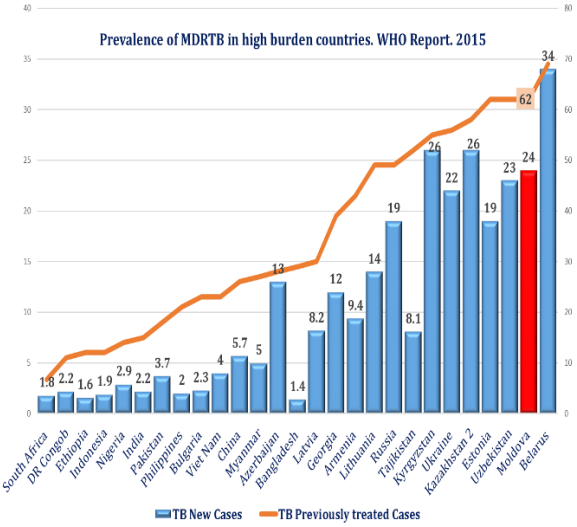
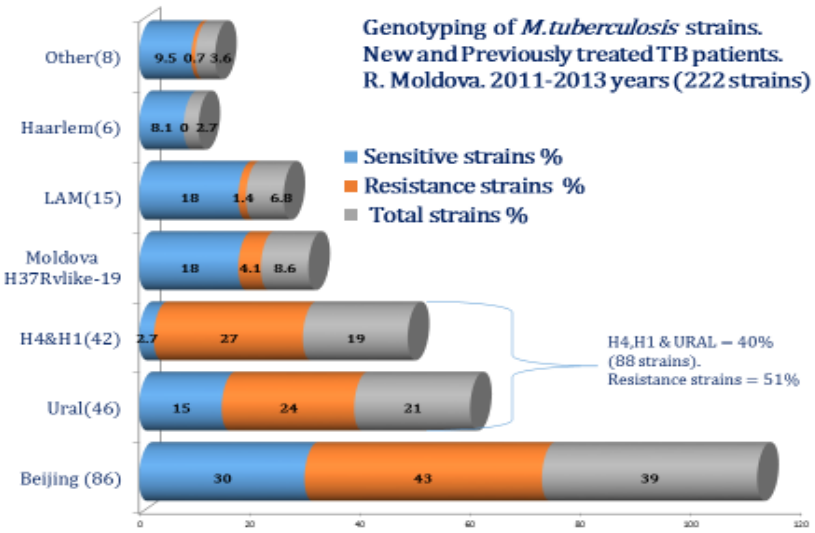


Diagram 2. Prevalence of MDRTB in Europe, 2014



Reasons of high TB and MDR-TB burden in country include poverty, lack of rapid diagnostic capacities and inconsistent availability of anti-TB drugs, especially for the treatment of MDR-TB (6,7). Re-infection, or nosocomial transmission of resistance strains are common for former Union countries. Patients with TB, especially with MDR-TB, are long-term hospitalized and hospitals are inadequately equipped with infection control measures to prevent nosocomial infection [8,9,10]. Others reasons of high MDRTB prevalence could be the large, predominance distributions of Beijing genotype of M. tuberculosis among TB patients in country, who are linked with drug resistance, in special among MDRTB patients. According the last study, performed by National Reference Laboratory from Chisinau in collaborations with Research Center Borstel from Germany and California University from San Diego, US, the Beijing and H4(Ural) genotypes of M. tuberculosis were presents among MDRTB patients in most of 75% of cases (11). The study results of the genotyping of M. tuberculosis strains are presented in diagram 3.

Diagram 3. Distribution of M. tuberculosis genotypes among susceptible and MDR&XDRTB patients



Sequencing of genomes for MDR-TB and XDR-TB is essential, as the presence of expected sequence diversity in M. tuberculosis would provide a basis for understanding pathogenesis, immune mechanisms, and bacterial evolution. The bacterial factors that contribute to disease severity and type, in addition to host genetics, and the environment, remain still largely ill-defined. Understanding the mechanisms of drug resistance, virulence, spreading of M. tuberculosis, manifestation and clinical course of TB disease, based on a full genomic analysis is extremely important both for Moldova health programs and to support worldwide efforts to combat the disease.

