

## Work package 7

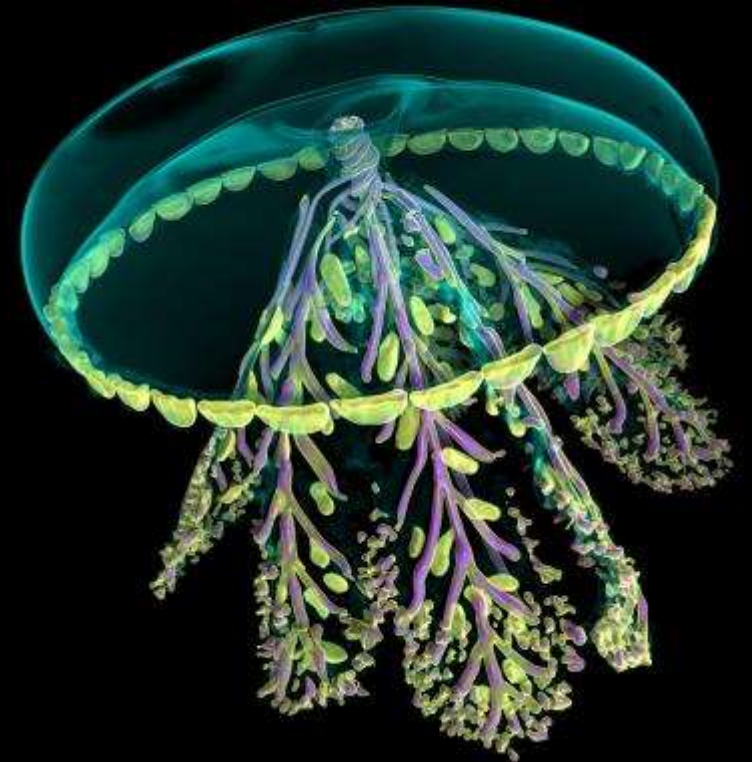
### JRA2: Collections on Demand

Christos Arvanitidis (HCMR)

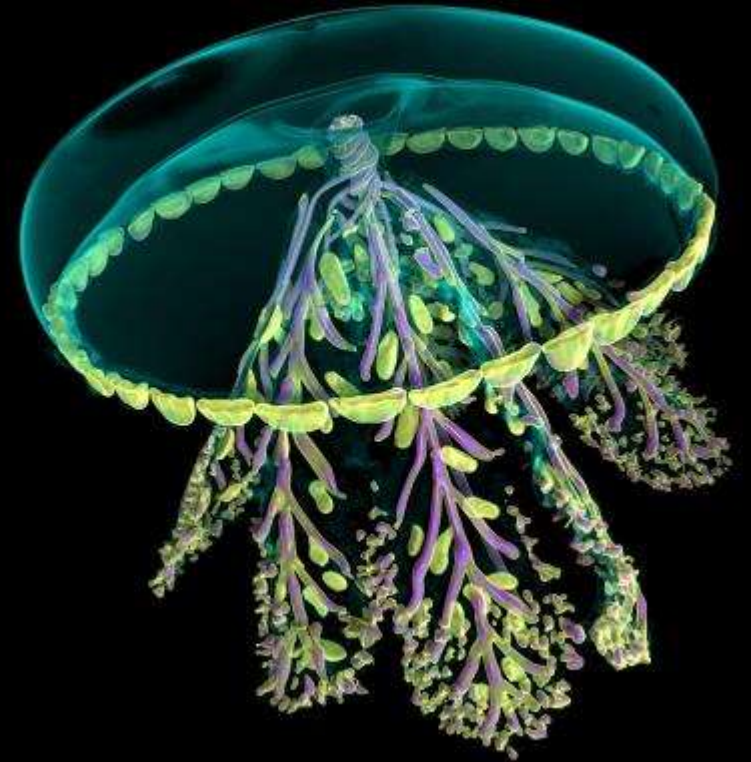
Peter Hollingsworth (RBGE)

Patricia Mergen (BGM)

Patrick Semal (RBINS)



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Nesrine Akkari, Dominik Zimmermann, Silke Schweiger, Karin Wiltschke;  
RBINS: Patrick Semal, Jonathan Brecko, Thierry Bakeljau; RMCA: Didier  
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Steven Janssens; BGBM: Gabriele Droege, Eva Häffner; MfN: Christiane  
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Arvanitidis, Eva Chatzinikolaou, Niki Keklikoglou, Emmanouella Panteri,  
Eirini Filiopoulou, Dimitra Mavraki, Panagiotis Kasapidis, Georgios Kotoulas,  
Dimitris Tsaparis, Jon Bent Kristoffersen; Naturalis: Wouter Addink; TDWG  
Ana Casino; RBGE: Peter Hollingsworth, Rachael Brewer, Suzanne Cube  
Michelle Hart, Laura Forrest; RBGK: Alan Paton, Tim Fulcher; NMP: Jiří  
Frank; SMNS: Joachim Holstein, Juan Carlos Monje; ZFMK: Claudia Koch,  
Katharina Schmidt-Loske; UCPH: Nina Rønsted; LUOMUS: Aino Juslén;  
HNHM: Gábor Csorba; HUJ: Gila Kahila Bar-Gal; NRM: Irene Bisang



