TEMPLATE FOR THE PREPARATION OF A TECHNICAL BACKGROUND DOCUMENT FOR A NATIONAL STRATEGIC ACTION PLAN FOR THE CONSERVATION AND SUSTAINABLE USE OF CROP WILD RELATIVES

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INTRODUCTION TO THE TEMPLATE

This template has been prepared in the context of the ACP-EU funded '*In situ* conservation and use of crop wild relatives in three ACP countries of the SADC region'[1] (SADC Crop Wild Relatives for short) project to assist countries in documenting and detailing the scientific aspects of the development of National Strategic Action Plans (NSAP) for the conservation and sustainable use of crop wild relatives (CWR). This document will thus constitute a technical background document that forms the scientific basis of the NSAP and complements the main NSAP document for which a template is also provided[2]. The scientific information contained here should be reviewed and updated if a future iteration of the NSAP is to be undertaken.

The template has been prepared based on the *Resource Book for Preparation of National Conservation Plans for Crop Wild Relatives and Landraces* (Maxted *et al.* 2013), commissioned by the FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) as part of the ongoing work on implementing the Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture (GPA), and the *National Level Conservation of Crop Wild Relatives and Wild Food Plants: Revised Draft Voluntary Guidelines* (CGRFA 2017).

The template is for guidance only and it is not essential that all sections are completed (optional sections are indicated in the text). However, the more detail that is provided, the stronger is the scientific and technical background of the NSAP.

[1] '*In situ* conservation and use of crop wild relatives in three ACP countries of the SADC region' (SADC Crop Wild Relatives for short) is a three-year project (2014-2016) co-funded by the European Union and implemented through the ACP-EU Co-operation Programme in Science and Technology (S&T II) by the African, Caribbean and Pacific (ACP) Group of States. Grant agreement no. FED/2013/330-210. http://www.cropwildrelatives.org/sadc-cwr-project/

[2] See Dulloo E, Magos Brehm J, Kell S, Thormann I and Maxted N (2017) Template for the preparation of a National Strategic Action Plan for the conservation and sustainable use of crop wild relatives. Bioversity International and University of Birmingham. doi:10.7910/DVN/QH9XWB. Available at: https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/QH9XWB

CONTENTS OF THE TEMPLATE – INSTRUCTIONS TO USE THE TEMPLATE

The technical background document to the NSAP should be written in technical language where all the information is explained, detailed and properly referenced when needed. This template has been created in Microsoft Word and some the sections mentioned below are automatically generated.

- 'Table of contents'. Lists all sections of the document organized in the order in which they appear. To update it, right click anywhere in the table and the 'Update Field' will appear. You can either choose to update the entire table (if changes to headings or the structure have been made in the document, or to only update the page numbers if only changes to the layout and body text have been made. If new sections/headings are needed then they need to be created by using the same heading style of the document in order to be automatically included in the table of contents.
- 'Acknowledgements'. All the contributors (experts, institutions) to the NSAP should be acknowledged in this section, including advisors, data providers and researchers involved in the work. Any sources of funding that supported the development of the NSAP should also be accredited.
- 'List of figures'. List of all figures included in the document; to ensure that all figures are included in the list of figures, the captions of all figures need to be added via the menu 'References' followed by the 'Insert Caption' option and choosing 'Figure' as the label; this procedure is needed so all figures are automatically listed in the 'List of figures'. If the label 'Figure' does not exist it needs to be created in the menu 'References' > 'Insert Caption' > 'New Label'.
- 'List of tables'. List of all tables included in the document; to ensure that all table are included in the list of tables, their captions need to be added via the menu 'References' followed by the 'Insert Caption' option and choosing 'Table' as the label; this procedure is needed so all tables are automatically listed in the 'List of tables'. If the label 'Table' does not exist it needs to be created in the menu 'References' > 'Insert Caption' > 'New Label'.
- 'List of acronyms'. All the main abbreviations used throughout the text should be listed in this section.
- 'Goals and specific objectives of the National Strategic Action Plan' where these are detailed.
- 1 'National CWR checklist'. This section details the type of checklist developed, data sources used, how it was generated and provides an overview of the checklist.
- 2 'Prioritizing the CWR checklist'. It includes a description of how the checklist was prioritized for conservation including the criteria and methodlogy used, the list of priority taxa as well as details on how the CWR inventory for priority taxa was created.

