Abstract

The invasive plant species Common Ragweed (*Ambrosia artemisiifolia* , L. 1753) has spread in Switzerland over the last decades. Serious health illness (hight fever, asthma) are induced by its pollen and ca. 12% of citizens are subject to ragweed allergy. In heavily infested area in Europe, the annual cost of Common ragweed can be very high. Therefore, ways to anticipate future invasions are desirable. One possible approach to forecast the future is to understand past-to-present invasions.

In this study, we tested whether current Ragweed populations are randomly distributed, as a consequence of multiple independent introductions, or whether they show a dispersal gradient pattern from surrounding countries. To answer this, we combined species distribution models, dispersal models and population genetics.

Dynamic dispersal scenarios initiated from Geneva and Chiasso were significantly more similar to the current distribution than the null model of random appearance. Preliminary population genetics analyses did not show a significant structure but more work is needed. These results show that only a dispersal scenario from a few limited initial populations located at the Swiss border can explain the spread patterns in Western Switzerland and Ticino. Prioritizing management on these particular populations could be an efficient way to limit the further spread of Common Ragweed in Switzerland. In the future, the approach could be refined with more accurate dispersal parameters and realistic scenarios could then be derived to predict future spread pattern, pollen dispersal or management cost.

Abstract

Au cours des ces derniers décennies, l'espèce invasive Ambroisie à feuilles d'armoise (*Ambrosia artemisiifolia*) s'est largement répandue en Suisse. Cette éspece est connue pour causer des sérieuse sinthomes (fièvre, asthme) causées par ses pollens, qui provoquent des allergies dans le 12% environs de la population. Dans les régions d'Europe très envahies par cette espèce, le coût annuel lié à l'Ambroisie à feuilles d'armoise peut être très élevé. La prévention d'une telle invasion est donc souhaitable. Une approche possible pour une prévision de la situation future en Suisse est la compréhension des invasions passées et présentes.

Dans cet étude, la répartition de l'Ambroisie a été testée afin de comprendre s'il s'agit d'un phénomène dû au hasard, conséquence de plusieurs introductions indépendantes, ou lié à des schémas de colonisations à partir des pays limitrophes. Pour répondre à cette question, des modèles de distribution et de dispersion ainsi que la génétique des populations ont été combinés.

Les scénarios de dispersion dynamique à partir de Genève et Chiasso sont significativement plus semblables à la distribution actuelle que le modèle d'apparition casuelle. Les analyses préliminaires sur la génétique des populations n'ont pas montré une structure significative, d'ultérieurs recherches sont néanmoins nécessaires.

Les résultats obtenus montrent que seulement un scénario de dispersion à partir de quelque population d'origine localisées aux frontières suisse peut expliquer la répartition de l'espèce dans le ouest suisse et au Tessin.

Donner la priorité à la lutte à ces populations d'origine peut constituer un moyen efficace pour éviter une ultérieure colonisation de l'Ambroisie à feuilles d'armoise en Suisse. Dans le futur, un affinement de l'approche à l'aide de paramètres de dispersion plus spécifiques peut être envisagé. Ainsi, des scénarios réalistes prédisant les coûts liés à la gestion de l'envahissement ainsi que une distribution future des plantes et des pollens peuvent être mis en place.

Introduction

Natural barriers constituted for a long time strong limitations to the dispersal of species . Human-mediated modifications of the landscape and the intensification of international exchanges resulted in a breakdown of these barriers with effect on interactions between species that were never found together previously (…). As a result, no region is today isolated as it was in the past (Mckinney, 2006; Rahel, 2002). Alien invasive, by definition, are species established in the wild beyond their natural distribution range and dispersal potential (Walther et al., 2009; Mooney & Hobbs, 2000). They are usually aided by some form of disturbance (Williamson, 1996), and can locally displace native species and provoke major transformation of ecosystems. Therefore, they are considered one of the main threats to biodiversity (Pimm *et al.,* 1995). Invasive alien are also source of important economical damage for humans, as agriculture and health are in some cases affected by invasive animal and plant species.

Common Ragweed (*Ambrosia artemisiifolia*) is a plant from the Asteraceae family and is native to North America. The first European appearance of this species occurred in the middle of the 19th century, but it began to spread rapidly only since the middle of the 20th century (Chauvel et al., 2006). Where local founder populations have established, common ragweed is able to disperse quickly and efficiently along the linear structures such as communication networks (e.g.; railways, highways; Brandes & Nitzsche, 2006). Transient soil deposits and subsequent reuse of the ground and the excavation of contaminated sites clearly help the species' spread, increasing the problem. Commuter daily traffic between an infested area, such as the Rhône-Alpes region, and a non-infested area, such as the Geneva area, could generate seeds deposition on the side of the main communication ways (Taramarcaz et al., 2005). Moreover there are several examples of farming machinery rented and transported from the Lyon infested region and employed in Geneva or Lausanne area (Taramarcaz et al., 2005).

