

Deliverable D-JRP19 **Workpackage** WP1.1

Responsible Partner: ISS Contributing partners: SVA





GENERAL INFORMATION

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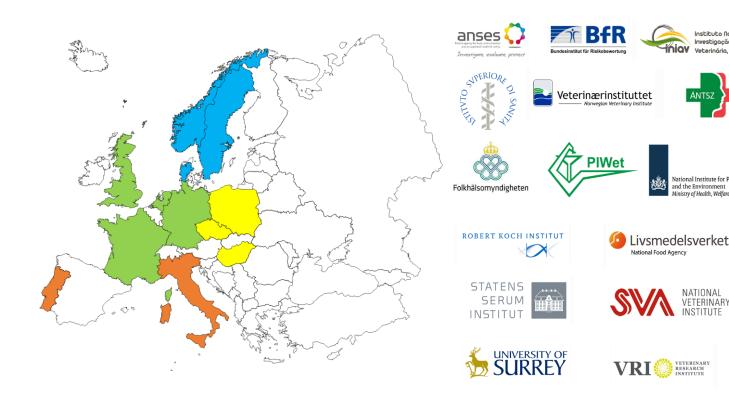
DOCUMENT MANAGEMENT

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Other contributors	Karin Troell				
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KICK-OFF ANNUAL MEETING of PARADISE PROJECT ORGANIZED by ISS in ROME (ITALY)





1.1. The PARADISE PROJECT

PARADISE (https://onehealthejp.eu/jrp-paradise/) is a multicentre collaborative international project (2020-2022) composed by 15 partners from 12 Europena countries. PARADISE aims at delivering informative typing schemes and innovative detection strategies applicable to food matrices for both parasites. Using NGS technologies (genomics and metagenomics), the project will generate much needed data that will enrich our understanding of the epidemiology and genomics of these organisms, and provide the basis on which improved strain-typing schemes will be developed and rigorously tested. In parallel, strategies (nanobodies, aptamers, use of hybridization probes) to enrich for the target pathogens in different matrices will also be developed and tested. Furthermore, PARADISE will engage in multicentre studies to validate the newly developed methods, testing their applicability across the spectrum of



[03/04/2020]



relevant matrices in an unprecedented effort at the EU level. These new methodologies will form the basis for integrated approaches aimed at controlling FBPs in the European food chain. Technical workshops on milti-locus typing schene and on enrichment strategies will be organized.

1.2 AGENDA of THE KICK-OFF MEETING HELD on 10-11 FEBRUARY in ROME, ITALY

Here we report all the activities launched and discussed during the 1.5 working days of the PARADISE project.

DAY 1 (10/02/2020)

8:45 - 9:00	Registration (ISS)
9:00 - 9:05 Deputy)	Welcome – Simone M. Cacciò (Project Coordinator, ISS) and Karin Troell (SVA,
09:05 - 09:30	Tour of the Table: Quick consortium presentation (All)
9:30 - 9:45	Introduction to One Health EJP (Simone M Cacciò, ISS)
9:45 – 11:00	 Introduction to the PARADISE project Overall goals and strategy (K Troell, SVA)
11:30 – 12:30	WP1: Coordination and impact (Simone M Cacciò, ISS)
11:00 - 11:30	Coffee/tea break
11:30 – 12:30	WP2: NGS-based genomics and metagenomics[General intro: Yannick Blachard, ANSES]
	 Task 2.1 NGS-based genome study of selected isolates of <i>C. parvum</i> and <i>G. duodenalis</i> (SM Cacciò, ISS, Yannick Blanchard, ANSES) Task 2.2 In silico analyses of metagenomes for detection of foodborne parasites (Frits Franssen, RIVM) Task 2.3 Experimental amplicon-based and shotgun metagenomics for detection of foodborne parasites (Rune Stensvold, SSI) Discussion
12:30 - 13:30	Lunch break
13:30 – 14:30	WP3: Design, implementation and validation of multi-locus typing schemes • [General intro: Karin Troell SVA, Christian Klotz, RKI]
	 Task 3.1 In silico selection of informative loci from comparative genomics data (Karin Troell SVA, Christian Klotz, RKI) Task 3.2 Development of MLST schemes for C. parvum and G. duodenalis (Martha Benson, UoS, Simone M Cacciò, ISS) Task 3.3 Interlaboratory comparison of typing schemes (Anne Mayer Scholl, Bfr) Discussion
14:30 – 15:30	WP4: Parasite enrichment strategies • [General intro: Marco Lalle, ISS]
	Task 4.1 Development of pre-DNA extraction enrichment strategies (Christian Klotz, RKI, Gregory Karadjan, ANSES) Page 4

