

Exploration and exploitation of the GxGxE space spanned by multi-environment intercropping experiments

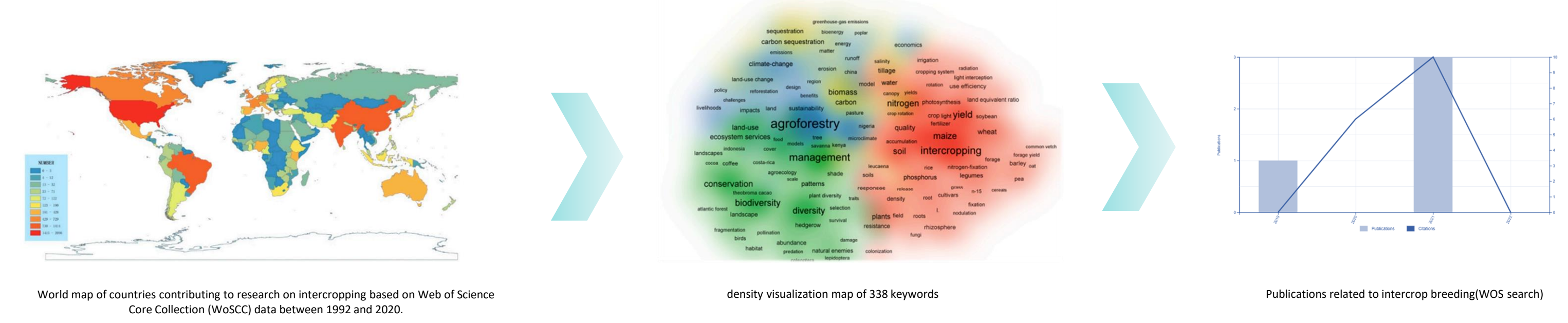
INTRODUCTION

Intercropping is the cultivation of at least two crop species on the same land for the entire or a substantial percentage of the growth cycle. Intercropping legumes and cereal species is useful for a myriad of reasons including yield stability, nutritional content and numerous agro-ecosystem services (Brooker et al., 2013, Zhang et al., 2010, Ofori et al., 1987, Annicchiarico et al., 2019). However, intercropping also creates diverse competition effects for the mixed partners, which can have a significant impact on their agronomic performance. Therefore, selecting complimentary intercropping partners is the key to the realisation of a good mixed crop yield. Both Annicchiarico et al. (2019) and Wolfe et al. (2021) suggest the use of specialized intercrop breeding methods to develop complementary varieties as reciprocal intercropping partners. Intercrop breeders face the same issues as single-crop breeders in the sense that newly developed varieties should perform well in a wide range of environments. This quest for all-around performers generally implies a search in the so-called Genotype-by-Environment (GxE) space for which numerous strategies have been described in the literature (Freeman 1983, Romagosa 1993, Hill 1975). Intercrop breeders search for pairs of genotypes belonging to different species, giving rise to vast GxGxE search space. The existence and potential of this GxGxE space and related GxG, GxGxE and GxExG spaces are discussed extensively in the literature (de Vos et al., 2013, Subrahmaniam et al., 2017, Subrahmaniam et al., 2020, Subrahmaniam et al., 2021) but no efficient exploitation strategy is currently available.

