

# Using multiple factor analysis to compare expert opinions with conservation assessment results for the wild relatives of oat (*Avena sativa* L.) and pigeon pea (*Cajanus cajan* (L.) Millsp.)

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## Introduction

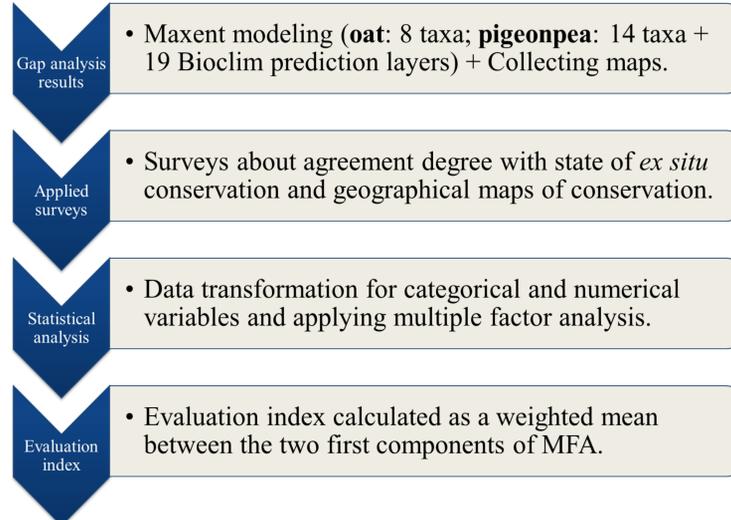
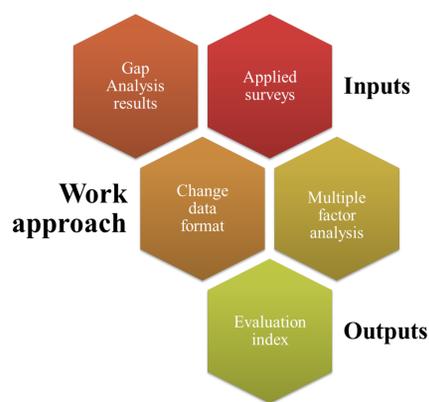
The gap analysis methodology (GA) is a tool that enables an assessment of the state of *ex situ* conservation of crop wild relatives (CWR), undomesticated plant species important for agriculture due to their wide genetic diversity and their relatively close genetic relationship to cultivated species (Maxted et al., 2006). GA methodology evaluates the gaps in conservation from the taxonomic, geographic and environmental point of view (Ramírez-Villegas et al., 2010). This methodology provides a Final Priority Score (FPS) identifying the CWR that require urgent conservation, as well as distribution maps and collecting gaps maps and evaluation statistics derived from the spatial modelling algorithm. These results are then provided to experts with widely recognized experience in botany, genetic resources and conservation, for their assessment.

Including information derived from the participation of experts in the analysis provides greater robustness of the results obtained from GA, allowing us both to have more confidence in results, as well as to further refine them. Here we display GA and expert opinion results for the wild relatives of oat and pigeon pea using a multiple factor analysis (MFA). MFA is a multivariate statistical technique that allows the analysis of multiple data formats (Abdi et al., 2013). Using the MFA to assess quantitative and qualitative results by a number of experts, we derived an expert evaluation index of accordance with GA results.

## Main objective

Evaluate the degree of agreement between the experts' opinions and results of the GA methodology in order to better inform collecting priorities for *ex situ* conservation.

## Materials and Methods



## Results

Here we present the variables evaluated, the GA results (including the FPS score of prioritization for each of the gene pools analyzed (Table 1) and hotspots for proposed further collecting of plant material (Figure 1 and Figure 3).

**Gap analysis results:** FPS from GA methodology rank from 0 (high priority species) to 10 (no further collecting recommended).

### Evaluation variables:

1. Comparable evaluation (CMP). Expert evaluation per species purely of comprehensiveness of existing germplasm collections. This score is directly comparable with GA outputs and is performed before experts are shown GA results.
2. Contextual evaluation (CNT). Expert evaluation per species including all contexts in regard to conservation of species, including threats and usefulness in plant breeding.
3. GA results agreement (EVL). Expert's direct evaluation per species of GA results.
4. Expert's evaluation per species of the occurrence data used for the GA (OCC).
5. Expert's evaluation per species of the distribution maps/Ecological Niche Models produced for the GA (ENM).
6. Expert's evaluation per species of collecting gaps maps (GAP).

If the cumulative percentage of variance in the first and second component is greater than 60%, then construct evaluation index (Gutiérrez et al, 2012).

Expert evaluation index ranked species with low degree of agreement (0) between expert opinion and GA results, to high degree of agreement (100).