In heavily infested areas, this specie causes considerable negative impacts on human health, as caused by pollen (allergies, asthma; Laaidi et al., 2003) and on crop yield (potato, beets, sunflowers; Brandes & Nitzsche, 2006). For example, in neighbouring countries such as France and Italy, up to 12% of the population suffers from allergies to ragweed pollen (Taramarcaz et al., 2005). The costs of preventing a Swiss ragweed spread are for the moment lower than the treatment of a significant percentage of the population for pollen allergy (Taramarcaz et al., 2005). In the Rhône-Alpes area CHF 250'000 are spent yearly just on educating people. The state hospital of Milano 1 (ITA) spent aproximatly 1'390'000 € to treat people with allergies to Ambrosia pollen in 2002 (Zanon, 2002). The yearly illness cost in Germany was estimated at 32'000'000€ (Reinhardt et al., 2003 (Brandes & Nitzsche, 2006), in Quebec the cost of health care and prevention is at 49'000'000CHF (Taramarcaz et al., 2005).

In Switzerland during the 90'S, no prevention activities and eradication programs were initiated. However during the first years of the XIXth century, Common ragweed was not anymore only presence casual species, but in Geneva and in Ticino the situation began to become worrying, with important yearly increases in the populations. In Ticino, 80 population were detected in 2003, 110 in 2004 (Ciotti & Maspoli, 2005), and 33 in 2003 in Geneva (Taramarcaz et al., 2005). Different prevention activities were started and an important eradication programme was set-up. Today 300 populations were censored in Ticino and 200 in Geneva (Centre du Réseau Suisse de Floristique, CRSF).

Yet, despite these population increases, Switzerland is still at an early stage of *Ambrosia* invasion, but areas can change from low to heavy ragweed colonization in a few years (Taramarcaz et al., 2005).. Therefore, action can still be undertaken today to successfully prevent or limit the future spread of this species (Taramarcaz et al., 2005).Explaining the specie-environment relationships and predicting the spatial distribution of invasive species

is of great importance for developing and implementing early warning and prevention systems (Waage et al, 2001; Wang et al., 2006). One approach for predicting species involves the use of habitat-suitability or niche-based models, whereby environmental conditions, suitable for the maintenance of populations of species, are identified and mapped out onto geographic space (H. Chen, 2007).

We designed our study to understand whether the Swiss populations of *Ambrosia artemisiifolia* are randomly distributed over the landscape as a consequence of multiple and independent introductions in the recent past, or whether they show diffusion-like patterns from Geneva to Lausanne and from Chiasso to Bellinzona, starting from respectively nearby countries, i.e. France and Italy.

To attain our objective, we first characterized the native niche and investigated whether it was conserved between the native and invaded range. Starting from the native distribution, we estimated the importance of different climatic variables, and how they affected the projection in the invaded range. We derived a global model, projectable into the future. We then focused on Switzerland to get a map of the potential distribution of *A. artemisiifolia* created for present and future conditions, with a mix of climatic and human disturbance variables. Using a dispersal model (MigClim; Engler & A. Guisan, 2009), we integrated a dispersal simulation integrating the previously developed habitat suitability models and maps.

In this study, we tested whether dispersal from Geneva and Chiasso was more probable than dispersal from random introductions. Then, population genetic analyses were used to support or infirm the results obtained from the MigClim simulations.

This study produces new and interesting information on the ecology and biogeography of *A. artemisifolia* , which should prove useful for its management in Switzerland Our results

also provide Swiss authorities with useful maps of the species' distribution, for present and future scenarios, at the national, European and world levels.. In a research perspective, our approach and findings may suggest new ideas for future studies, integrating the proposed habitat-dispersal model and genetic data with, for instance, atmospheric models of pollen transport.