- 3 ‘Diversity analysis of priority CWR’. This section is the first that contains a large part of the scientific analysis that forms the basis of the NSAP. It includes the distribution or priority taxa, hotspot and complementarity analysis, ecogeographic and genetic diversity analyses. These analyses will form (together with the results obtained in sections 4 ‘Gap analysis of priority CWR’, 5 ‘Climate change analysis’ and 6.1 ‘Predictive characterization’ of this document) the basis of the conservation actions recommended in section 8 ‘Concrete actions for conservation and sustainable use of CWR’ of the NSAP’[2]. Note that not all types of analyses (distribution, hotspots and complementarity, ecogeographic and genetic diversity) have to be undertaken, they are OPTIONAL.
- 4 ‘Gap analysis of priority CWR’. Provides important background data for the NSAP, namely on *in situ* and *ex situ* gap analyses.
- 5 ‘Climate change analysis’. Details what priority taxa and populations of those taxa are most affected by climate change. The results presented in this section will be combined with the results presented in sections 3 ‘Diversity analysis of priority CWR’, 4 ‘Gap analysis of priority CWR’ and 6.1 ‘Predictive characterization’ of this document to form the basis of the conservation actions recommended in section 8 ‘Concrete actions for conservation and sustainable use of CWR’ of the NSAP[2].
- 6 ‘CWR utilization potential’. In this section a brief overview of the current users’ demands should be provided which will form the starting point of the predictive characterization studies.
- 7 ‘Monitoring CWR diversity’. This section describes how CWR conserved *in situ* and *ex situ* should be monitored in the long-term.
- 8 ‘Lessons learnt’. In this section reflections on what could be improved when planning for CWR conservation and sustainable utilization can be included.

Some of these sections are inter-related and the results obtained in one might be used in another. For example, current users’ demands (section 6.2 of the NSAP[2]) are closely linked to CWR prioritization for conservation (section 2), and the results obtained from taxon prioritization (section 2), diversity (section 3), gap (section 4) and climate change analyses (section 5) and predictive characterization (section 6.1) will be analyzed jointly and encapsulated into specific concrete conservation actions (section 8 of the NSAP[2]).

[INSERT NATIONAL EMBLEM OF THE COUNTRY]

NATIONAL STRATEGIC ACTION PLAN FOR THE CONSERVATION AND SUSTAINABLE USE OF CROP WILD RELATIVES IN [NAME OF COUNTRY] – TECHNICAL BACKGROUND DOCUMENT

Citation: [Insert the reference of the technical background document ot he NSAP]

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ACKNOWLEDGEMENTS

All the contributors (experts, institutions) to the NSAP should be acknowledged in this section, including advisors, data providers and researchers involved in the work. Any sources of funding that supported the development of the NSAP should also be accredited.

LIST OF FIGURES

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LIST OF ACRONYMS

List hereunder all the main abbreviations used throughout the text.

GOALS AND SPECIFIC OBJECTIVES OF THE NATIONAL STRATEGIC ACTION PLAN

Define the goals (overall purpose and desired overall outcomes) and specific objectives of the NSAP that should be endorsed by national stakeholders[3].

[3] For more detail and examples of goals and objectives, see part V, *'Writing the strategic plan'* from page 28 in CGRFA (2017). National Level Conservation of Crop Wild Relatives and Wild Food Plants: Revised Draft Voluntary Guidelines. CGRFA-16/17/Inf.19. Sixteenth Regular Session, 30 January–3 February 2017, Rome.

1 NATIONAL CWR CHECKLIST

1.1 Type of CWR checklist

- Describe what type of checklist[4] has been created.

1.2 Data sources to produce the CWR checklist

1.2.1 National flora checklist

- Explain how the national flora checklist was obtained and provide the reference.
- Specify whether a digitized version of the checklist has been used or whether it had to be created.
- State whether the checklist contains both native and introduced taxa.
- Note how many taxa are included in the flora checklist. When referring to taxa, make sure to distinguish between the number of species and the number of taxa (ie, including subspecific taxa).
- Say how many taxa are included in the flora checklist.

1.2.2 List of crops or crop genera

- Describe what kind of crops (or crop genera) it includes (nationally and/or regionally and/or globally cultivated, major and/or known neglected and under-utilized crops, crop use categories[5], priority crops and how they were selected).
- Refer to the source(s) consulted to compile the list of crops or crop genera.
- How the list of crops or crop genera was compiled.
- Refer how many crops and crop genera were compiled and used to created the CWR checklist.

1.3 Generation of the national CWR checklist

- Describe the method used to generate the CWR checklist.
- State whether the CWR checklist has been validated through broad stakeholder consultation.
- Indicate whether the CWR checklist has been made available online and provide the URL.