Table 1: FPS score and evaluation index per crop wild relative taxon

Crop	Taxon	FPS	Evaluation index	Crop	Taxon	FPS	Evaluation index
Oat	<i>A. strigosa</i>	0.5	61.5	Pigeonpea	<i>C. lanceolatus</i>	1.1	63.7
Oat	<i>A. prostrata</i>	1.6	57.2	Pigeonpea	<i>C. trinervius</i>	1.1	32.1
Oat	<i>A. insularis</i>	2.0	58.7	Pigeonpea	<i>C. confertiflorus</i>	1.2	75.2
Oat	<i>A. abyssinica</i>	6.3	62.9	Pigeonpea	<i>C. acutifolius</i>	1.5	66.3
Oat	<i>A. fatua</i>	6.4	14.3	Pigeonpea	<i>C. crassus</i>	1.5	47.9
Oat	<i>A. sterilis</i>	6.6	18.6	Pigeonpea	<i>C. lineatus</i>	1.7	49.2
Oat	<i>A. murphyi</i>	6.6	72.0	Pigeonpea	<i>C. sericeus</i>	1.8	33.5
Oat	<i>A. maroccana</i>	8.3	66.5	Pigeonpea	<i>C. cajanifolius</i>	2.4	45.0
Pigeonpea	<i>C. latisepalus</i>	0.1	68.6	Pigeonpea	<i>C. albicans</i>	2.7	29.8
Pigeonpea	<i>C. cinereus</i>	0.1	67.9	Pigeonpea	<i>C. platycarpus</i>	3.7	39.4
Pigeonpea	<i>C. reticulatus</i>	0.1	62.5	Pigeonpea	<i>C. mollis</i>	4.6	33.4

## Oat case

For the oat gene pool we found a high degree of correlation between variables in regard to the first principal component (PC), except for EVL variables (Figure 2).



Figure 1: Map showing hotspots for proposed collecting of high priority crop wild relatives of oat

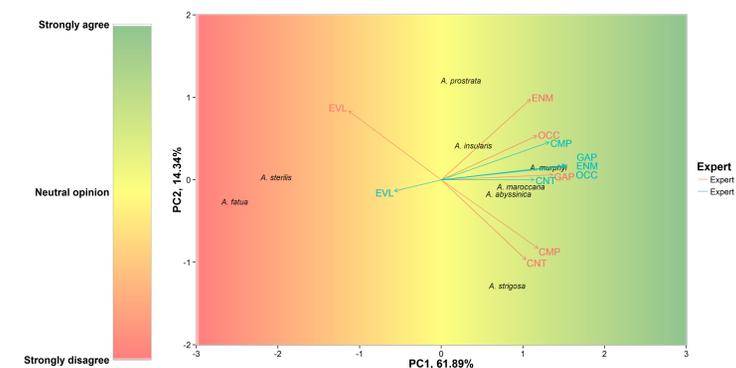


Figure 2: Biplot for oat results

## Pigeon pea case

We found a high degree of correlation between the variables obtained from each of the three experts in regard to the first principal component (PC). *C. confertiflorus*, *C. latisepalus*, *C. cinereus*, *C. acutifolius*, *C. lanceolatus* and *C. reticulatus* displayed the highest accord between experts and GA results.

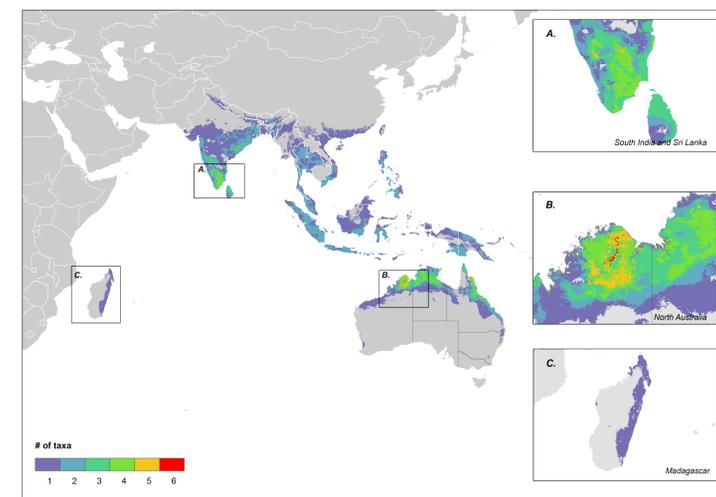


Figure 3: Map showing hotspots for proposed collecting of high priority crop wild relatives of pigeon pea

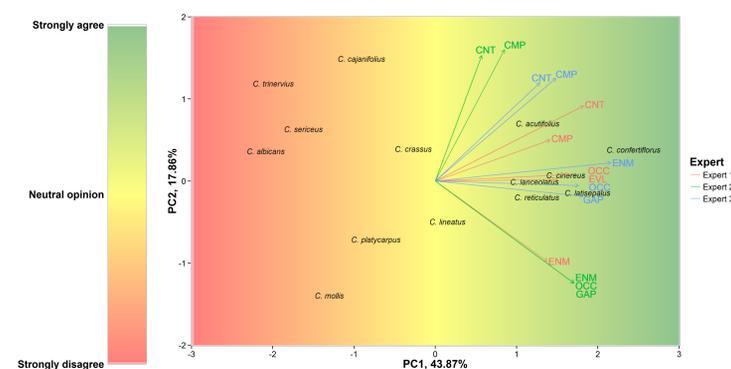


Figure 4: Biplot for pigeonpea results

## Conclusions

- The methodology presented permits the utilization of quantitative and qualitative expert evaluation data from various experts in assessing the quality of gap analysis results, providing a quantitative medium by which the valuable knowledge of recognized experts in botany, conservation and plant genetic resources can input on conservation analyses.
- The integration of the opinions of the different experts into a single metric (evaluation index) is a useful tool for summarizing such quantitative and qualitative evaluations and for comparing these to the gap analysis results.
- For both case study crop gene pools, expert evaluation provided further support to confidence in gap analysis results for most species. The evaluation also identified species in need of further analyses in order to resolve high discord between experts and the gap analysis results. The expert evaluation method can be applied to other crop gene pools to assess the reliability of conservation priorities scores and areas recommended for further collecting.

## Acknowledgements

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<http://www.cwrdiversity.org/>

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