Clinical Infectious Diseases Advance Access published May 14, 2015



# *PTX3* Polymorphisms and Invasive Mold Infections after Solid Organ Transplantation

**A. Wójtowicz[1], T. Doco Lecompte[2], S. Bibert[1], O. Manuel[1,3], S. Rüeger[4,5], C. Berger[6], K. Boggian[7], A. Cusini[8], C. Garzoni[8,12], H. Hirsch[9], N. Khanna[9], N.J. Mueller[10], P.R. Meylan[1,11], M. Pascual[3], C. van Delden[2], P-Y. Bochud[1,*], and the Swiss Transplant Cohort Study (STCS)[‡]**

[1]Infectious Diseases Service, University Hospital (CHUV) and University of Lausanne, Lausanne, Switzerland

[2]Service of Transplantation and Service of Infectious Diseases, University Hospitals of Geneva, Geneva, Switzerland

[3]Transplantation Center, Department of Surgery, University Hospital (CHUV) and University of Lausanne, Lausanne, Switzerland

[4]Institute of Social and Preventive Medicine, University Hospital (CHUV) and University of Lausanne, Lausanne, Switzerland

[5]Swiss Institute of Bioinformatics, Lausanne, Switzerland

[6]Division of Infectious Diseases and Hospital Epidemiology, University Children's Hospital Zürich, Zürich, Switzerland

[7]Division of Infectious Diseases and Hospital Epidemiology, Cantonal Hospital St. Gallen, St. Gallen, Switzerland

[8]Department of Infectious Diseases, Inselspital, Bern University Hospital and University of Bern, Bern, Switzerland

[9]Division of Infectious Diseases and Hospital Epidemiology, University Hospital of Basel, Basel, Switzerland

[10]Division of Infectious Diseases and Hospital Epidemiology, University Hospital Zürich, University of Zurich, Zürich, Switzerland

[11]Institute of Microbiology, University Hospital (CHUV) and University of Lausanne, Lausanne, Switzerland

[12]Departments of Internal Medicine and Infectious Disease, Clinica Luganese, Lugano, Switzerland

[*]Corresponding Author Contact Information: Dr. Pierre-Yves Bochud, Infectious Diseases Service, Department of Medicine, Centre Hospitalier Universitaire Vaudois (CHUV), BH 19-105, Rue du Bugnon 46 ,1011 Lausanne (Suisse), Tel.: +41 21 314 43 79, Fax: +41 21 314 10 33, E-mail: Pierre-Yves.Bochud@chuv.ch

Alternate Corresponding Author Contact Information: Dr. Agnieszka Wójtowicz, Infectious Diseases Service, Department of Medicine, Centre Hospitalier Universitaire Vaudois (CHUV), CLE, D04-406, Ch. des Boveresses 155, 1066 Epalinges (Suisse), Tel.: +41 21 314 10 25, E-mail: Agnieszka.Wojtowicz@chuv.ch

[‡]This study has been conducted in the framework of the Swiss Transplant Cohort Study, supported by the Swiss National Science Foundation and the Swiss University Hospitals (G15) and transplant centers.

The members of the Swiss Transplant Cohort Study are: Rita Achermann, John-David Aubert, Philippe Baumann, Guido Beldi, Christian Benden, Christoph Berger, Isabelle Binet, Pierre-Yves Bochud, Elsa Boely (Head of local data management), Heiner Bucher, Leo Bühler, Thierry Carell, Emmanuelle Catana, Yves Chalandon, Sabina de Geest, Olivier de Rougemont, Michael Dickenmann, Michel Duchosal, Thomas Fehr, Sylvie Ferrari-Lacraz, Christian Garzoni, Yvan Gasche, Paola Gasche Soccal, Emiliano Giostra, Déla Golshayan, Daniel Good, Karine Hadaya, Christoph Hess, Sven Hillinger, Hans H. Hirsch, Günther Hofbauer, Uyen Huynh-Do, Franz Immer, Richard Klaghofer, Michael Koller (Head of the data center), Thomas Kuntzen, Bettina Laesser, Roger Lehmann, Christian Lovis, Oriol Manuel, Hans-Peter Marti, Pierre Yves Martin,