OBJECTIVE

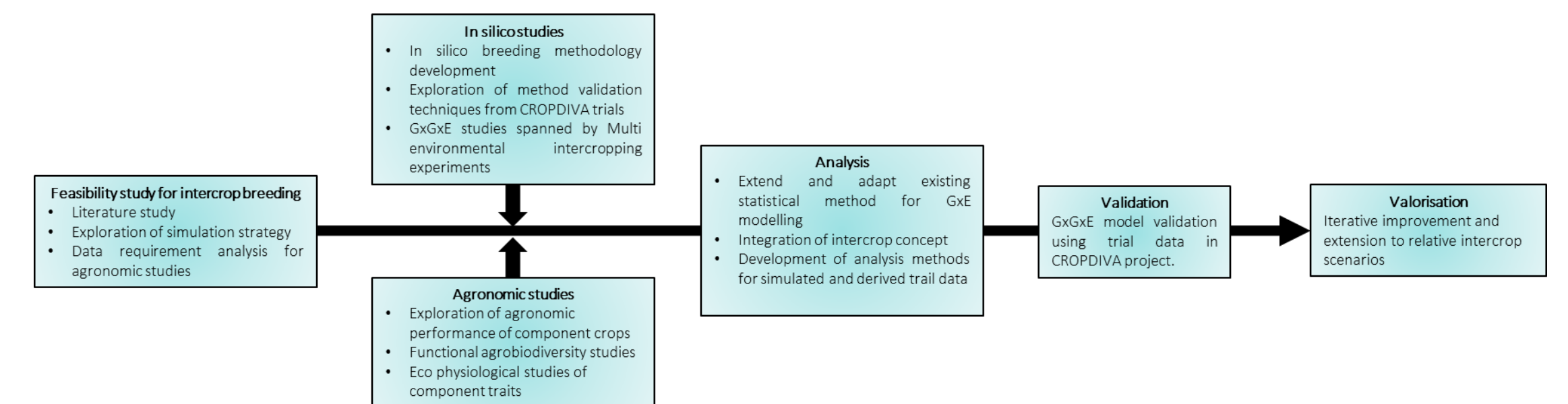
The presented research project aims to develop an optimal breeding strategy for intercrops by extending existing approaches for intercrop breeding with ecophysiological intercrop growth modelling. In-silico developed methods will be calibrated by means of the multi-year, multi-environment intercrop trial data that is generated in the Horizon2020 CROPDIVA project. The developed methods and tools will be most valuable to intercrop breeding and research communities, further catalysing the wide-scale adoption of this sustainable cropping system.