1.4 Information documentation

Describe the data management system used to compile the CWR checklist.

1.5 CWR checklist and overview

This section may include:

- The number of CWR taxa (including subspecific taxa where relevant) in the checklist.

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[4] Complete CWR checklist – a list of all CWR found in the country, providing the botanical names and authorities. Priority CWR checklist – a partial list of CWR found in the country that is the result of a first prioritization, usually on crop genepools, providing the botanical names and authorities.

[5] The level 1 of the crop categories according to Economic Botany Standards can be used (available at: http://www.kew.org/tdwguses/rptLevel1_2States.htm).

- The number of CWR taxa (including subspecific taxa where relevant) endemic to country (%, list, graph).
- The number of CWR taxa (including subspecific taxa where relevant) that are related to each of the crops and/or crop use categories included in the list of crops (or a graph).
- A table listing the crops, the genera containing the related CWR and the number of species (and subspecific taxa where relevant) within each gene pool or crop group (include it in an annex if too long).
- The number of CWR taxa (and subspecific taxa where relevant) that are native (vs. introduced) and those that are endemic to the country.
- The full checklist can be included as an annex or published online (the URL must be provided).

2 PRIORITIZING THE CWR CHECKLIST

'The national CWR checklist can be prioritized to produce a shorter list for which specific active conservation is considered most necessary. The prioritized national CWR checklist forms the basis of the national CWR inventory'[6,7].

2.1 Prioritization criteria

The criteria used to prioritize the national CWR checklist should be listed and thoroughly explained and justified. Data sources of information related to each criterion should be also included. This section is closely linked to section 6.2, 'Current users' demands' of the NSAP[2].

2.2 Prioritization method

- The prioritization method used should be explained in detail.
- The annotated checklist together with the scoring of the taxa can be included as an annex or published online (the URL must be provided).

2.3 Priority taxa

- Provide the number of priority CWR species (and subspecific taxa where relevant).
- List the priority taxa (can be included as an annex).
- Provide overview of priority taxa (native/naturalized, endemics, threatened taxa, GP/TG concept, number of wild relatives per crop/crop genus, etc) (graphs, tables).

[6] CGRFA (2017). National Level Conservation of Crop Wild Relatives and Wild Food Plants: Revised Draft Voluntary Guidelines. CGRFA-16/17/Inf.19. Sixteenth Regular Session, 30 January–3 February 2017, Rome.

[7] Here we distinguish CWR checklist from CWR inventory, where a CWR checklist is a list of all CWR taxa found in certain geographic unit (region, country, etc) comprising a list of taxon names and authorities, whereas an inventory of CWR is the list of CWR taxa present in a country with ancillary information, such as gene pool or taxon group concept applied, biology, general distribution, threats, threat assessments and conservation actions; an inventory is usually created after prioritizing the CWR checklist and for the priority taxa (Maxted *et al.* 2013).

2.4 Compilation of the CWR inventory for priority taxa

- Refer to the data sources used to compile the information in the CWR inventory.
- Indicate whether the CWR inventory has been made available online and provide the URL.

2.5 Information documentation

Describe the data management system used to compile the CWR inventory.

3 DIVERSITY ANALYSIS OF PRIORITY CWR

This section describes the diversity analyses that can be undertaken for all priority CWR taxa. These analyses will form (together with the results obtained in sections 4 'Gap analysis of priority CWR', 5 'Climate change analysis' and 6.1 'Predictive characterization' of this document) the basis of the conservation actions recommended in section 8, 'Concrete actions for conservation and sustainable use of CWR' of the NSAP[2]. Note that not all types of analyses (distribution, hotspots and complementarity, ecogeographic and genetic diversity) have to be undertaken, they are OPTIONAL.

3.1 Compilation of occurrence data

May include:

- Sources of CWR occurrence data (online databases, *ex situ* accessions, herbarium records, bibliographic references, personal communications, etc).
- Whether a field survey has been conducted in order to collect priority taxa occurrence and population data, and description of the survey.
- Qualitative evaluation of the type and comprehensiveness of the data sources used to compile the occurrence data (overview of completeness of data collated and any gaps regarding for example in terms of coordinates).
- Whether there are any data sources that were not surveyed and why.

3.2 Occurrence data quality verification and control and overview of data

Methodology – may include:

- Description of how the data was verified (checked for duplicates and spelling errors, formatted and standardized).
- Provide details on whether georeferencing was undertaken and how (method, software).
- Description of method used to assess data quality.
- Sampling bias assessment (explanation of data analysis as well as software used).

