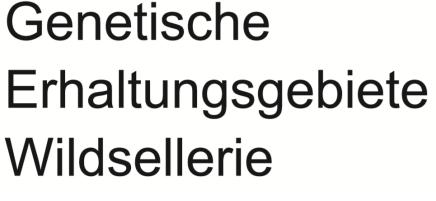
# **Establishment of Genetic Reserves for Crop Wild Relatives**

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#### Introduction

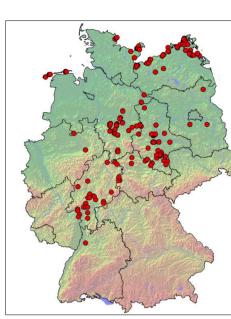
While great progress has been achieved in organizing ex situ plant genetic resources conservation programs, the implementation of the *in situ* conservation strategy is lagging behind. The deployment of the genetic reserve conservation technique has been suggested to facilitate in situ conservation measures. A four step methodology for the identification of genetic reserve sites for a target crop gene pool has been developed (Maxted et al., 1997, Maxted and Kell, 2009) and is operative. The technique entails the identification of occurrence representing the spectrum of intraspecific diversity of a species. The establishment of genetic reserves in a formal, regulatory sense has not been achieved so far. The latter is the main objective of the model- and demonstration project "Genetic reserves for wild celeriac species (Apium and Helosciadium) as component of a network of genetic reserves in Germany". Four wild celery species distributed in Germany were chosen as model objects for two reasons. Firstly, the species are suited to enhance the crop breeding pool (Melchinger and Lübberstedt, 2003; Wang et al., 2011). Secondly, the species have been classified as threatened. The agricultural and nature conservation sector thus have a common interest in improving the conservation status of the species.



# Species, habitats, distribution pattern







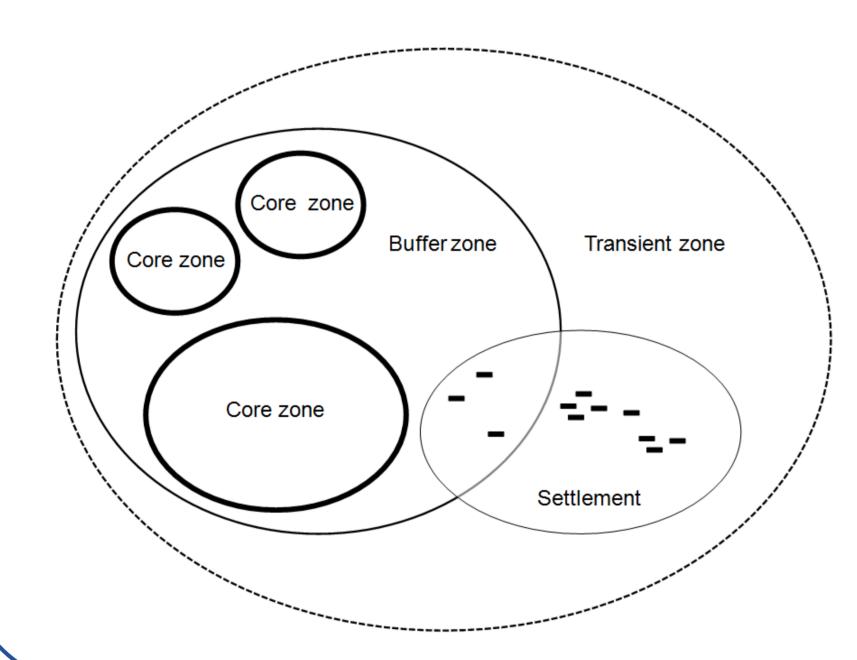


The project is implemented by the Julius Kühn-Institut, Institute for Breeding Research on Agricultural Crops, Quedlinburg (coordinator)<sup>1</sup>), the Botanical Garden of the University of Osnabrück<sup>2</sup>), and the Albrecht Daniel Thaer-Institute for Agricultural and Horticultural Sciences of the Humboldt-University, Berlin<sup>3</sup>). The project team is supported by the Federal Nature Conservation Agency, Bonn, the German Federation for Plant Innovations, Bonn, the Bavarian Academy for Nature Conservation and Landscape Management, Laufen, and ten nature conservation agencies located in the Federal States.



