

Population Genetics on *Ambrosia* genus: **past**, **present** and **future**

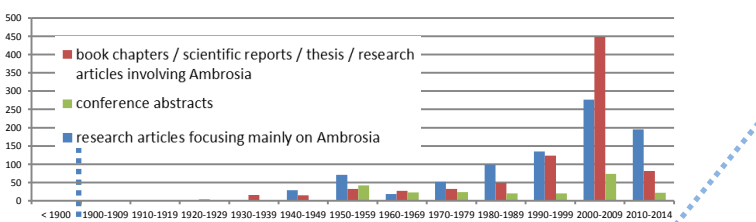


Coordinators* and members of the **Genetic Task Force** of COST-SMARTER (affiliations noted in the "Present" part):
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Introduction:

A new Task Force within the COST-SMARTER has recently been created. This group is composed of population geneticists from several European countries in charge of focusing on "**Genetics on *Ambrosia***" (Austria, France, Hungary, Italy, Poland, Sweden). Their mission was to review molecular methods used in published genetics studies on common ragweed and to discuss about future projects.

Scientific contributions involving *Ambrosia* plants



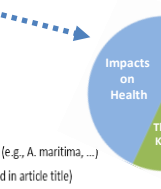
Scientific journals:



Ambrosia species studied:



3 different interests of research articles:



Literature about Molecular Population Genetics^A / Genomics^B of *Ambrosia*:

From	Authors	Year	Journal	Method/Marker	Pop. Studied	Main conclusion
USA	Martin et al. ^A	2014	MolEcol	SSR (n=6) ^A	USA	historical pattern of agricultural density
USA	Hodgins et al. ^A	2012	MolEcol	12-plex array ^B	USA/French/Swiss/Hungary	identification of invasiveness genes
USA	Lai et al. ^B	2012	AmBot	EST library (n=22)	USA/Hungary (A.art) USA/China (A.trif)	no introgression between A.art x A.trif
France	Mityás et al. ^A	2012	Maygar	Scot (n=11)	French/German/Czech/Hungarian	East EU pop. are only one metapopulation
China	Li et al. ^A	2012	Plos	AFLP (n=4 pairs)	USA/China	multiple introductions in China
Hungary	Mityás et al. ^A	2011	Biotelet	Bi-Pasa (n=4)	Hungarian	technical report
Australia	Gaudeul et al. ^A	2011	Plos	SSR (n=9) ^A	UE/USA/Asia/Russia/Argentina/Australia	absence of isolation by distance
France	Chun et al. ^A	2011	Biolvas	SSR (n=5) ^B	French/East EU/USA	two distinct origins in EU (West/East)
France	Chun et al. ^A	2010	NewPhy	SSR (n=8) ^B	French	increase of genetic diversity in France
France	Genton et al. ^A	2009	MolEcol	SSR (n=5) ^B	French/USA	active gene flow - admixture in France
France	Genton et al. ^A	2009	MolEcolNat	SSR (n=5) ^B	French/USA	multiple introductions in France
						technical report

PAST

PRESENT

Today, several national research projects are conducted in:

- Inra Dijon: R. Causse, B. Chauvel*, C. Délye, V. Le Corre, Q. Martinez
«Evolution and spread of resistance-inhibiting herbicides in two ragweed species (*A. artemisiifolia* & *A. trifida*)»
«Genetic structure of ragweed populations»
Several Ho: Role of non-agricultural habitats: sources or sinks for the ragweed populations? Isolation by distance: decrease on diversity with distance?
See poster of Lucy Meyer entitled: "New polymorphic markers for genetic diversity studies in an invasive plant: the common ragweed (*A. artemisiifolia*)"

- BOKU Vienna: G. Karrer*, M. Kropf, H. Meimberg
«Migration routes of *A. artemisiifolia* throughout Austria and neighbouring countries indicated by DNA microsatellite and AFLP analyses»
CC: 3 different ways of spreading processes are running in Austria;
no distinct migration routes at small geographical scale were found.

