**Call for collaborative PhD projects**

**The Graduate School of Chinese Academy of Agricultural Sciences**

**and Wageningen University**

**Joint PhD Programme**

**2022**

**Applicants**

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**Title**

*Accelerating Genetic mapping in non-recombinant Brassicaceae genomes*

**Proposal**

The association of genetic variation with phenotypic variation is one of the cornerstones of molecular plant breeding approaches. The use of genetic mapping populations in model species has greatly enhanced our understanding of the effects of genome sequence variation. Nonetheless, the development and application of such experimental populations is notoriously more complicated in crops with large and redundant genomes.

Recently, however, WUR-Genetics has developed the technology for generating so-called chromosome substitution lines (CSLs), which consist of assemblies of non-recombined chromosomes. The size of a panel of unique segregating lines depends on the chromosome number of the species involved (2n) but is finite since crossovers between homologous chromosomes do not occur. In the model species *Arabidopsis thaliana* CSL libraries have been shown to reduce the costs and time of generating a genetic mapping population while increasing the mapping power and cost efficiency of phenotyping, especially in detecting epistatic interactions.

The development of CSLs depends on two crucial steps: i) suppression of crossovers and ii) generation of doubled haploids. The latter step is a standard procedure in Brassicaceae while the reduction of crossover formation in the hybrid of a cross between two genotypes can be achieved in different ways. In Arabidopsis this was accomplished by means of a dominant-negative RNAi construct silencing an essential meiosis related gene. However, CAAS-IVF has established an EMS mutant library of ~2,000 Chinese cabbage lines, each sequenced at 10x coverage. This library can be screened for mutations in genes involved in crossover formation, which than can be introduced into target lines to generate CSLs. In addition, CAAS-IVF has sequenced (20x) more than a thousand *B. rapa* germplasm lines that can be screened for natural variation in recombination frequency.

Yet, although the two species are related, the Brassica genome is considerably more complex than the Arabidopsis genome, involving more chromosomes and multiple redundant copies of homologous genes that might hamper the complete suppression of crossover formation. Therefore, in addition to the mutant approach, we suggest an alternative methodology that does not rely on the suppression of crossovers and generation of doubled haploids. Instead, we propose a massive genotyping approach of a backcross population from which progeny with non-recombinant chromosomes are selected and inter- or back-crossed again to obtain CSLs. During synapsis of homologous chromosome pairs in prophase I of meiosis, prior to segregation, crossovers often only occur between two sister chromatids while the two other chromatids remain unchanged. The method thus aims at selecting progeny from a cross between a hybrid and one of the recurrent parents containing high numbers of such nonrecombinant chromosomes. Residual heterozygosity can then be removed by further back-crossing while novel constellations can be achieved by intercrossing. A representative CSL library can be obtained within two generations of backcrossing and genotyping of a few thousand offspring with as little as 20 molecular markers.

Here we propose to develop these two complementary methods of generating CSLs in Brassicaceae in parallel, which will greatly assist in mapping complex traits in an important crop species.

**PhD candidate**

No potential PhD candidate available.

**Joint intent**

The CAAS-Institute of Vegetables and Flowers and the WUR-Laboratory of Genetics declare a joint intent of collaboration in the outlined PhD project and agree with the financial arrangements as stated below.

• *The CAAS Institute will cover:*

- A basic allowance for living costs for the duration of the project, including the required living allowance of the PhD candidate in the time that (s)he is in Wageningen. According to Dutch Immigration law this allowance should at least be € 1225,-. The costs of living when the candidate is in the Netherlands will be covered by the IVF lab budget or via a CSC visiting scientist grant.

- A bench fee of € 1000,- per month that the PhD candidate is in Wageningen, to be paid to the chair group, of which € 900,- is covered by the CAAS institute and € 100,- by Wageningen University. The Laboratory of Genetics will send an invoice after each visiting period of the PhD candidate to be paid by IVF.

- All local research expenses.

- Travel costs of candidates (2 return tickets).

• *The Wageningen University Chair Group will cover:*

- All local facilities required for the candidate at Wageningen University.

- The candidate’s visa costs.

- At least one trip of the Wageningen supervisor to China (CAAS Institute).

- € 3500,- to cover training and education activities. Note that, like all other PhD’s of Wageningen University, the Graduate School of Wageningen University that the PhD candidate will be part of, will cover an additional € 2500,- for organisation of PhD training and education.

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Jian Wu Joost J.B. Keurentjes

Institute of Vegetables and Flowers Laboratory of Genetics

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