Methods

<u>*Object of study:*</u>

Common Ragweed (*Ambrosia artemisifolia*) is an annual monoecious weed, from the Asteraceae family (Taramarcaz et al., 2005). Its maximum height is between 120 and 180 cm and it is strongly dependent on its habitat, especially water supply and lack of competition (Brandes & Nitzsche, 2006). A. artemisiifolia grows best in warm and moist conditions, while low temperature and inadequate water supply delay its development (Deen & Swanton, 1998). Common ragweed responds to mycrorrihzai inoculum in a positive way, increasing its dry matter significantly (Crowell & Boerner, 1988). Flowering is induced by a dark period of app. 8 hours (Deen & Swanton, 1998), in Switzerland it coincides at the period between beginning of August to mid October (Taramarcaz et al., 2005). Under optimum conditions the plant takes only 30 days to flower and 50 days for its seeds to reach maturity (Brandes & Nitzsche, 2006). The quantity of seeds produced varies between a few thousand up to 60'000 (Lavoie, 2007). The seeds remain germinable in the seed bank for at least 20 years (Silc, 2002), up to 35 years (Oberdorfer, 2001). Is a non-competitive specie and it germinate preferably on open site.

Species Distribution Modeling:

Our approach was based on ecological niche modeling(ENM) (Guisan & Zimmermann, 2000; Peterson, 2003; Guisan & Thuiller, 2005), consent the prediction of the species distribution. The climatic niche is a climatic space condition in which species could survive and reproduce. To use ENM different assumption are needed, first of all climatic factor are assumed to have the main role on the specie distribution at the continent scale

(Woodward, 1987). Second, the distributions of occurrence need to represent the entire realized niche, the distribution area on the native country need to be at the equilibrium (movement of colonization in a new environments of the fundamental niche are not suitable). Finally the models are affected if there is not a conservation of the niche between the native area and the invasive range (Broennimann & Guisan 2008). The ENM are base on the climatic factors and any other information about environmental and biotic variables, (for example soil type, disturbance regime, interspecific interactions and competition) are considered. These additional variables characterizing the realized niche could change between the native and invasive area, affecting for consequence the result of specie distribution models (SDM) based on ENM.

Native niche conservatism on global scale:

Species occurrence data:

Common Ragweed distribution was based on 4 different databases, Global Biodiversity Information Facility (www.gbif.org), Australian Virtual Herbarium (avh.rbg.vic.gov.au/avh/), Atlas Flora Europea (Meusel & Jäger) and the Jepson California Herbarium (ucjeps.berkeley.edu), that give an index of presence/absence with a 50 KmX50 Km coordinates resolution (Fig. 1a, 1b, 1c). Three different regions were considered, the native range in North America (NA). Eurasian territory (EU) with parts of Northern Sahara Countries (neighboring the Mediterranean Sea) and Australia (AUS) were integrated as invasive range.

Climate data:

We used the CRU05 climate data at 0.5° (New et all. 2000) to derive (Tab. 1): the mean annual temperature (temp), annual sum of precipitation (p), minimum temperature (tmin),

maximum temperature (tmax), humidity index (aetpet), growing degree days (gdd), standard deviation of precipitations (stdpd).

Statistical modelling:

As we used only bioclimatic variables, we modelled the bioclimatic niche.

We used the BIOMOD platform (Thuiller, 2003) for computing ensemble models combining 5 different modeling techniques: GLM (generalisedlinear model (McCullagh & Nelder, 1989)), GAM (generalised additive models (Hastie & Tibshirani 1990)), GBM (generalised boosted models (Ridgeway, 1999)), MDA (mixture discriminant analysis (Hastie et al. 1994)). These models, relating the species distribution of the native lands, to the 8 climatic variables, were calibrated (10 replicates) using a random sample of the data (70%).To validate our prediction in North America, the predictive power of each model was evaluated on the remaining 30% of the data using AUC (area under the curve criteria (Thuiller, 2003)). The following appreciation of AUC was used: 0.9<AUC<0.95 good model; 0.95<AUC1 very good model (Thuiller & al. 2005). The weighted mean (of the mean AUC of 10 replicates) of the AUC obtained on the five different model's techniques was used to evaluate the calibrations and projections. Whit a permutation procedure, BIOMOD can extract a measure of relative importance of each variable that is independent of the model. The importance of each variable is one minus the correlation score between the original prediction and the prediction made with a permuted variable. High values will therefore reveal a high importance of the variable whereas a value of 0 mean that there is no importance.

The different models calibrated and evaluated in North America were then used to project the potential analogues areas throughout Europe and Australia. The projection were evaluated too, with the local correspondent distribution of Common Ragweed. To investigate the conservation of native niche on the invasive countries we applied exactly

the same procedure to obtain models calibrated in Europe/Australia and projected in North America and Australia/Europe.

We then reduced the number of climatic variables used to calibrate the model on the native area. A clustering of the 8 variables was done (Fig.2). We then separated the variables into 4 different groups and we calibrated the models 3 times separately; in exactly the same way explained before. Only the most important variables from each group were retained (Tab.2) and an ultimate model with the best 4 variables for the native niche was created.