1st row: Apium graveolens subsp. graveolens. Habitat at Sülldorf.
2nd row: Helosciadium repens. Habitat in Sachsen-Anhalt.
3rd row: H. nodiflorum. Habitat in Rheinland-Pfalz
4th row: H. inundatum. Habitat at Boye, Niedersachsen
Maps: © GeoBasis-DE / BKG 2007 und 2013

#### Genetic reserve: design



Model of a genetic reserve for crop wild relatives (based on Maxted *et al.*, 1997).

The figure depicts plant groups spread over three core zones altogether constituting a meta-population. These groups are united in the buffer zone. Together with the transition zone the buffer zone serves protecting the core zone and to allow for fluctuations and migration of the species on a small scale.

### **Related crops**

The continued adaptation of the wild species generates genetic variation which can be used for broadening the breeding pools of domesticated forms.



Apium graveolens subsp. graveolens is the wild ancestor of Cutting celery, Apium graveolens var. secalinum; Celery, Apium graveolens var. dulce; Celeriac, Apium graveolens var. rapaceum

# Identification of genetic-reserve sites: the work flow

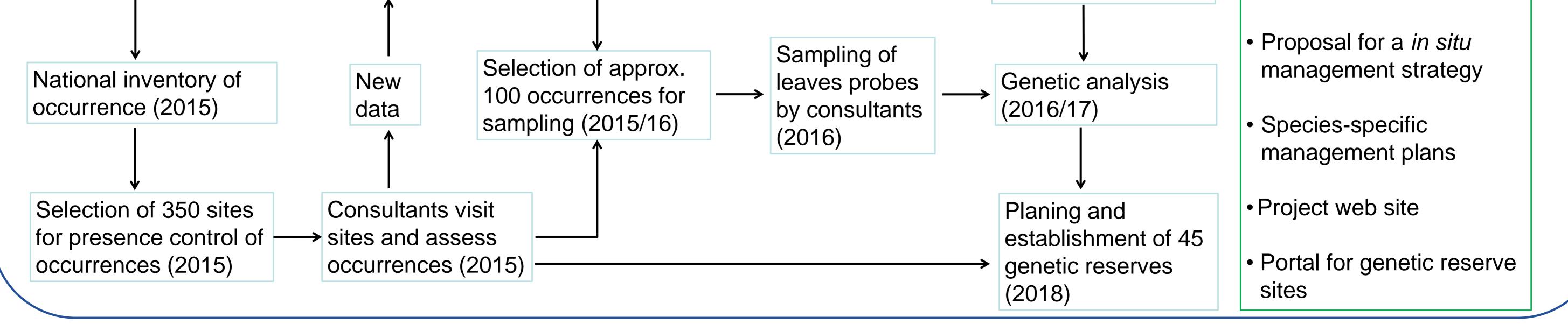
Distribution data from nature conservation agencies (2015)



Development and testing of polymorphic SSR (2015/16)

#### Accompanying actions

- Network Memorandum of Understanding
- Communication strategy



#### References

Maxted, N., Ford-Lloyd, B. V., Hawkes, J. G. (eds.), 1997. Plant genetic conservation: the *in situ* approach. – Chapman & Hall, London. Maxted, N. and Kell, S. P., 2009: Establishment of a global network for the in situ conservation of crop wild relatives: status and needs. – FAO Commission on Genetic Resources for Food & Agriculture, Rome: 266 pp. Melchinger, A. E. und Lübberstedt, T., 2003. Abschlussbericht zum GFP-Forschungsvorhaben ghg 1/98 (97 HS 044). Sortendifferenzierung und Verwandtschaftsuntersuchungen bei Feldsalat (*Valerianella locusta* L.), Radies (*Raphanus sativus* L.) und Knollensellerie (*Apium graveolens* L.) mit Hilfe PCR-gestützer genetischer Marker. Universität Hohenheim, Institut für Pflanzenzüchtung, Saatgutforschung und Populationsgenetik, Lehrstuhl Angewandte Genetik und Pflanzenzüchtung. Wang et al., 2011. Genetic diversity in Apium graveolens and related species revealed by SRAP and SSR markers. Scientia Horticulturae 129, 1–8.

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