A Scientometric Analysis of Worldwide Intercropping Research, Lv et al., 2021



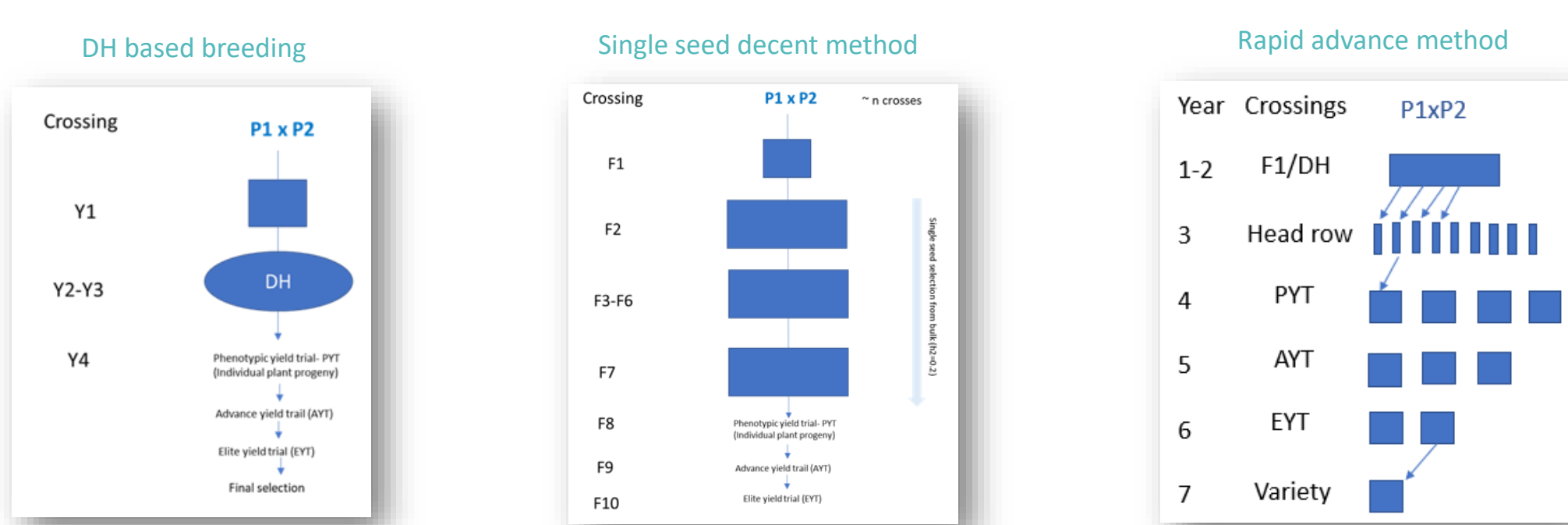
MATERIAL AND METHODS

The project aims to infer a maximally efficient breeding strategy for intercrops. Existing intercrop breeding strategies generally allow to explore but a limited part of the GxGxE interaction space due to operational constraints. We aim to develop and integrate an ecophysiological intercrop growth model in the breeding process to enlarge the explored subspace in the dimension of the environment. The calibration and validation of this growth model relies on the phenotypic data that is gathered in extensive multi-year, multi-environment intercrop trials across Europe as part of the Horizon2020 CROPDIVA project. The efficiency of this new breeding strategy will be benchmarked against that of existing intercrop breeding methods by means of simulations.