After an evaluation of the calibration region the model was projected across the European lands and in Australia. We then compared the AUC of the invasive countries for the model construct with all of the 8 initial variables and the final one where only 4 variables were selected .

Global model :

Broennimann & Guisan (Biol, Lett. 2008) suggested to use native and invasive occurrence to improve predictions of biological invasion, due to the modification of the realised and/or the fundamental niche. All the previous models may be able to give some interesting information about the conservatism of the niche, and could be important in predicting the distribution across the entire world. We assembled the presence/absence of North America, Europe and Australia to construct a global model, using the same models and the same 4 best variables cited before. We then projected this global model on the entire world (Fig.3). To evaluate the power of this global model, we projected it onto the NA, EU and AUS separately and we evaluated it with the presence/absence of these 3 regions, looking at the AUC value.

Projection of the global model in the future:

We finally projected the global model (World_2) for the future, on 2050. Aeotpet index was not available so we use the aridity index (a). we recalibrated the model with the 3 variables (Temp,P,Tmax) and the aridity index on the three main region, to project it on the entire world for the present and the future. To validate the replacement of Aeotpet with "a", a comparison between the two world model constructs for the present (Fig.4, Fig.3a) was done and the differences are irrelevant. Aeotpet for the future is not available but the replacement with "a" is then justifiable.

<u>*Present and future Swiss distribution of the Common Ragweed:*</u>

Species occurrence data:

The actual swiss occurrence of *Ambrosia artemisiifolia* was based on the CRSF database . Only records with a coordinate error less than 250m were taken into account. From that data two regions appeared to be particularly affected, (Fig. 5), a desegregation was performed. Only a single presence for each 1Km was considered. We reduced from 978 to 643 the number of occurrence, without affecting the importance of the two main affected regions.

Selection of a suitable environment:

Opposite to the world, and on the reason of the resolution increase of the model (i.e. pixel size = 100mX100m l), in Switzerland the absence doesn't cover the entire country. 3'000 pseudoabsence were randomly selected from a prior mask of suitable locations.
This mask excluded, all pixel at more than 1600m.s.m, Forests, glaciers, rocks, lakes, rivers, etc.

Swiss variables, related to climate and humans:

A pool of different variables were initially selected. A cluster analysis (Fig.6) allowed the definition of four different groups, and initial models were run separately following the same procedure as for the global scale calibrations (see above). This allowed selecting the four most important variables to be selected. The initial climatic variables were partially the same used at the global scale (Mind, Pdays, Prec, Sfroyy, Swb, Taveryy). Common ragweed distribution is commonly (Brandes & Nitzsche, 2006) related to human transportation; for this reason the distance from speedways, highways and main roads were chosen as additional variables. An index of urban density and agricultural density was also introduced. The both density index were obtained starting from the land use and performing a mobile window of 400m diameter that calculated the ratio of pixels attributed to urban/agricultural or other classes.

Statistical modeling:

In each of the 10 replicates, 70% of the data was used to calibrate the models and 30% was used for evaluation. We used the same modeling techniques as for the global scale (GLM,GBM,GAM,MARS,FDA).

Future Swiss risk of invasion:

The same auc procedure used for the global scale was performed to obtain an estimation of the future risk for a Swiss invasion. The model obtained with the actual Swiss occurrence of Common Ragweed was projected on the future climatic variables predicted for 2040. These values are extrapolated from the a1Fi ARIII climatical scenario (www.IPCC.ch).

Pattern of colonization in Switzerland using MigClim:

Model calibration:

The technique used on the previous part of the project gave us an idea of the maximum of potential expansion of this species and the geographical predilection. However our main objective was to investigate the pattern of colonization.

This part focuses on two regions, Lemanique and Italian, clearly the most affected in switzerland. MigClim is an application that permit to integrate a simulation of dispersion based on habitat suitability maps. According to the historical records (CRSF), *Ambrosia artemisifolia* appeared in Switzerland at the beginning of the '90th in Geneva; we chose a departing point on the speedway, close to the border with France. Smoolik & al. (2010) derived a dispersal Kernel that describe the probability of dispersion with the distance, based on 15 years of Austrian records. We used a leptokurtique version of our function (k=1000, l=21625, dist=distance between source), as they suggest (Fig.7).

$$f(x) = \frac{0.659}{f(1) * \frac{2 * k}{(\pi * l * (1 + (\frac{dist}{l})^2)}} * \frac{100}{3500}$$

Smoolik & al. (2010) used a pixel size of 7x5 Km, our pixel size is 100x100m, for this reason we divided the function by 3500. The maximum long dispersal distance was 100Km and between 50-100Km we use a unique probability value (0.0014).