Genomic comparison has shown that gene content can vary between strains of M. tuberculosis. The analysis of complete genome sequences from clinical isolates identified that single nucleotide polymorphisms (SNPs), large sequence polymorphisms (LSPs), and regions of difference (RDs) originate from small deletions, deletions in homologous repetitive elements, point mutations, genome rearrangements, frame-shift mutations, and multi-copy genes [14, 15].

Complete sequencing of the M. tuberculosis genome (21, 22) led to a large body of literature indicating that DR in M. tuberculosis is mainly due to single nucleotide mutations (SNPs) in specific genes (23-25). These well documented drug resistance-conferring mutations now form the basis of a variety of molecular R-DST platforms currently in use or being developed (26).

The main purpose of this study was to sequencing about 150 DNA genomes of M. tuberculosis strains collected from M&XDR TB patients from Moldova.

Goals:

- Reveal phylogenetic/phylogeographer peculiarities of M. tuberculosis strains in Moldova; study the local characteristics of causative agent circulation throughout the country.
- Establish the profiles of M. tuberculosis isolates genotypes and the importance of these in transmission of infection; investigate the differences between genomes of TB strains with varied drugs resistance and clinical manifestation of disease;
- Collect the clinical metadata that describes patients' history will allow for the selection of strains from hundreds of samples, providing a unique opportunity to study the variability and dynamics of TB genome mutations.

Eligibility

To be eligible for study enrollment, individuals were collected in concordance with Inclusion Criteria and Exclusion Criteria. HIV-positive individuals and HIV-negative individuals were included in this study.

Inclusion criteria

Male and female, New & Relapse TB patients of any ethnicity and race, HIV negative and positive, if they:

- have signed informed consent to specimen collection,
- are 18 years of age or older; and
- are known to be sputum smear-positive, based on prior examination of sputum; and
- have positive culture on liquid or solid media and
- have DST result by phenotypic or genotypic tests and
- are sensitive strain to all first line TB drugs, or
- are confirmed resistance to INH&RIF, or
- are confirmed resistance to INH&RIF and quinolone and one injectable drugs

After submission of the informed consent, participants were asked to provide at least 3 sputum specimens of min 3 ml in volume. The sputum was tested by SSM, GeneXpert MTB/RIF, MGIT, LJ culture.

Exclusion Criteria:

- Patients are not included for the study if the quantity of respiratory secretions was not sufficient;
- TB Patients with only extra-pulmonary disease;
- TB Patients under 18 years of age;
- Inability to provide informed consent.
- Subject enrollment

Screening.

Adult subjects meeting inclusion criteria was asked to participate. TB Patients was recruited at outpatient clinic office and inpatient hospital settings. Individuals was asked by clinic staff if they would be interested in participating in the study. Interested individuals were referred to study personnel for informed consent procedure. Participants was told that participation is voluntary and that they have the opportunity to ask questions individually.

For project implementation were selected 157 TB patients, new (64) and retreatment cases (93), with culture positive results, from 32 administrative territories of Moldova, who became ill in period from March 2015 up to February 2016. All patients were investigated microbiologically: sputum smear microscopy, GeneXpert MBT/RIF, culture and drug susceptibility testing. M.tuberculosis strains were isolated using solid (Lowenstein-Jensen) and liquid (BACTEC MGIT960) methods. The clinical and radiological metadata that describes the diseases history and treatment outcomes of selected patients, were collected using the special questionnaire. Most of selected patients were aged between 25 and 54 years – 77.1% (n=121). From these male was 77.1% (n=121) and male 22.9% (n=36) patients. Distribution of selected patients by sex and age is present in table 1.

Table 1. Distribution of selected TB patients by sex and age

Age groups	*18-24*	*25-34*	*35-44*	*45-54*	*55-64*	*65>*	*Total*
Male	8	26	37	32	15	3	121
Susceptible	0	5	7	3	4	0	19
%	0.0	4.1	5.8	2.5	3.3	0.0	15.7
MDRTB	6	12	14	11	7	2	52
%	5.0	9.9	11.6	9.1	5.8	1.7	43.0
XDRTB	2	9	16	18	4	1	50
%	1.7	7.4	13.2	14.9	3.3	0.8	41.3
Male, %	6.6	21.5	30.6	26.4	12.4	2.5	100.0
Female, no	5	13	10	3	2	3	36
Susceptible	1	1	3	1	1	1	8
%	2.8	2.8	8.3	2.8	2.8	2.8	22.2
MDRTB	4	3	3	1	1	1	13
%	11.1	8.3	8.3	2.8	2.8	2.8	36.1
XDRTB	0	9	4	1	0	1	15
%	0.0	25.0	11.1	2.8	0.0	2.8	41.7
Female, %	13.9	36.1	27.8	8.3	5.6	8.3	100.0

TB New cases were 64 patients (47 males and 17 female) and re-treatment cases were 93 patients (74 males and 19 females). The majority of selected patients were MDRTB and XDRTB – 82.8% (65 patients in each group), only 10.2% (n=16) of patients were non-MDR and 7.0% (n=11) was with pre-XDR resistance pattern. Distribution of selected patients by type of diseases and resistance pattern is present in table 2.