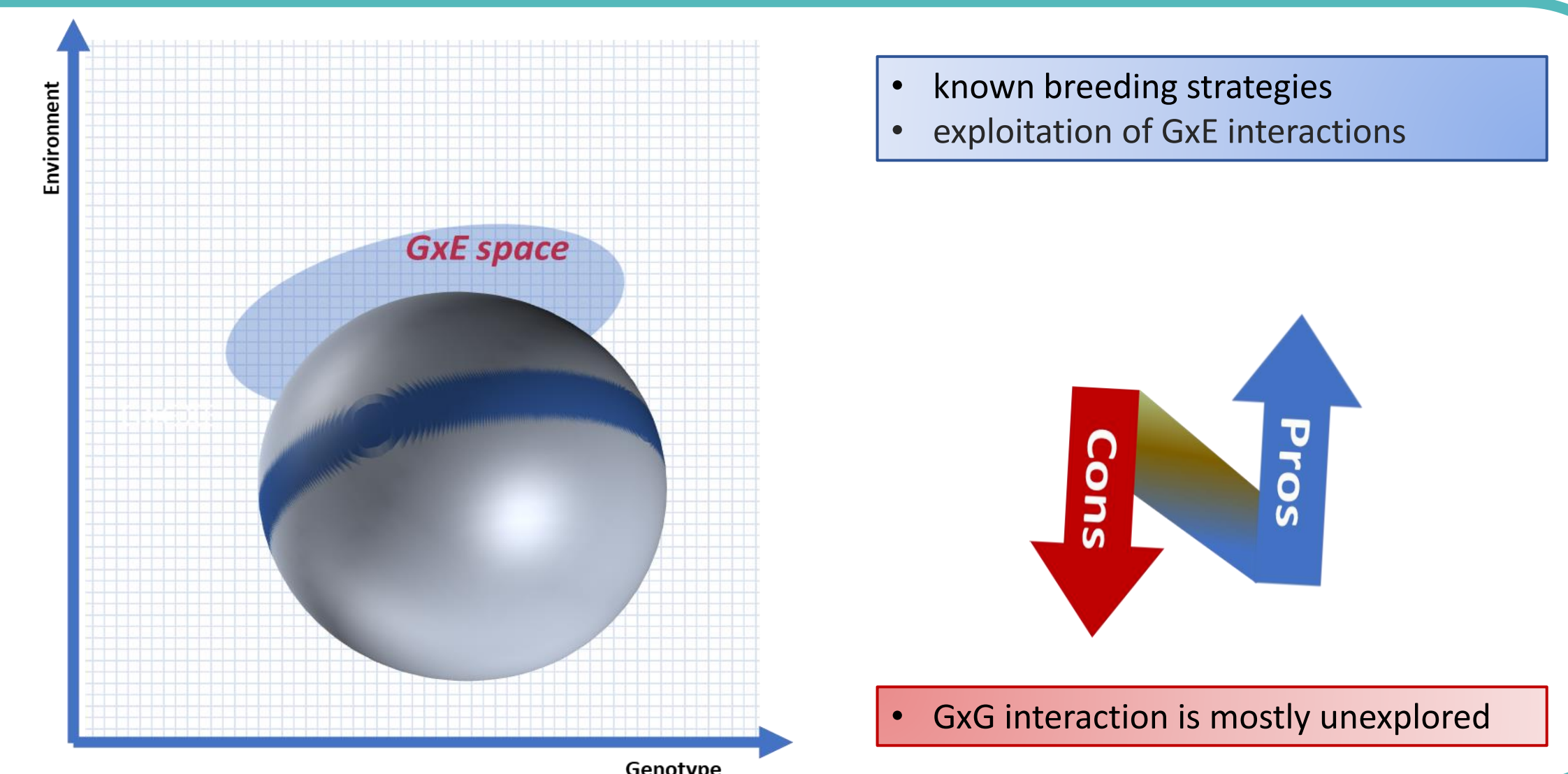
INTERCROP BREEDING STRATEGIES FOR DECOMPOSITION OF GXE MODELLING FRAMEWORK

Monocrop Breeding for Intercrops (MBI approach)

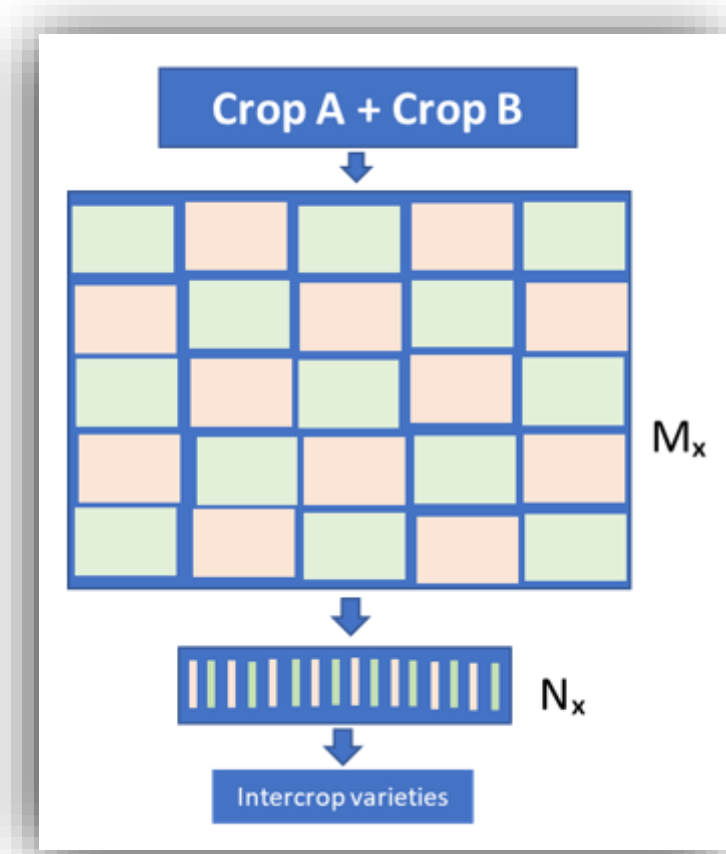


Concept: Breed the components of system as monocrops but select for intercrop compatibility. The breeding methods of the involved species are not necessarily alike but the breeding goals include various intercrop-specific traits such as growth habit and growth duration. This approach is mainly focused on the exploration of the GxE subspace and provides little opportunity to exploit GxG interactions during the breeding process.

- Main features:**
- standard monocrop breeding strategies
 - favourable, short-term rate of genetic gain
 - limited exploitation of GxG interaction