Which scenario is the best one:

Hundreds random departure points were selected on the two study area, that includes the states of Geneva, Vaud and Vallais for the first area, and the state of Ticino for the second. The suitability maps were obtained to the same modeling technics as the previous

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chapters. We assumed a potential of dispersion for the new colonized pixel at the next generation of 100%, any other parameter was   adjusted. MigClim was run during 13 steps (1step=1year), and the density of the colonized pixel was calculated on a mobile window of 7kmX4km height. The correlation between the density of the actual occurences and the density derived from the "realistique" model with a start point in Ghenf and Chiasso was calculate. This value of correlation was compared to a null model built with 100 random introduction points. This test answered the question if the dispersal from the a priori known source is more probable than dispersal from random introduction points.

Genetical approach to support MigClim method:

MigClim is based on a statistical approach, for this reason a genetic approach was added to confirm our modeling results. The objective was to derive preliminary information on the swiss genetic diversity of ambroisia.

Samples collection:

Samples of leaves from 5 individuals from each population were collected and dried on silica gel. Each Population was at least 100m distantance from each other (Henry et al., 2009),

A total of 85 populations were sampled during the season 2010, in Ticino, Vaud, Geneva, and Italy. In addition Doc.Gaudeol shared 4 italian populations collected during previous seasons by Dr. Levente (Plant Protection Institute of the Hungarian Academy of Science, Budapest) Prof. Bretagnolle (Dijon University) also shared 5 French populations collected in a previous season. The collected material covered the most affected regions in Switzerland and their nearly foreign lands (Fig.8).

DNA extraction:

For Economical and technical reason we reduced the number of populations in the analysis to 20 (Fig.8). A surface of approximately 25mm^2 of leaf material from each individual was pulverized on 2-mL Eppendorf tubes using two iron sphere and a mechanical shaker. DNA was extracted using the DNeasy Plant mini kit (QIAGEN), or with Robot extraction; according to the manufacturer's protocol. However the final dilution was done on 100 µl of Buffer AE contrary to the 200µl indicated. Extractions were stored at -20°C.

Molecular markers and plastid DNA sequencing:

Each individual was characterized by two nuclear microsattellites, Ambart17 (GeneBank nr. FJ595152) and Ambart18 (GeneBank nr. FJ595153) isolated by Bretagnolle & al. (Molecolar Ecology Resource, 2009).

Polymerase chain reaction (PCR) was performed in a total volume of 10µl, containing: 1 µl H_2O, 2 µl $MgCl_2$, 1 µl Primermix (250 µl H_2O and 5 µl (10 µM) of forward and revers primers), 5 µl Master Mix. Each forward primer was labelled with one florescent dye, HEX and FAM. Cycling was performed in a T3 Thermocycler (Biometra), with a initial denaturing of 95°C for 15min, 29 cycles at 95°C for 30", 50°C for 45s, 72°C for 45", and a final extension step of 72°C for 5mins. PCR products were loaded on an ABI PRISM 3100 with GeneScan 350 size standard, and alleles were sized using GeneMapper (version 3.7; Applied Biosystems).

Results

Models transferability:

The models calibrated in NA, EU and AUS have in general a good precision compare to the real presence, on the Fig.1 all the models and projections done with 8 climatic variables are showed. On Tab.3 all evaluations of the models are presented and in Tab.4 the details about the importance of the variables are showed. The different climatic variables use assume, for each of the three area of calibration different, different importance. The four most important variables on NA model (Pet, Temp, Gdd, Tmin) are different on EU (Tmin, Temp, Stdp, Gdd) and AUS (Aetpet, Gdd, Temp, Tmax), the best variables are different and the value of important change (Tab.4).

All variables were clusted Fig.2 and a choice of 4 groups was done. Group 1: tmin, temp - Group 2: tmax, gdd, pet - Group 3: aetpet - Group 4: p, stdp. The Tab.2 show the importance of the different variables use on the 3 model (Tab.5) ran separately and temp, tmax, p and aetpet explain the most important part of the models. We switch from 8 climatic variables to 4 and the correlation between the variables was reduce Fig.9. The NA model done with the 4 selected variables, have an evaluation a bit lower (0.988 auc) than the previous model at 8 variables (0.994 auc), but the european projections are consistently better (0.774 - 0.720 auc)   and the australian too (0.95 - 0.92 auc). The amelioration of the EU projections of the NA model after the clustering is relatively important on the geographical distribution as showed on Fig.10 .