Results – may include:

- Overview of collated data (number of records before and after data quality control, number of records per source, number of records per taxon, etc).
- Figure showing sampling bias map (number of occurrences) and discussion.

3.3 Distribution, hotspots and complementarity analyses

Methodology – may include:

- Explanation of the data analyses undertaken as well as reference to the software used:
    - Species distribution maps.

    - Predicted distribution maps (using species distribution modeling techniques – SDM) (model used, model validation, species occurrence data used, environmental data used).
    - Species richness assessment – hotspot analysis.
    - Complementarity analysis based on CWR diversity (at taxon level).
- List of the types and sources of GIS layers used in the analysis.

Results – may include:

- Figures showing priority species actual distribution, description/discussion of actual distribution.
- Figures showing priority species predicted distribution, description/discussion of predicted distribution).
- Figure showing species richness assessment (hotspot analysis), description/discussion of hotspots.
- Figure showing complementarity analysis, description [number of CWR species (and subspecific taxa where relevant) covered by complementarity sites, list of CWR species (and subspecific taxa where relevant) in each complementarity site] and discussion.

3.4 Ecogeographic diversity analysis

Methodology – may include:

- Creation of ecogeographic land characterization maps (ELC maps) (CAPFITOGEN tools)[8] (selection of ecogeographic variables, method of map creation).
- Mapping and detection of ecogeographic patterns (e.g. life cycle of the species in different areas, whether a particular CWR grows in a particular soil type, or whether the frequency of a character state changes along an environmental gradient).
- Complementarity analysis based on ecogeographic diversity of target taxa[9].

Results – may include:

- List of variables selected to create the ELC maps.
- ELC maps (generalized maps or species specific, variables used) overlapped with taxon distribution.
- Characterization of ecogeographic diversity for each CWR taxon (number of ecogeographic categories in which the taxon occurs, table with number/frequency of different populations[10] that occur in each ecogeographic category).

3.5 Genetic diversity analysis

Methodology and results – may include:

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[8] Parra-Quijano M, Torres E, Iriondo JM, López F and Molina A (2016) CAPFITOGEN tools user manual, version 2.0. International Treaty on Plant Genetic Resources for Food and Agriculture, FAO, Rome, Italy.

[9] For more details see Rubio Teso ML, Kinoshita KK and Iriondo JM (2014) Optimized site selection for the *in situ* conservation of forage and fodder CWRs: a combination of community and genetic level perspectives. Internaitonal Conference Enhanced Genepool Utilization – Capturing Wild Relative and Ladrace Diversity for Crop Improvement'. 17-20 June 2014. Cambridge, United Kingdom.

[10] Different accessions do not necessarily represent distinct populations; pragmatically, different populations are represented by accessions that have different pairs of coordinates.

- Review of existing studies on:
    - Breeding system, floral morphology, mode of reproduction, pollination mechanism.
    - Seed dispersal mechanism, seed dormancy.
    - Phenology, life cycle, timing of reproduction, successional stage.
    - Geographic range, population size, density and spatial distribution.
    - Patterns of allelic richness and eveness across the geographic breadth of the species against which change can be measured during later monitoring.
    - Identification of populations for conservation based on amount and patterns of genetic diversity both within and between populations of the species.
    - Identification of traits of interest for crop improvement.
    - Assessment of how natural selection and neutral evolutionary forces are affecting populations targeted for conservation.
    - For any of the studies mentioned above, data on techniques and markers, data analysis and software used should be described.
- Description of study specifically undertaken to inform the development of the NSAP (optional)[11]:
    - Definition of the aim and objectives of the study.
    - Techniques and markers used.
    - Data analysis undertaken and software used.
    - Main results obtained.

3.6 Information documentation

Describe the data management system used to compile the occurrence data as well as the genetic information gathered.

4 GAP ANALYSIS OF PRIORITY CWR

This section presents the results of gap analysis (i.e. identification of gaps in conservation – those taxa and respective relevant populations not conserved either *in situ* and/or *ex situ*). Together with sections 3 'Diversity analysis of priority CWR', 5 'Climate change analysis' and 6.1 'Predictive characterization' of this document, it forms the basis of the conservation actions recommended in section 8, 'Concrete actions for conservation and sustainable use of CWR' of the NSAP[2]. Note that both *in situ* and *ex situ* gap analyses can be undertaken at several levels: at taxon and/or at infra-specific level. The analysis at infra-specific level includes analyses at ecogeographic, genetic and/or trait[12] levels, and not all of them have to be undertaken.