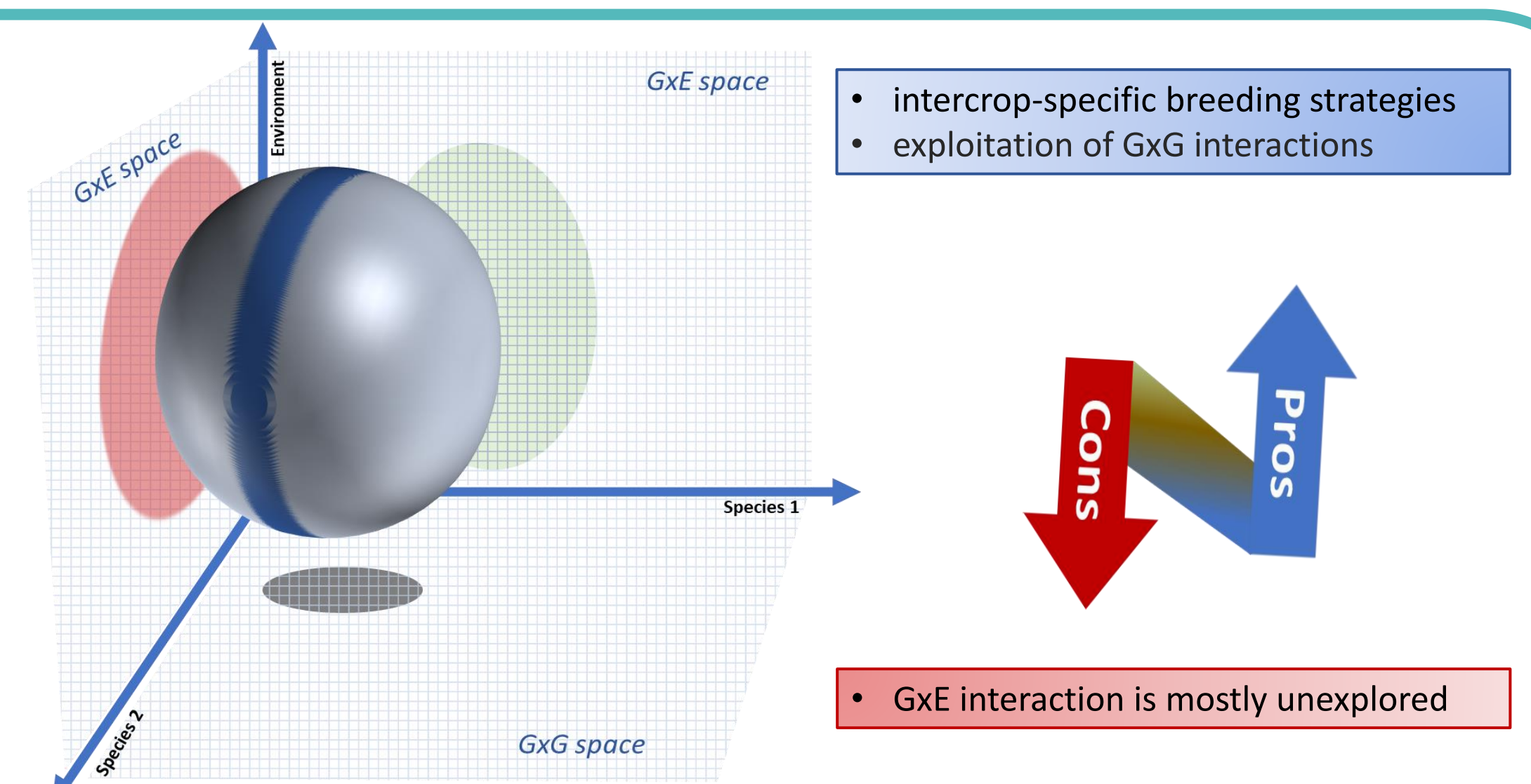


Integrated Intercrop Breeding (IIB Approach)