The co-morbidities were notified at 42.3% (n=25) of MDR TB and at 45.7% (n=27) of XDR TB patients. HIV infected were 11 patients (8 males and 3 female); from these five with MDR, one with pre-XDR and five with XDRTB. 55% (n=6) of patients with TB/HIV co-infection died during first year of treatment. In total from cohort of patients with pre- and XDRTB (n=76) in the first year of treatment 33% (n=25) died.

Table 2. Distribution of selected patients by type of diseases and resistance pattern

TB Patients, Male	*Susceptible*	*MDRTB*	*Pre-XDRTB*	*XDRTB*	*Total Male*
New Cases, no	10	30	0	7	47
%	21.3	63.8	0	14.9	100
Relapse, no	0	13	1	8	22
%	0	59.1	4.5	36.4	100
After Default, no	0	3	3	11	17
%	0	17.6	17.6	64.7	100
After Failure, no	0	6	5	24	35
%	0	17.1	14.3	68.6	100
TB Patients, Female	*Susceptible*	*MDRTB*	*Pre-XDRTB*	*XDRTB*	*Total Female*
New Cases, no	6	8	0	3	17
%	35.1	47.1	0	17.7	100
Relapse, no	0	2	0	3	5
%	0	40	0	60	100
After Default, no	0	0	0	3	3
%	0	0	0	100	100
After Failure, no	0	3	2	6	11
%	0	27.3	18.2	54.6	100
Total patients, no	**16**	**65**	**11**	**65**	**157**

All information of selected patients was included in the TB Portal site. The DNA extraction was performed from 96 M. tuberculosis strains for future WGS examination. The WGS results will promote the possibilities to perform comparative analysis of all existing TB genomes, find SNPs and find correlations of genome variations with patients' medical history, and resistance of corresponding bacteria to known drugs. Will be possible to look for variants with high association to the MDR and XDR phenotypes, as well as resistance to specific drugs using the clinical and in vitro data available for these samples.

Conclusions:

1. For purpose of project were collected 157 M. tuberculosis strains of TB patients, with sensitive and resistant form of TB, from different territories of Moldova.
2. The results of microbiological investigations, the clinical and radiological data of examinations were collected. The majority of selected patients was with MDR TB and XDR TB – 82.8% (65 patients in each group), only 10.2% (n=16) of patients were non-MDR and 7.0% (n=11) were with pre-XDR resistance pattern.
3. All information of selected patients was included in the TB Portal site. For the future WGS examination, 96 M. tuberculosis isolated strains were selected, the DNA extraction was performed and was organized the shipment to Broad Institute, US.
4. The WGS results will promote the possibilities to perform comparative analysis of all existing TB genomes, find SNPs and find correlations of genome variations with patients' medical history, and resistance of corresponding bacteria to known drugs. Will be possible to look for variants with high association to the MDR and XDR phenotypes, as well as resistance to specific drugs using the clinical and in vitro data available for these samples.

SECTION III: BIBLIOGRAPHY OF PROJECT-RELATED PUBLICATIONS

Instructions:

In this section, please list the following:

1) Peer reviewed journal publications; and
2) Other non-peer reviewed journals; or
3) If no publications resulted from your research, an explanation for why and a plan for publishing results in the future.

Please use the format provided below to list publications for both the peer reviewed journals and the other non-peer reviewed journals or articles.

For a journal or magazine article:

Format:

Author Name(s). "Article Title." Journal Name Volume (Year): Page Numbers. (Country of publication)

Note:

- It is imperative to list the country of publication in addition to other citation information.
- Please do not abbreviate the titles of journals or other publications.
- Please do not include abstracts from conferences and conference proceedings. Such abstracts should be cited in Section VI, Conference Presentation List.
- If you include items that have been submitted for publication but have not yet been accepted for publication, please clearly mark these items as "submitted" at the end of the citation.