PARADISE kick-off meeting hosted by ISS in Rome, Italy





- Task 4.2 Development of post-DNA extraction enrichment strategies (Marts Isaksson, SVA)
- Discussion

15:30 - 16:00 Coffee/tea break

16:00 – 17:00 General Discussion

[Moderators: Simone M Cacciò, ISS, Karin Troell SVA]

17:00 End of day 1

20:00 - Social dinner in Rome (Organized by ISS)

DAY 2 (11/02/2020)

09:00 - 09:30	Communication and dissemination in OHEJP projects (Pikka Jokelainen, SSI)
9:30 – 10:30	 General Discussion [Moderators: Simone M Cacciò, ISS, Karin Troell SVA] Focus on Year 3: work plan, milestones and deliverables
10:30 - 11:00	Coffee/tea break
11:00 – 13:00	 General Discussion [Moderators: Simone M Cacciò, ISS, Karin Troell SVA] Task allocation Any other business
13:00	End of the meeting

Major discussion points

The discussion focused on three main topics: bioinformatics, collection of samples and SOPs for procedures.

Bioinformatics:

- *Cryptosporidium and Giardia need different appraoches for sequence data processing
- *A pipeline is available for *Cryptosporidium*, while for *Giardia* it should be developed (although it may be possible to start by testing that for *Cryptosporidium*)
- *There are good reference genomes for *C. parvum*. RKI should soon have reference genomes of high quality (from combined PacBio and Illumina experiments) for *Giardia* Assemblages AII and B.
- *There is a need for a shared platform to store genome data (those available and those to be generated) so that all bioinforaticians can access them.
- *There is a need for a questionaire/sheet to gather metadata from collected samples in a harmonised way

Collection of samples:

*The nature fo the metadata to be collected was discussed. The minimum information should comprise the host/matrix, geographic origin, and time of collection. Additional information may





include presence of clinical symptoms, possble link to outbreak and all other relevant epidemiological data

*For WP2, Whole Genome Sequencing

- -Send samples to ISS or SVA for clean up and DNA extraction
- -Minimum requierment is that they are rich/semirich on (oo)cysts and that typing is performed (at least species identification)
- -preferrably a broad range of samples representing different countries and/or different hosts
- -all partners involved except SLV

*For WP3 testing markers

- -An informative panel of samples is needed. Ideally, the panel should include samples from outbreak and sporadic cases, from different hosts and different subtypes (for *Cryptosporidium*)
- -If genomic DNA cannot be sent, at least speciation needs to be done before sending feces.
- -Four different partners will run the initial tests (ISS, RKI, SVA and UoS)

*For WP2 metagenomics

- -spiking with three organisms (Giardia, Cryptosporidium and Toxoplasma)
- -VRI is responsible for spiking the food matrix
- -if partners have metagenomic datasets with known occurence of these parasites, send to RIVM

SOPs

- *SOPs for DNA extraction and (oo)cyst cleanup will be sent to partners
- *SOPs for spiking salad
- *SOPs for species identification of both *Cryptosporidium* and *Giardia* ISS/SVA will compile and share the documents.

Other points of discussion:

- *The OHEJP has set specific communication and dissemination rules. Adherence to these rules is important
- *A steering committee, with one representative for each partner Institute, is needed. ISS will contact by e-mail all partners and ask to nominate the person.
- *A common place to share data and ensure good flow of information is desirable. The OHEJP web page is a logical choice.
- *Suggestions of experts to be included in the advisory board are needed. The advisory board should to meet 1-2 times per year.





1.3 LIST of PARTICIPANTS

Funded partners

INSTITUTE	NAME and SURNAME	COUNTRY
ANSES	Yannick Blanchard Gregory Karadjan	France
Bfr	Anne Mayer-Scholl Smita Sutrave	Germany
INIAV	Jacinto Gomes	Portugal
ISS	Simone M Cacciò Marco Lalle Paolo Vatta Anna Rosa Sannella Federica Santolamazza Azzurra Santoro Alessandra Ludovisi	Italy
NVI	Rebecca Davidson	Norway
OKI	Judith Olutzer István Kucsera	Hungary
PHA	Ioana Bujila	Sweden
PIWET	Jacek Sroka Weronika Piotrowska	Poland
RIVM	Frits Franssen	the Netherlands
RKI	Christian Klotz	Germany
SSI	Rune Stensvold Pikka Jokelainen	Denmark
SVA	Karin Troell Mats Isaksson Emma Östlund	Sweden
VRI	Iva Slana Bretislav Koudela	Czech Republic
UoS	Martha Benson	United Kingdom
Associate partner		
INSTITUTE	NAME and SURNAME	COUNTRY
CRU	Rachel M Chalmers	United Kingdom





Picture of the participants to the kick-off meeting of the PARADISE project organized by ISS in Rome, Italy on 10-11 February 2020.