Pascal Meylan, (Head, Biological samples management group), Paul Mohacsi, Isabelle Morard, Philippe Morel, Ulrike Mueller, Nicolas J Mueller (Chairman Scientific Committee), Helen Mueller-McKenna, Thomas Müller, Beat Müllhaupt, David Nadal, Gayathri Nair, Manuel Pascual (Executive office), Jakob Passweg, Chantal Piot Ziegler, Juliane Rick, Eddy Roosnek, Anne Rosselet, Silvia Rothlin, Frank Ruschitzka, Urs Schanz, Stefan Schaub, Christian Seiler, Nasser Semmo, Susanne Stampf, Jürg Steiger (Head, Executive Office), Christian Toso, Dimitri Tsinalis, Christian Van Delden (Executive office), Jean-Pierre Venetz, Jean Villard, Madeleine Wick (STCS coordinator), Markus Wilhelm, Patrick Yerly.

**Key points:** (40) 39

Donor polymorphisms in *PTX3* were previously associated with susceptibility to invasive aspergillosis in hematopoietic stem cell transplant recipients. Here, we show that *PTX3* polymorphisms also increase the risk of mold colonization and infection when detected among solid organ transplant recipients.

**Abstract**

Donor *PTX3* polymorphisms were shown to influence the risk of invasive aspergillosis among hematopoietic stem cell transplant recipients. Here, we show that *PTX3* polymorphisms are independent risk factors for invasive mold infection among 1101 solid organ transplant recipients, thereby strengthening their role in mold infection pathogenesis and patient's risk stratification.

## Introduction

Invasive mold infections (IMI) represent an important cause of morbidity and mortality in transplant recipients [1, 2]. While specific risk factors have been identified in both hematopoietic stem-cell (HSCT) and solid organ transplant (SOT) recipients, such as patient age, co-morbidities, conditioning regiments, cytomegalovirus (CMV) infection, renal failure, reoperation and level of immunosuppression [1, 3], it is still difficult to accurately predict which patients will develop this complication [4].

An increasing number of studies are highlighting a role for genetic polymorphisms in susceptibility to invasive fungal infections [4]. So far, due to numerous limitations, existing data have not supported the use of such polymorphisms for individual risk stratification in the clinical practice. A major limiting factor is the inability to replicate the association, especially when studies are performed in populations that differ in terms of baseline characteristics or immunosuppressive regimen [4].

Pentraxin 3 (PTX3) is a soluble pattern recognition receptor (PRR) produced by neutrophils, dendritic cells, macrophages and epithelial cells that was shown to exert important antifungal protection [5]. Polymorphisms in *PTX3* gene in the donor have been recently associated with increased susceptibility to invasive aspergillosis (IA) among HSCT recipients [6]. Here, we show that polymorphisms in *PTX3* also increase susceptibility to IMI among SOT recipients. This observation strengthens the role of these polymorphisms in immune defenses against fungal pathogen and its potential use as a predictor for infection in the clinical practice.

## Materials and Methods

**Patients and study design.** The Swiss Transplant Cohort Study (STCS) is a large national cohort of SOT followed at 6 Swiss university centers [7, 8]. For the present study, SOT recipients enrolled prospectively from May 2008 to December 2011 who provided an informed consent for participation to genetic studies within the STCS were included. The protocol was approved by the Ethics committees of all participating centers. Patient's data were collected at enrollment, at 6 months and every 12 months after transplant on standardized case report forms. Mold colonization and proven or probable IMI were diagnosed according to MSG/EORTC definitions as previously described [8, 9]. Only patients that underwent their first organ transplantation were included. Patients who had mold infection before receiving transplant (N=5) were disqualified from the study.

**Genotyping.** Genomic DNA was extracted from patient's blood using the Gentra Puregene Blood Kit (Qiagen, Hombrechtikon, Switzerland). Three single nucleotide polymorphisms (SNPs) in *PTX3*, including *rs2305619* (+281A/G), *rs1840680* (+1449A/G) and *rs3816527* (+734A/C [D48A]) were selected based on previous observations [6]. The *rs2305619* and *rs1840680* SNPs were genotyped as a part of a customized GoldenGate Genotyping Assay® (BeadXpress, Veracode® technology, Illumina®). The *rs3816527* SNP was genotyped using Competitive Allele-Specific PCR (KASP™) system (LGC Genomics, UK).