[11] For more detail and examples of typical research questions, see section A5, *'Genetic data analysis of priority species*' from page 112 in the *Resource Book for Preparation of National Conservation Plans for Crop Wild Relatives and Landraces* (Maxted *et al.* 2013).

[12] Trait diversity comes directly from section 6.1 'Predictive characterization' of this document.

4.1 *In situ* gap analysis

Methodology – may include:

- Data sources used in the analysis (e.g., priority taxon occurrence data; protected area shapefiles).
- At taxon level: identification of taxa actively conserved *in situ*.
- At taxon level: method used to identify taxa found within and outside protected areas.
- At infra-specific level: method used to identify infra-specific (ecogeographic, genetic[13] and/or trait[14]) diversity found within and outside protected areas (if results of ecogeographic, genetic and/or trait diversity analyses are available).

Results at taxon level – may include:

- List of species that do not occur within any existing protected areas.
- Table with priority CWR taxa requiring urgent *in situ* conservation and justification based on *in situ* gap analysis.
- Figure and % of priority CWR taxa actually found within existing protected areas.
- List of priority CWR taxa present in each protected area.
- Figure and % of priority CWR taxa predicted to be found within existing protected areas as a result of SDM (from section 3.3, 'Distribution, hotspots and complementarity analyses').
- List of priority CWR taxa predicted to be found in each protected area as a result of SDM (from 3.3, 'Distribution, hotspots and complementarity analyses').

Results at infra-specific diversity level – may include:

- Table with the ecogeographic categories/genetically important populations/with relevant traits already conserved and not conserved *in situ* for each CWR taxa.
- Table and figure showing priority sites/populations for active *in situ* conservation action of priority CWR (Most Appropriate Wild Populations, MAWP)[15] based on infra-specific diversity and discussion. These should include:
    - List of protected areas where genetic reserves for individual taxa could be established based on infra-specific diversity data.
    - Sites outside of protected areas where genetic reserves for individual taxa could be established based on infra-specific data.

4.2 *Ex situ* gap analysis

Methodology – may include:

- Genebank data sources used in the analysis (linked to the sources of CWR occurrence data surveyed in section 3.1, 'Compilation of occurrence data').
- At taxon level: method used to identify taxa conserved *ex situ*.

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[13] The genetic diversity analysis should be based on data obtained in section 3.4 'Ecogeographic diversity analysis' of this document.

[14] The trait diversity analysis should be based on data obtained in 6.1 'Predictive characterization'.

[15] Most Appropriate Wild Populations (MAWPs) are those populations that are considered to be of most value to target limited conservation resources [see more details in Maxted N, Avagyan A, Frese L, Iriondo JM, Magos Brehm J, Singer A, Kell SP (2015) ECPGR Concept for *in situ* conservation of crop wild relatives in Europe. Wild Species Conservation in Genetic Reserves Working Group, European Cooperative Programme for Plant Genetic Resources, Rome, Italy].

- At infra-specific level: method used to identify infra-specific (ecogeographic, genetic[16] and/or trait[17]) diversity conserved *ex situ* (if results of ecogeographic, genetic and/or trait diversity analyses are available).

Results at taxon level – may include:

- List of taxa not conserved *ex situ*.
- Table with priority CWR taxa requiring urgent *ex situ* conservation and justification based on *ex situ* gap analysis.
- List of CWR taxa with populations found in *ex situ* collections.
- List of CWR taxa with five or more different populations conserved *ex situ*[18,19].
- Figure showing *ex situ* conservation priorities and discussion.
- List of priority collecting areas where multiple taxa could be sampled for *ex situ* conservation.

Results at infra-specific diversity level – may include:

- Table with the ecogeographic categories/genetically important populations/with relevant traits already conserved and not conserved *ex situ* for each CWR taxa.
- Table and figure showing priority populations/areas for *ex situ* conservation of priority CWR based on infra-specific diversity.

5 CLIMATE CHANGE ANALYSIS

The results presented in this section will be combined with the results presented in sections 3 'Diversity analysis of priority CWR', 4 'Gap analysis of priority CWR' and 6.1 'Predictive characterization' of this document to form the basis of the conservation actions recommended in section 8, 'Concrete actions for conservation and sustainable use of CWR' of the NSAP[2].