Example:

Feldstein, M.M., I.M. Raigarodskii, A.L. Iordanskii, and J. Hadgraft. "Modeling of percutaneous drug transport in vitro using skin-imitating Carbosil membrane." Journal of Controlled Release 52 (1998): 25-40. (Country of publication)

For a book:

Format:

Author Name. Title. Place: Publisher, Copyright Year. (Country of publication)

Example:

Ebbing, Darrell D. General Chemistry. Boston: Houghton Mifflin Company, 1996. (Country of publication)

Peer Reviewed Journals List:

1.
2.
3.
4.

Other Non-Peer Reviewed Journals List:

1.
2.
3.
4.

1. If you do not have any project-related publications to cite, please explain:

Is planning to publish then the results of WGS assay will be finished. The WGS results will promote the possibilities to perform comparative analysis of all existing TB genomes, find SNPs and find correlations of genome variations with patients' medical history, and resistance of corresponding bacteria to known drugs. Will be possible to look for variants with high association to the MDR and XDR phenotypes, as well as resistance to specific drugs using the clinical and in vitro data available for these samples.

2. Are you planning on publishing in the near future?

   ___**Yes.**

3. If yes, please provide details about planned publications, including the expected journal/book title(s) and submission date(s).

The publication will be published in the local journal "Bulletin of Academy of Science from Moldova".

Also the presentation on UNION conference and abstract will be submitted.

SECTION IV: PROJECT-RELATED CONFERENCE PRESENTATIONS

Instructions:

In this section, please list any project-related conference presentations made by any team members.

Please use the format below to list conference presentations.

Format:

Presenter's Name(s). "Presentation Title, (Type of Presentation*), Conference/Workshop Name, Dates of Conference, Location of Conference.

> **Note*:*** For "Type of Presentation," please indicate either "Oral Presentation" or "Poster Presentation."

Example:

KIordanskii, A. L. "Diffusion Modeling of the Propranol Drug Delivery from a Hydrophilic Transdermal Therapeutic System," (Oral Presentation), Third Spanish-Portuguese Conference on Controlled Drug Delivery, September 6-9, 1998, Lisbon, Portugal.

Project-Related Conference Presentation List:

1.
2.
3.
4.

1. If you have not made any conference presentations, please explain:

2. Are you planning to make any conference presentations in the near future?

   ___Yes

3. If yes, please describe planned presentations and list the titles, dates and locations of the respective conferences.

Annually Conference of Phthisiopneumology Society from Moldova, September 2016. Chisinau

SECTION V: SUPPLEMENTAL INFORMATION (optional)

Instructions:

CRDF Global appreciates receiving supplemental information, such as photographs, publicity articles, publication copies, Power Point presentations, or other materials. Please send such materials along with your Final Report to finalreports@crdfglobal.org.

If you submit photographs, please be sure to identify all persons pictured and indicate their roles in the CRDF Global project. Please be aware that unless you indicate otherwise, CRDF Global reserves the right to use photographs and other materials above in publicly distributed CRDF Global documents.

1. Do you have supplemental information you would like to provide to CRDF Global at this time?

   ___No

2. If yes, please list supplemental information.

1.
2.
3.
4.
5.

Final Report Checklist

Please make sure that **all** sections listed below are included and properly indicated in your report. For your own reference, review your final report and check off each item that is included.

Section I: CGP Project results & Accomplishments

☒ Brief Statement of Major Accomplishments

☒ Public Summary

Section II: Technical Report

☒ Technical Report (**no longer than five (5) pages**)

Section III: Bibliography of Project-Related Publications

☒ Peer Reviewed Journals List

☒ Other Non-Peer Reviewed Journals List

☒ Plans for publishing if no project-related articles have been published or submitted

☐ Citation Index

Section IV: Project-Related Conference Presentations

☒ Project-Related Conference Presentation List

☒ Plans for making project-related conference presentations if none have been made

Section V: Supplemental Information (optional)

Do you have supplemental information you would like to include:

☐ Yes ☐ List of Supplemental Information (if applicable)

☒ No

Note: For your Final Report to be considered complete, the Team Surveys completed by the respective teams must also be submitted to finalreports@crdfglobal.org. Download all Final Report documents at http://www.crdfglobal.org/grants-and-grantees/forms-templates.