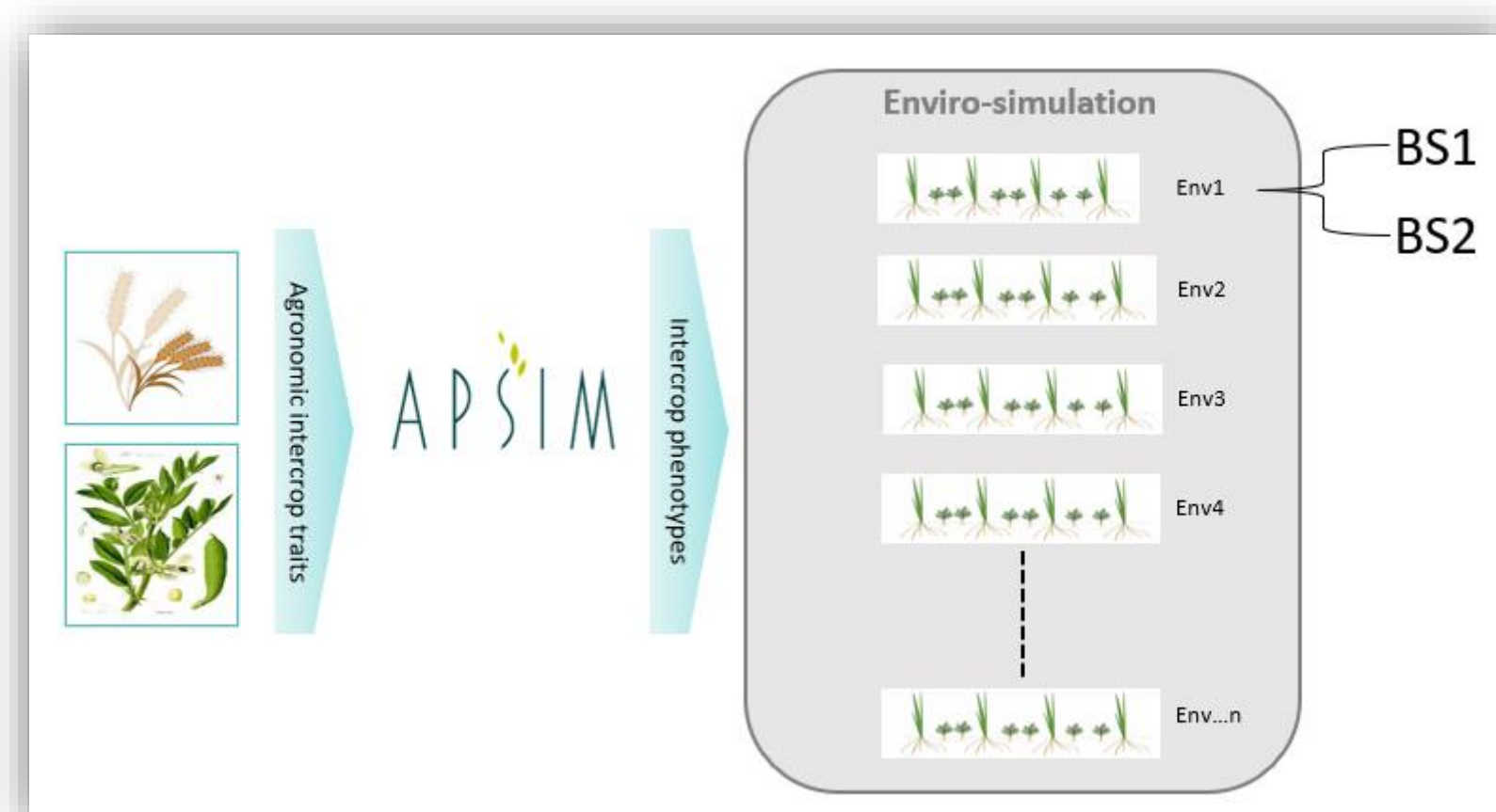


Concept: Partner crops are bred together in terms of phenotypic evaluation. Relies on intercrop-specific breeding concepts such as the estimation of producer/associate effects and general/specific mixing abilities to identify combinations of accessions with superior, intercropping performance. The number of candidate combinations in each stage of the breeding process is generally very high, reducing opportunities for extensive multi-environment phenotyping.

- Main features:**
- intercrop breeding strategies
 - exploitation of GxG interactions
 - limited exploration of GxE interactions