**Statistical analysis.** Statistical analysis was carried out by using Stata 13.1® software (StataCorp LP, College Station, Texas, USA). The association between mold colonization and IMI by *PTX3* variants were assessed by 36-months cumulative incident curves (with censoring at lost to follow-up or death date) and by using the log-rank test [8]. Furthermore, stepwise Cox

regression model were used to estimate risk factors that were independently associated with the phenotypes. Based on previous studies [6], the associations were tested for the recessive mode of inheritance. The linkage disequilibrium (LD) and Hardy-Weinberg equilibrium (HWE) tests were assessed by using the pwld and hwe softwares implemented in Stata. Since *rs2305619* and rs1840680 were in almost perfect LD ($R^2$=0.99), analyses are shown only for *rs2305619*. *PTX3* haplotypes were generated using PHASE version 2.1 (University of Washington, Seattle, WA, USA). Power calculation was performed by using powerSurvEpi package 0.0.6 in R (R Core Team, Vienna, Austria).

**Results**

The study included 1101 Caucasian patients who received a SOT form kidney (N=670), liver (N=190), lung (N=102), heart (N=79), islet/pancreas (N=15), or combined organ transplants (N=45). Among those, 45 were diagnosed with mold colonization (21 lung, 11 kidney, 7 heart, 4 liver and 2 mixed organ recipients, supplementary **Table S1**) and 26 developed IMI (11 kidney, 5 lung, 5 heart, 3 liver and 2 mixed organ recipients). IMI was mainly caused by *Aspergillus* species (N=21 [81%]) or due to other fungi (*Fusarium* [N=2], *Alternaria* [N=1], *Zygomycetes* [N=1], and mixed pathogens [*Zygomycetes* and *Fusarium*, N=1]). The PTX3 rs2305619 and rs3816527 SNPs had minor allele frequencies (MAF) of 0.48 and 0.42, respectively, and both were at HWE (supplementary **Tables S2** and **S3**).

To assess the risk of mold colonization and IMI according to *PTX3* polymorphisms, we first analyzed the 36-month cumulative incidence of colonization and infection after transplantation in patients carrying the different genotypes/diplotypes. These incidences were significantly higher among patients carrying the *rs3816527* AA genotype compared to those carrying the CC or CA genotypes (colonization 0.0621 versus 0.0320, log rank test P=0.03; IMI 0.0394 versus 0.0166,

P=0.03; supplementary **Figure 1** A and B). Similar though less significant associations were observed when comparing patients carrying the *rs2305619* GG genotype to those carrying the AA or AG genotypes (colonization P=0.09 and IMI P=0.08; supplementary **Figure S1** A and B) or patients carrying the h2/h2 diplotype (combining the minor alleles of both *rs2305619* and *rs3816527*) to the other diplotypes (colonization P=0.08 and IMI P=0.07; supplementary **Figure S2** A and B).

To determine whether the polymorphisms were independent risk factors for the fungal phenotypes, we used multivariate stepwise Cox regression models adjusted for all relevant covariates. The associations between *rs3816527* and fungal colonization or infection were even more significant after adjustment for age and sex, CMV infection or disease, CMV sero-status, immunosuppressive drugs, acute/chronic rejection and/or type of transplanted organ (colonization HR=2.57, 95%CI 1.42-4.65, P=0.002 and IMI HR=3.18, 95%CI 1.45-6.98, P=0.004; supplementary **Table S4**). Significant associations were also observed for *rs2305619* (colonization HR=1.97, 95%CI 1.06-3.58, P=0.03 and IMI HR=2.29, 95%CI 1.04-5.03, P=0.04; supplementary **Table S5**) and the h2/h2 diplotype (colonization HR=2.06, 95%CI 1.12-3.79, P=0.02 and IMI HR=2.43, 95%CI 1.11-5.34, P=0.03; supplementary **Table S6**).

