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# **Biotic Risks and Climate Change in Forests**

10<sup>th</sup> IUFRO Workshop of WP 7.03.10 "Methodology of Forest Insect and Disease Survey in Central Europe", September 20-23, 2010 Freiburg, Germany

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# Biotic Risks and Climate Change in Forests

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# Preface

The tenth regular workshop of the IUFRO Working Party WP 7.03.10 "Methodology of Forest Insect and Disease Survey in Central Europe" was held in Freiburg im Breisgau, Germany, September 20-23, 2010. It was organized and hosted by the Forest Research Institute of Baden-Württemberg, Department of Forest Protection. The workshop topics focused to the following themes: Biotic Risks and Climate Change in Forests, with respect of three subtopics in context to Climate Change: 1) Risk assessment of actual and introduced pests and diseases; 2) Survey of actual and introduced pests and diseases and 3) Information platform on pests and diseases occurrence in Central Europe.

All together 77 participants attended the meeting. During the scientific program, 29 oral and 29 poster presentations were organized as well as a guided tour through the historical part of the city of Freiburg. The whole day field excursion introduced us the local forest protection highlights of the famous Black Forest - including the strictly protected forest reserve Napf with its bark beetle situation.

Our working group is mainly engaged in biotic influences to the forest health condition in Central Europe, but although researchers from elsewhere are welcome to attend. Meetings are an ideal platform to exchange information on methods and techniques in forest protection, conducting of forest pest and disease survey and advisory service, which have a long tradition within European forest research institutes and faculties. It is a unique platform for both, forest entomologists and forest pathologists to meet together in one place to discuss and share experiences, practices and scientific results.

The IUFRO group wish to express their gratitude to the German colleagues who perfectly organized the fruitful meeting in Freiburg: Dr. Horst Delb, Silvia Pontuali and staff from the Forest Research Institute of Baden-Württemberg (FVA). Our special thanks go to Prof. Konstantin von Teuffel, director of the institute, who hosted us in Freiburg and to Dr. Hansjochen Schröter, section leader of forest protection, for his impressive contribution at the Black Forest excursion. We also thank the organizers and Renate Krieg for bringing the manuscripts together and preparing the proceedings.

Milos Knizek Beat Forster Wojciech Grodzki

Coordinator and deputy coordinators of WP 7.03.10



Participants of the Workshop at the excursion to the Black Forest, Feldberg-Stübenwasen, September 22<sup>nd</sup>, 2010

# 1.3 MYCOLOGY

# Distribution and genetic variability of *Heterobasidion annosum* s. l. in the Northwest German Lowland

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## Introduction

The *Heterobasidion annosum*-complex contains significant root-rot pathogens of mainly conifers in Germany. Since the last decade new damage patterns are obvious in the German Lowland beside the so-called "Ackersterbe". There are devastating root rot phenomena in conifer plantations and natural forests especially Pine forest in Lower Saxony and in Lusatian mining district. Currently, in the forest of the Northwest German Lowland there were observed massive continuance damages in forest stands ranging from the dying of single trees to the loss of whole forest stands. Beside the normal, latent distribution in the forests, in the last years, a more aggressive infestation, which could not be explained by the common and presently known epidemiology and pathogenicity of *Heterobasidion* is obvious. Actually estimations in Lower Saxony show more than 100.000 ha infested forest stands. The infestation of precultivations of Douglas Fir and Beech in Pine forests is remarkably, and has negative influence of the sustaining and economical forest management.

Due to a population study of *H. annosum* s. I. specimens were treated in PCR experiments. Different DNA-regions like ribosomal ITS, (Internal Transcribed Spacer), portions of nuclear glyceraldehyde 3-phosphate dehydrogenase (GPD), nuclear elongation factor 1-a (EF1), and a part of the mitochondrial ATP synthase subunit 6 coding region (ATP 6) were sequenced, to perform a phylogenetic analysis via parsimony, Bayesian and median-joining network analysis (BLANDELT *et al.* 1999).

### Results

89 *H. annosum* s. I. specimens were collected in Lower Saxony and Hesse. DNA was isolated after EDWARDS *et al.* (1991) and upon other terms. Several *H. annosum* s.I. specimens were preliminary treated in PCR experiments. The sequence data of the different DNA regions were compared with other published phylogeographical and sequence data of European and North American specimens (mainly data published by LINZER *et al.* 2008). There was no evidence of the occurrence of invasive species like *Heterobasidion irregulare* Otrosina & Garbelotto (= North American P ISG (pine)) or *H. occidentale* Otrosina & Garbelotto (= North American S ISG) (OTROSINA & GARBELOTTO 2010)

Two of the three European *Heterobasidion* species, *H. annosum* (Fr.) Bref s. str. and *H. parviporum* Niemelä & Korh. in Woodw. were found on different coniferous and deciduous host trees in Lower Saxony and Hesse. The specimens were identified by morphology and ITS-sequences. From 89 collected vouchers three from spruce were determined as *H. parviporum*. For an example the phylogenetic results of the GPD (Figure 1) and EF1 Loci (Figure 2) of the investigated *Heterobasidion* species were shown. The used other data were published by LINZER *et al.* (2008) and retrieved from Genebank.



Figure 1: Bayesian analysis of the GPD-locus. The GPD-locus-analysis was rooted with the outgroup Heterobasidon insulare. 50% majority tree with posterior-probabilities printed on nodes. The genetical distance is given in the bar. The investigated *H. annosum* s. str. specimens sequenced by the authors are printed in green. *H. parviporum* collected in Lower Saxony is printed in blue. The used other data were published by LINZER *et al.* (2008) and retrieved from Genebank.



Figure 2: Median joining network analysis of the Nuclear elongation factor 1-a (EF1). Analysis was rooted with the outgroup *H. insulare* (pink). *H. annosum* s.str. specimens collected by the NW-FVA are marked red. *H. parviporum* collected in Lower Saxony are marked dark blue (others pale blue). H. irregulare (dark gray, NAm-P-ISG) H. occidentale (light gray, NAm-S-ISG) and *H. abietinum* (green). The used other data were published by LINZER *et al.* 2008 and retrieved from Genebank.

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