A global model created with the assembling of the presence/absence on the three region studied, has a good evaluation (0.93 auc) and it was projected on the entire world (Fig.3a) and in the future two (Fig.3b). The actually distribution of Common ragweed could cover, if

present in every favourable places, the 29% of the terrestrial world surface (AUC CutOff 0.3057), with an increase of 6% during the next 40 years.

Switzerland and Common Ragweed:

The selection of the 14 variables used in Switzerland was done 4 groups of clustered variables (Fig. 6). A model was built with each group of varibales (Ta. 6) and the most important variables (Tab.7) of the 4 different models were: temp, P, tot-roads, urban-density. The fjnal model (Fig.5) created with the 4 selected variable had a good evaluation (auc 0.94), with two highly important variables, temp (0.73) and urban-density (0.17). The projections done for the 2040 clime (Fig.11, Annex A) is apparently not so different to the present, but there is an increase of 750Km2 on the area affected by *Ambrosia artemisifolia* witch corresponds to the approximation of a 4% increase in the Swiss mask.

MigClim

MigClim was run first under a scenario corresponding to the hypothetized pathway of colonization. This model was run for 20 generation steps. After 20 generations, all the suitable area was colonized.   Step nr. 13 gives the closest results from the actual distribution. The correlation of the real density (Fig.12a) of this specie and the modeled one (Fig.12b) is 0.42. This correlation is significantly higher than the null model (p-val =0.97). Only on 3 random models (Fig.12c)showed a higher correlation with the actual density (0.426%, 0.44%, 0.50%). The start points randomly assigned to these 3 models were all on Geneva region. The second region considered was the Ticino, with an hypothesis of introduction on the Chiasso region. This scenario (Fig.12b) is the most correlated one (0.61%) with the real occurrence (Fig.12a.), and any other random scenario

attains this value.

Genetical results:

We assigned the haplotypes for two micro satellite loci at 120 individuals. 16 haplotypes on locus Ambart 17 and 6 on Ambart18 were found. Different investigation on the structure of population, on the lost of genetically diversity were done. Due to the small number of different loci sequenced, no significant result were founded.

Discussion

This research was structured on three different parts. The common objective was to understand the pattern of colonization, in Switzerland, of Common ragweed. A global investigation into the conservation of the ecological niche, was done first. Temp, Tmax, P and aetpet appear the most important climatic variables at the global scale. A non negligible improvement is obtained with a cluster selection of variables to transfer models from the native niche. The future climatic scenario shows an expansion in the area affected by this species, especially in the non native regions. A new statistical approach coupled with the MigClim application offers an interesting way to investigate the colonization pathways. Following our results Geneva and Chiasso the most probable source of introduction in western Switzerland and Ticino respectively.

The global model projected throughout the world is projected in two vast areas not used during the calibration. These two areas were excluded from the analysis because little data was available. However the little data found confirmed the presence of common ragweed in two regions (one in South Africa and one in Paraguay), also predicted by the model developed. This fact clearly supported the model's reliability. The future predictions for 2050 show an increase of 6% in the favorable territory. There will not be an important shift in the most affected area, the region affected today will remain affected in the future; but the intensity of the risks and the favorability of the environment will increase. This can only warn authorities concerned not to hesitate, and to engage serious effort into the management of Ambrosia for the future. Hopefully in some region of South America, Africa and Australia, the future distribution seems to be vaguely smaller than on the present. Future clime will probably assume on these regions a less favorable characteristic compare to the present. Unfortunately during this study we didn't deepen for understand

which variables are more responsible of this change. More focused research, on regional scale, could be source of interesting information for the future risk of invasion for *A.artemisiifolia.*

The climatic variables used during the different model's calibration (on invasive or native area), assume different importance due to the different types of climates found. Multiple examples can be extrapolate from Tab.4, we focus here on the tmin. Tmin on the Australian calibration is not an important variable (0.001), as appose to the European model, where tmin assumes an important role (0.71). The projection of the Australian model in EU (FIG.1h) is in consequence not realistic; in fact Sweden, Finland and the west part of Russia are erroneously predicted. In this case different information about the physiology of the plant (Deen & Swanton, 1998; Strandhede, 2000; Chauvel B. personal communication) was known, but in other cases some erroneous projections could be considered as correct. This show how the global extent of the calibration area can affect models results and transferability.

A selection of the most important variables using a cluster way, and a pooling (Broenniman & Guisan) of all data on the occurrence of the native and invasive areas for the calibration, is probably one of the best ways for a correct prediction.

In our case an amelioration for the European projection (+0.054 auc), derived from the reduced number of variables is obtained. The European area predicted following this method approach more the model calibrated on EU than the non-clusted one, calibrated on NA.