Since the occurrence of colonization and IMI was significantly higher among thoracic transplant recipients, we performed a supplementary analysis that was limited to this group of patients. The associations between *PTX3* polymorphisms and fungal colonization and infection were even stronger, especially for *rs3816527* (log-rank test, colonization P=0.002 and IMI P=0.006; **Figure 1** C and D; multivariate model, colonization HR=3.64, 95%CI 1.67-7.92, P=0.001, IMI HR=7.33, 95%CI 1.86-28.9, P=0.004; supplementary **Table S4**). Significant associations were also observed for *rs2305619* (colonization HR=2.74, 95%CI 1.26-5.96, P=0.01 and IMI HR=5.30, 95%CI 1.41-19.9, P=0.01; supplementary **Figure S1** C and D, **Table S5**) and for the h2/h2

diplotype (colonization HR=3.06, 95%CI 1.39-6.75, P=0.006 and IMI HR=5.68, 95%CI 1.56-20.7, P=0.009; **Figure S2** C and D, supplementary **Table S6**).

## Discussion

A number of studies have reported associations between polymorphisms in host immune genes and susceptibility to fungal infections in immunocompromised patients [4]. Many were limited by several factors, including a lack of replication and/or the absence of functional evidence supporting the association [4]. Polymorphisms in *PTX3* in the donor have been recently associated with an increased risk for the development of IA among HSCT recipients [6]. We report for the first time an association between such polymorphisms and susceptibility to mold colonization and IMI among SOT recipients. Thus, the validation in a different patient population suggests that *PTX3* polymorphisms may represent a valuable marker of increased risk for fungal infection.

The two *PTX3* polymorphisms have a relatively high frequency (MAF ~0.4) [6] compared to polymorphisms previously associated with IA, such as *rs4986790*/1 in Toll-like receptor 4 (*TLR4,* MAF ~0.05) [10] and *rs16910526* in Dectin-1 (MAF 0.08) [11]. Rare SNPs require very large cohorts for replication, while frequent ones can be replicated in smaller datasets. The association between *PTX3* polymorphisms was initially replicated in two independent cohorts of HSCT recipients from different centers [6]. In the present study, we provide further validation in a population whose clinical condition and type of immunosuppressive regimen is different. Thus, these polymorphisms may be more universal than other population-specific risk factors.

There is strong evidence for the involvement of PTX3 in the immune responses against *Aspergillus* spp [5]. PTX3 can directly bind *Aspergillus* conidia by recognizing galactomannan,

thereby acting as an opsonizing factor for complement activation and subsequent phagocytosis [12]. PTX3 can also interact with PRRs such as Dectin-1 or TLR4 to increase fungal patterns recognition and thus promote adaptive immune responses [12, 13]. *In vivo*, *PTX3* knockout mice have been shown to be highly susceptible to IA due to defective recognition of *A. fumigatus* by macrophages and their phagocytic activities as well as imbalanced adaptive responses to this fungus [5].

In addition, there is evidence that polymorphisms in *PTX3* are associated with reduced immunity against fungal pathogens. The missense +734A *rs3816527* allele was suggested to influence *PTX3* mRNA stability, thereby affecting its secondary structure and leading to its lower expression. *PTX3* variants were also associated with a reduced PTX3 production in neutrophils with defective phagocytic activities and reduced *Aspergillus* clearance [6]. Of note, neutrophils originate from the donor stem cells in HSCT and from the recipient in SOT. Consistently, polymorphisms associated with IA in the previous study of HSCT patients were issued from the donor [6], while those associated with IMI in the present study of SOT are from the recipient. Since most patients who develop infection are previously colonized, it is difficult to determine whether the polymorphisms influence colonization alone, or colonization and infection.

Our findings indicate that specific genetic polymorphisms in *PTX3* are responsible for susceptibility to IMI in SOT recipients. This study reinforces the validity of *PTX3* polymorphisms as an important risk factor for mold infection risk stratification in immunocompromised patients.

**Funding**

P.-Y.B. was supported by the Swiss National Foundation (Grand number 324730-144054), the Leenaards Foundation, the Santos-Suarez Foundation, and the Loterie Romande. P.-Y.B. is recipient of Mérieux Research Grant (MRG) and is a participant in the European Union's Seventh Framework Program (FP7/2007-2013) under grant agreement n° HEALTH-2010-260338 (ALLFUN). Furthermore, this project was supported by STCS project No 12, a grant from the Emma Muschamp Foundation and the FLTO Foundation (Fondation Lausannoise pour la transplantation d'organes). The Swiss Transplant Cohort Study is funded by a grant from the Swiss National Research Foundation (Grant number 33CS30_148512).