- University of Pannonia: J. Taller
«Population genetic analysis of common ragweed (*Ambrosia artemisiifolia* L.) in the Carpathian-basin»
«Development of a simple PCR-based assay for the identification of triazine resistance in the noxious plant common ragweed (*Ambrosia artemisiifolia*) and its applicability in higher plants»

- SLU Uppsala: A.-K. Kolseth, R. Scalone*
«Will photoperiod requirement serve as a barrier to establishment of common ragweed *or* genetic diversity will enable its establishment in Sweden?»
CC: certain European pop. are already adapted to Scandinavian photoperiodic conditions

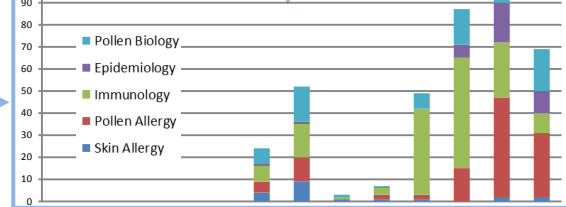
- University of Milan: S. Citterio, R. Gentili
«Study of intra & inter population genetic variability of common ragweed (*Ambrosia artemisiifolia* L.) in relation to Amb 1 isoforms and their allergenicity»
CC: Italian pop. seem to come from the Eastern part of the native area (Canada), as the French pop.

- University of Silesia: K. Bzduga, B. Tokarska-Guzik
«Genetic diversity of *Ambrosia artemisiifolia* in Polish populations and coming from bordering countries»
See poster of Katarzyna Bzduga entitled: "The allergenic invasive plant *A. artemisiifolia*: a new research platform in Poland"

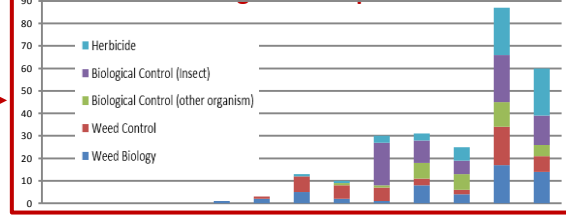
Observations

- Countries largely affected by the common ragweed's invasion are the ones using the most frequently molecular population genetics methods (e.g., France, Hungary, Austria).
- However, these population genetics studies are currently associated with other aspects of the ragweed problem (herbicide-resistance, pollen allergy, late-flowering, ...).

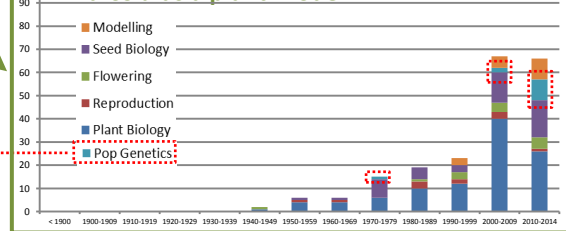
Ambrosia as a health problem:



Ambrosia as an agricultural problem:



Ambrosia as a plant-model:



SCIENTIFIC CONCLUSIONS FROM THE LITERATURE REVIEW:

- European common ragweed populations were originating from two different areas in the native range: Eastern European populations (Russia, Ukraine, ...) are coming from the Western part of the native range (USA-UT, USA-MT), while Central European populations (Hungary, Austria, ...) are forming one meta-population coming from the Eastern part of the native range (Canada, USA-NY).
- However, multiple introductions occurred since the start of the invasion and increased the genetic diversity of the originally introduced populations. Genetic bottlenecks are detectable difficultly due to an active gene flow between the introduced populations.
- Moreover, historical pattern of agricultural density and history can be found in the native range and showed clearly that invasive genotypes of common ragweed were already selected before their introductions in Europe.
- The invasiveness of common ragweed does not seem to come from genetic introgressions with its invasive sister-species, giant ragweed (*Ambrosia trifida*), but from a process of selection of plants possessing genes that facilitate "invasiveness".

FUTURE

- Molecular Population Genetics studies represent a very small part of the *Ambrosia* literature (< 1%), even if it grew significantly during the last 5 years. More works using population genetics have to be done in the future.
- The number of population genetic studies is clearly limited by the number of SSR markers available in the literature (only 13 nuclear SSR and 6 chloroplast SSR). The increase of the number of SSR markers will permit to possess efficient tools to answer more questions about the invasion biology of common ragweed. Moreover, the increase of the number of SSR markers is primordial for genomic mapping investigations. Today, several studies are focusing on the identification of specific genes (herbicide-resistances, invasiveness, flowering, ...) and would probably require their localisation on a genetic map of the common ragweed's genome.
- The use of molecular markers related to resistances (e.g., Scot) permits to estimate the impact of resistances on the selection process occurred during the invasion. Markers specific to an adaptive traits (resistance, flowering, germination) should be used more often in population genetic studies.
- The transition between population genetics to population genomics should start within the research groups of the members of the COST-SMARTER, as it has been done by external research groups (Lai et al. 2012; Hodgins et al., 2012).

Acknowledgement:

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