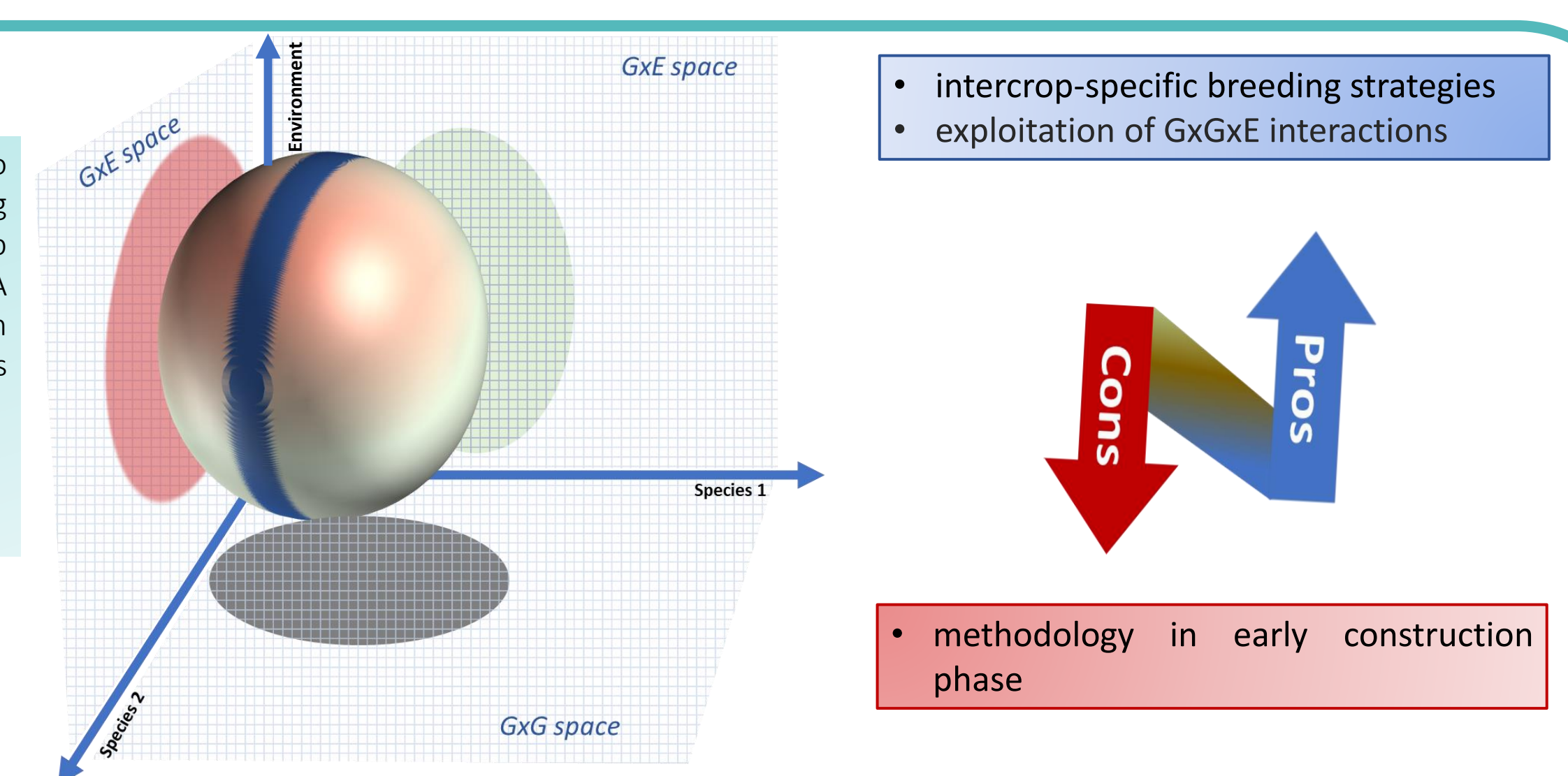


Ecophysiological intercrop modelling (EIM Approach)



Concept: This approach aims to take advantage of ecophysiological intercrop modelling to explore and exploit the relevant parts of the GxGxE interaction space in the breeding process. The envisioned ecophysiological model will be constructed from intercrop phenotypes that are gathered in the European trial network of the Horizon2020 CROPDIVA project. The initial methodology will be developed for intercropping systems of faba bean and triticale for which crop modules are available in the Agricultural Production Systems simulator (APSIM).

- Main features:**
- expand GxGxE exploration by ecophysiological intercrop modelling
 - integration of existing intercrop breeding strategies



CONCLUSION:

Ecophysiological intercrop modelling is put forward as a convenient way for intercrop breeders to explore the vast GxGxE interaction space that is spanned by multi-year, multi-location intercrop field trials. The project aims to develop an efficient intercrop breeding strategy that integrates ecophysiological crop growth modelling to enhance the exploration of the environmental dimension of the search space. Calibration data for these models is obtained from the multi-year, multi-location intercrop trials that are part of the CROPDIVA Horizon2020 project. This novel method will be benchmarked in-silico against other intercrop breeding strategies in terms of breeding efficiency and rate of genetic progress.

REFERENCES