Methodology – may include:

- Predicted distribution of species with various climate change scenarios (using species distribution modeling techniques – SDM) (model used, model validation, species occurrence data used, environmental data used).
- Selection of priority CWR taxa most affected by climate change.
- Selection of populations of priority CWR taxa for *in situ* and *ex situ* conservation based on the assessment of the impact of climate change on species distribution[20].

[16] The genetic diversity analysis should be based on data obtained in section 3.5 'Genetic diversity analysis'.

[17] The trait diversity analysis should be based on data obtained in section 6.1 'Predictive characterization'.

[18] Five different accessions do not necessarily represent five distinct populations; pragmatically, different populations here are represented by accessions that have different pairs of coordinates.

[19] See discussion in Dulloo ME, Labokas J, Iriondo JM, Maxted N, Lane A, Laguna E, Jarvis A and Kell SP (2008) "Genetic Reserve Location and Design." In: Iriondo JM, Maxted N and Dulloo E (eds) Plant Genetic Population Management. CAB International, Wallingford, UK, pp. 23-64.

[20] Populations of priority taxa predicted to be negatively affected by climate change should be prioritized for *ex situ* conservation because they are likely to go extinct, whereas populations predicted to be either not affected or positively affected by climate changes should be prioritized for *in situ* conservation because they are likely to persist in the long-term [see more details in Magos Brehm J, Saifan S, Taifour H, Abu Laila K, Al-Sheyab F, Alassaf

- Predicted impact of climate change on potential sites for *in situ* conservation (with reference to the hotspot and complementarity analysis results obtained in section 3.3 'Distribution, hotspots and complementarity analyses', the priority sites for *in situ* conservation that resulted from the taxon level analysis, the protected areas and sites outside of protected areas where genetic reserves could be established obtained in section 4.1 '*In situ* gap analysis').

Results – may include:

- Maps of potential distribution with climate change for CWR taxa.
- Priority CWR taxa for *in situ* and *ex situ* conservation based on climate change analysis.
- Priority populations for *in situ* and *ex situ* conservation based on climate change analysis.

6 CWR UTILIZATION POTENTIAL

6.1 Predictive characterization

This analysis can be undertaken for priority CWR taxa.

Methodology – may include:

- Information on target traits and taxa.
- Details on data preparation (compilation, cleaning, georeferencing, quality control).
- Details on the method applied.

Results – may include:

- Priority populations or accessions of target CWR taxa that are predicted to have target traits (figure and details of populations), and whether these are already conserved *in situ* and *ex situ*.
- Distribution map of specific target traits among CWR populations of a particular taxon.

6.2 Information documentation

Describe the data management system used to compile the information that was compiled to document CWR utilization potential as well the information that has resulted from predictive characterization.

7 MONITORING CWR DIVERSITY

7.1 Development of monitoring plans for CWR

Description of monitoring plans for CWR conserved *in situ* and *ex situ* (at taxon or population level).

In situ conserved diversity – may include details on:

- Identification and selection of the variables to monitor.
- Design of the sampling strategy.

A, Bani-Hani R, El-Oqlah AA, Ghazanfar S, Haddad N, Shibli R, Abu Taleb T, Ali B and Maxted N (2014) Wild socioeconomic plant conservation strategy for Jordan. Royal Botanic Garden of Jordan (in press)].

- Selection and positioning of the sampling units.
- Timing and frequency of monitoring.
- Implementation of a pilot study.
- Planned data analysis.
- Associated PGRFA indicators achieved[21].

Ex situ conserved diversity – may include details on:

- Whether the identified gaps in *ex situ* conservation are being filled.
- Whether CWR diversity conserved *ex situ* is effectively conserved, regenerated and used.

7.2 Information documentation

Describe the data management system used to compile the monitoring information and how it will be used to manage and monitor CWR diversity.

8 LESSONS LEARNT

Lessons learnt and reflections on what could be improved when planning for the conservation and sustainable use of CWR. Examples may include stakeholders that should have been involved in e.g. prioritization of CWR, missing occurrence data that should have been included in the analysis (linked to 3.1 'Compilation of occurrence data'), etc.

[21] See the PGRFA indicators for monitoring the implementation the Second Global Plan of Action for Plant Genetic Resources (Second GPA) in appendix C of the FAO (2013) Report of the Commission on Genetic Resources for Food and Agriculture. Fourteenth Regular Session, 15–19 April 2013, Rome. Also see the reporting format for monitoring the implementation of the Second GPA in CGRFA (2015) Reporting Format for Monitoring the Implementation of the Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture. Fifteenth Regular Session, 19–23 January 2015, Rome.

9 REFERENCES