The pollen distributions could be important in helping to screen for its occurrence and to provide information for global databases. In fact not all the occurrences found on the databases have a complete life cycles, until the seeds have been produced and dormancy has occurred (Chauvel personal communication). These occurrences can be explained by human's role in seed dispersion creating a continuous flow that constantly brings new seeds to different areas. Otherwise in the past there may have been an important contamination of these seeds banks, due to their long life (Silic, 2002), and the non competitive behavior (Bazzaz, 1974), affecting the seeds germinating today again. We found a study which delimited a minimal gdd to conclude the entire life cycle of common ragweed; for this reason the world wide presence of the Ragweed was considered. In this particular case, the apparent distribution of A. artemiisifolia in Europe may represent an overestimation of the realized niche. This once again made us realize how important the choice of variables were, not only for the calibration of the model. But also for the projections produced for other countries and other climates.

The model created for Switzerland is at a fine scale, compared to the world work; for this reason some inhospitable geographical regions of Switzerland were excluded. This procedure reduced the number of errors produced, with the exclusion of some variables during the calibration.

For example in North America, Temp is a very important variable; however in Eu Tmin is much more important. To reduce the variables, for Switzerland, especially the correlated ones, we used Temp and we deleted from the mask all of the points higher than 1'600s.m.s (the highest FR population founded is at 1200 m.s.m). In consequence it is possible to exclude Tmin from the model. The importance of frodays, one of the variables used during the cluster selection, is very low (0.14). This confirms that for the mask, where also the pseudo-absence was selected, tmin (very correlate with frodays) is not useful.

Switzerland is still in an early stage of invasion, for this reason the distribution of population is not stable but in expansion. Probably Swiss occurrences inform only partially, about the fundamental Swiss niche of Common ragweed, and the derived models are certainly negatively affected.

Downscaling global models at a fine regional scale is delicate because the ecological factors driving species distribution can be quite different depending the resolution of the study. However, the selection of the pseudo-absence could be based on the projection of the global model onto the regional study area. With this procedure, the climate result from the major part of the pseudo absence, taking in account not only the present Swiss situation, (probably not at the equilibrium) but also the world distribution (Thuiller personal communication). The pseudo absence assumes more credit than the pseudo-absence which is randomly selected on the Swiss-mask.

The first model ran separately, during the selection of the Swiss variables, group(model1 Tab.X) only climatically variables and the second (model 2 Tab.X) only variables related to humans. Both models obtained a greet evaluation (AUC 0.92 clime / 0.88 human). This confirms that, in Switzerland, humans have an important role on the occurrence of Ambrosia (Taramarcaz et al., 2005) (the two models variables are not very correlated, the models are independent).

The Swiss model projected for the future has an important factor of incertitude due to the climatic forcaste. However it is interesting to see that for 2040 the situation will be geographically similar, compared to the current situation. The points with a high risk of colonization are the same, but the concerned areas will be a bit broader compared to the present situation (+750Km^2).

The presence of this species in the Western Switzerland is far from covering all of the potential environment (Fig.X), therefore these maps could be used as a utility to facilitate the effort in preventing this species from taking over this environment. By recognizing the target areas, it will be easier for people/authorities to create an effort to prevent this plants spread. The Vallais region is a good example of an important area, fortunately until now only one population has been able to colonize the area. This means that at this present time there is still a chance to prevent the spread of this ragweed; however if action is not taken now then in a few years the land may be covered in multiple populations which could cause significant damage for the areas and its inhabitants.

This movement of spread is well simulated by MigClim. This application gives an idea of the potential dispersion of the ragweed, while also giving an idea of the density of the populations in a specific area. MigClim is based on a probability model and the more favorable the area is, the higher the likelyhood that different populations will become present. The spread probability for each population is given by a kernel function, decreasing with the distance. But in any case simulated populations appear at the true place compared to the real populations. Otherwise the density of the populations in a limited area is comparable to the reality, and if today the model predicts less than 5 populations in Vallais, in a few years the situation will have dramatically changed. Following this model a large number of new populations will appear and spread on to this uncontaminated region.

MigClim follows a Kernel function that assigns the probability for a pixel to be colonized from a peopled one (this probability decreases with the distance). Smolik & al. (2010), calibrated the Kernel function using 15 years of records for the Common ragweed in Austria. Their model, evaluate the probability of a pixel to be colonized (at the next step), taking in account only the closest population as a source. This function of spread is the

only one available for Ambrosia and due to the geographical similarity with Austria, we decided to transfer it in Switzerland.