Raise the current TRL3 to TRL7; Combine  
scientific knowledge of biodiversity and natural ecosystems with the societal demands by  
enhancing availability of digital Collections on Demand (CoD)

Develop a workflow  
to support requests  
for VA to collections

Establish the IoD for  
collections as a  
service

Develop laboratory  
protocols and workflows,  
increasing success,  
scalability and  
cost-effectiveness of DNA  
sequence recovery

## Innovation-1: Laying the foundations of the VMNH

Expanding  
and  
developing  
cost models  
for CoD

Developing  
standards and  
guidelines for  
exchange of  
collection-  
derived imaging  
data

New data pipelines  
and standard  
workflows,  
enabling access to  
complex digital  
content  
such as 3D scans

Novel molecular  
lab protocols,  
workflows and  
informatics  
pipelines, to  
enable large scale  
DNA sequencing  
of NH collections

## Innovation-2: Mobilising resources

Strong focus on use cases (tasks 7.2, 7.3) that exploit NH collections to address high-profile research questions  
and/or tackle contemporary societal challenges

Combined high-throughput imaging and sequencing:  
in some cases (e.g. specific collections of insects),  
the same samples will be used in 3D imaging and DNA sequencing protocol development

### Task 7.1

- Digitisation-as-a-Service (DaaS) model
- BGM
- Prioritise requests
- Refine evaluation criteria
- Run two calls (in year 2 and year 3)
- Workflow will be integrated into ELViS (JRA1)

### Task 7.2

- Developing processes and pipelines for high resolution imaging services, including 3D models of NH specimens: Imaging on Demand (IoD)
- RBINS + HCMR
- Develop a high throughput process for delivering research data supporting VA to complex imaging data sets
- Review the techniques used for high resolution 2D, 2D+ and 3D digitisation of NH specimens
- Standardisation, protocols, best practice, efficient use of resources, semantics, storage capabilities and data access

### Task 7.3

- Developing the protocol infrastructure for DNA Sequencing on Demand (DNAoD)
- RBGE
- Enhance genetic and genomic accessibility of preserved collections
- Enhance protocols for amplicon free approaches
- Protocols: (a) organelle genome recovery via targeted capture, (b) hyb-seq recovery of 100s of nuclear loci, and (c) genome skimming

### Del 7.1

- Peer-reviewed paper on the implementation, assessments and sustainability business plan of VA
- M40

### Del 7.2

- Data pipelines and standard workflows, enabling online access to complex digital content (3D scans)
- M30

### Del 7.3

- Peer-reviewed publication providing synthesis of cost-effective and scalable work flows for DNA sequencing NH collections
- M44



## Dissemination Plans



Peer-reviewed  
journal or  
Conference  
Publications



Calls for proposals,  
Meetings, Workshops,  
Conferences, engaged  
SMEs



Pipelines and  
workflows  
available on the  
web



Web media, such  
as facebook,  
twitter, emailing  
lists



## CoD is placed centrally in the activities of DiSSCo (High-level Objectives)

### Other RIs and (similar) initiatives:

- LifeWatch ERIC
- EMBRC ERIC
- eLTER
- BioImaging
- IBOL Phase 2 'Bioscan': DNA identification of life on earth
- Earth Biogenomes: Genome sequencing life on earth
- Veterinary science (ichthyopathology vLab)
- Medical science (STEMI vLab)
- Material science
- Space geology (meteorite material)



- Planned meetings
  - WP meeting during the kick-off
  - WP meetings during Project meetings
  - Extra VideoConf meetings where needed
- Key stakeholders
  - Partners: **HCMR, BGM, RBGE, RBINS**, NHM, NHMW, RMCA, CSIC, MNHN, Naturalis, TDWG, RBGE, MfN, RBGK
  - Main stakeholders: TDWG, Data and Standards Consortia (e.g. GBIF/OBIS, GSC, etc.), IBOL (International Barcode of Life), ERICs and RIs at many scales and from many disciplines, Industry

- Risks
  - Multi-tasking
  - Delays and difficulties in WP cooperation
  - Long-time investment to start “paying-off”
  - Communication / dependencies between work in different institutions (mitigated by regular scheduled dialogue, and clarity at the outset of expectations and responsibilities)
  - Technical barriers to protocol development (mitigated by effective troubleshooting networks in place and extensive experience of the project team)
  - Others???

**Any questions?**