**Conflict of Interest**

The authors have no conflicting financial interests.

**Acknowledgement**

This study was conducted on behalf of all members of the Swiss Transplant Cohort Study. We thank all patients who participate in the Swiss Transplant Cohort Study, the study nurses, the central and local data managers and all the investigators involved in the STCS.

References


1. Morgan J, Wannemuehler KA, Marr KA, et al. Incidence of invasive aspergillosis following hematopoietic stem cell and solid organ transplantation: interim results of a prospective multicenter surveillance program. Medical mycology **2005**; 43 Suppl 1: S49-58.
2. Pappas PG, Alexander BD, Andes DR, et al. Invasive fungal infections among organ transplant recipients: results of the Transplant-Associated Infection Surveillance Network (TRANSNET). Clinical infectious diseases : an official publication of the Infectious Diseases Society of America **2010**; 50(8): 1101-11.
3. Neofytos D, Treadway S, Ostrander D, et al. Epidemiology, outcomes, and mortality predictors of invasive mold infections among transplant recipients: a 10-year, single-center experience. Transplant infectious disease : an official journal of the Transplantation Society **2013**; 15(3): 233-42.
4. Wojtowicz A, Bochud PY. Host genetics of invasive Aspergillus and Candida infections. Seminars in immunopathology **2014**.
5. Garlanda C, Hirsch E, Bozza S, et al. Non-redundant role of the long pentraxin PTX3 in anti-fungal innate immune response. Nature **2002**; 420(6912): 182-6.
6. Cunha C, Aversa F, Lacerda JF, et al. Genetic PTX3 deficiency and aspergillosis in stem-cell transplantation. The New England journal of medicine **2014**; 370(5): 421-32.
7. Koller MT, van Delden C, Muller NJ, et al. Design and methodology of the Swiss Transplant Cohort Study (STCS): a comprehensive prospective nationwide long-term follow-up cohort. European journal of epidemiology **2013**; 28(4): 347-55.
8. Wojtowicz A, Gresnigt MS, Lecompte T, et al. IL1B and DEFB1 Polymorphisms Increase Susceptibility to Invasive Mold Infection After Solid Organ Transplantation. The Journal of infectious diseases **2014**.
9. De Pauw B, Walsh TJ, Donnelly JP, et al. Revised definitions of invasive fungal disease from the European Organization for Research and Treatment of Cancer/Invasive Fungal Infections Cooperative Group and the National Institute of Allergy and Infectious Diseases Mycoses Study Group (EORTC/MSG) Consensus Group. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America **2008**; 46(12): 1813-21.
10. Bochud PY, Chien JW, Marr KA, et al. Toll-like receptor 4 polymorphisms and aspergillosis in stem-cell transplantation. The New England journal of medicine **2008**; 359(17): 1766-77.
11. Cunha C, Di Ianni M, Bozza S, et al. Dectin-1 Y238X polymorphism associates with susceptibility to invasive aspergillosis in hematopoietic transplantation through impairment of both recipient- and donor-dependent mechanisms of antifungal immunity. Blood **2010**; 116(24): 5394-402.
12. Salvatori G, Campo S. Current understanding of PTX3 protective activity on Aspergillus fumigatus infection. Medical mycology **2012**; 50(3): 225-33.
13. Bozza S, Campo S, Arseni B, et al. PTX3 binds MD-2 and promotes TRIF-dependent immune protection in aspergillosis. J Immunol **2014**; 193(5): 2340-8.

**Figure legend**

**Figure 1. Cumulative incidence of mold colonization and invasive mold infection according to *PTX3 rs3816527* SNP in all (panel A and B) and thoracic (panel C and D) solid organ transplant recipients.** Patients who were colonized or infected with mold before transplantation were excluded from the analyses. P values were calculated by log-rank test, recessive mode (patients homozygous for the rare alleles are compared to the other).