Smolik & al. suggest to use a leptokurtique version of our function to ameliorate the precision and to consider each colonized pixel as a source for another pixel. This amelioration was applied to the function used in Switzerland.

The leptokurtique version reduce the probability of spread for the court distance, but assuming the same f(0), and the same area under the curb (of the non leptokurtique), the long distance spreads have more chance of occurring. Every contaminated pixel could be a source of a new population in another pixel, (at the next step) and not only the closest one, this increment the probability for a pixel to be invaded. The increase of long distance events and the fact that each contaminated pixel could be a source of a new population, the colonization simulated with MigClim is faster than the reality. Due to a different density of villages and towns, a different morphology of territory and other differences on the human exploitation of the territory; a considerable error could also affect the Swiss model. However MigClim analyses were based on the density of population and the speed of colonization is a marginal data that didn't affected the accuracy of our result. Also the error derive from the geographically difference between Austria and Switzerland is not important because all the Swiss simulation are concerned at the same level.

The simulation show the situation after only 13 steps, since the introduction in Geneva. However historical records locate the introduction in the first half of '90, between 15 and 20 steps ago (CRSF). The MigClim simulation show how a single introduction of the Common Ragweed in Geneva could in 13 steps produce the actual situation. This means that any other independent introductions are needed to explain the present situation. In Ticino we have the same result, a single introduction in the Chiasso region could produce the same present situation. However in Ticino the mask available for the colonization is much more restricted compared to the Western Swizzerlan region. A large part of the mask

has a high suitability index and the geographical distance between Nord-South is lower than on the west Swiss part. These three characteristics, added to the Kernel problems cited before, can produce a likely simulation of the situation and gain results quickly; probably faster than the real history. In fact in the second step different populations are dispersed throughout the entire Ticino and they contribute to Ambrosia's progression. Considered this limitation, in Ticino, any other scenario that the single introduction in Chiasso region, is more correlated with the reality.

We used a leptokurtique version of the function, and we coupled it with a suitability map of territory. We then considered each contaminated pixel as a potential source. As the next step of amelioration, we suggested adding a function that assigned a probability to a new population, which would spread across the time. A new population is composed from few individuals and the probability to germinate, complete the life cycle, and to be a source for a new population, is less than a 3-4 years population compose from hundred of individuals (Auld, 1980). This means that to be a source, a population needs to wait some years (with also a small probability of extinction). This amelioration could slacken the speed of colonization across the territory and create the simulation with an increased accuracy compare to the real situation. However the main objective of our study was to detail the possible origin of the Swiss colonization and not to create an accurate Swiss dispersion model for Common ragweed.

Due to the small number of different loci sequenced, no significant result could be extrapolate from our genetically data at present. The program Structure (Pritchard, 2000) seems to be an interesting utility to confirm the origin of our populations, but the restricted number of loci prevent any reasonable conclusion. At present we will add 6 new microsatellite loci (Molecolar Ecology Reseurce, 2009) and complete our present data. For

the moment we couldn't confirm with our previous and partial genetically result the MigClim scenarios. However if the 5 new loci will confirm the actually trend offered by the two sequenced loci, interesting genetically information could definitely support the MigClim predictions

The Swiss suitability map obtained in our study is important for the management of this invasive species. The problem is that it only shows the maximum territory that could be colonized by Ambrosia, or the probability that a specific place could be colonized. On the contrary an ameliorated version of the model obtained with MigClim could give information about the density of the Common ragweed year after year and important information about the next region that will be affected could be obtained; allowing it to then be extrapolated. Scientists from Meteo Suisse, who work on predictions of pollen dispersion could ameliorate their prediction, as they will know the real progression and density of Ambrosia across time.

Conclusion:

The mains objectives of this study are attained, in fact new interesting information on Swiss Common ragweed pattern are found. Thanks to MigClim we can at present support the hypothesis of a development of Swiss invasion from Geneva and Chiasso regions. As, the present situation could derive from a single old population introduced on the first '90, the future expansions could be realized from the present populations. For this reasons serious provisions need to be considered for delimitate the future expansion of *A. artemisiifolia* on the Swiss territory. New important information about the habitat suitability in Switzerland were described on this study and the basis for future additional research were build. Following the methods applied during our research, future genetically information could confirm our statistically analysis. Our work will be integrate on models of pollen distribution by Katrin Zink (Meteo Suisse). Important information for prevent health problems concerning the Swiss population will be assembled. This is probably the best reward for our effort.

Aknowlegement

I woul like to thankyou all people that in a way or in anhother had an interaction with my master project. Thank you.