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*Pseudomonas syringae* pv. *actinidiae* isolated from *Actinidia chinensis* var. *deliciosa* in northern Italy: genetic diversity and virulence

Simona Prencipe¹, Maria Lodovica Gullino¹, Davide Spadaro¹,²*

¹ DISAFA – Dipartimento di Scienze Agrarie, Forestali ed Alimentari, Università degli Studi di Torino, Largo P. Braccini 2, 10095 Grugliasco (TO), Italy.
² Centro di Competenza per l’Innovazione in campo agro-ambientale (AGROINNOVA), Università degli Studi di Torino, Largo P. Braccini 2, 10095 Grugliasco (TO), Italy.

Abstract

Bacterial canker of kiwifruit, caused by *Pseudomonas syringae* pv. *actinidiae*, is responsible for significant economic losses, both in yield and quality. A collection of *P.s.* pv. *actinidiae* isolated in Northern and Central Italy, during the first severe outbreak (2008-2010) and a few years afterwards (2014), when the pathogen became endemic and established, was gathered. The genetic diversity was evaluated with rep-PCR, RAPD-PCR, and MLSA of six housekeeping and effector genes. On the same strains, the virulence was evaluated *in vitro* and *in vivo*, showing a higher disease index for the strains isolated in 2014, compared with the strains of 2010. The molecular fingerprinting, obtained by rep and RAPD analysis, revealed a high level of variability in the population of strains of *P.s.* pv. *actinidiae* from Northern Italy. All the parameters considered – *Na*, *Ne*, *H*, *I*, polymorphic loci, and AMOVA – showed a higher genetic diversity within the population of Northern Italy isolated in 2014, compared to the older population. The study of the genetic diversity and virulence permitted to show an increase of virulence and genetic diversity of the strains. The fast and dramatic epidemics caused by *P. s.* pv. *actinidiae* could be an interesting model to study the changes in the genetic diversity and virulence of a bacterial pathogen.

Keywords: bacterial canker, kiwifruit, pathogenicity, MLSA, rep-PRC, RAPD-PCR

*e-mail: davide.spadaro@unito.it*
**Introduction**

The causal agent of bacterial canker on kiwifruit, *Pseudomonas syringae pv. actinidiae*, was first isolated and described in Japan in 1984 (Takikawa et al., 1989). In Italy, the first severe outbreak occurred in 2008 (Balestra et al., 2009). As reported by the European and Mediterranean Plant Protection Organization (EPPO), the disease spread worldwide reaching France, Spain, Portugal, Switzerland, New Zealand, Chile, Turkey and South Korea (EPPO, 2012). Bacterial canker causes significant economic losses, both in yield at harvest and in reducing the postharvest quality, shelf life, and susceptibility to postharvest rots (Prencipe et al., 2016). Italy produces more kiwifruit than any other country, apart from China, with 384,000 tons and 24,800 cultivated hectares (FAOSTAT, 2014). Currently, there are not chemical or biological products on the market able to completely control *P. s. pv. actinidiae* on kiwifruit, but in the framework of integrated control strategies, copper compounds alternated with resistance inducers could be used to develop new strategies to reduce the disease development and spread (Monchiero et al., 2015).

Different populations of *P. s. pv. actinidiae* have been described: Psa 1 or biovar 1, with the strains responsible for the first occurrence of kiwifruit bacterial disease in Japan and Italy, producing phaseolotoxin; Psa 2 or biovar 2, including the Korean population of Psa isolated in 1990, producing coronatine; Psa 3 or biovar 3, grouped strains isolated in Europe, China, Chile and New Zealand responsible for the current pandemic disease, which do not produce phaseolotoxin and coronatine; Psa 4 or biovar 4 isolated in New Zealand, Australia and France, which do not produce phaseolotoxin and coronatine (Cunty et al., 2015). During 2010-2014, around 1,922 hectares of kiwifruit were removed in the different Italian regions, due to the attack of the highly virulent biovar 3.

The characterization of the population structure of the pathogen has been performed using biological characteristics, as pathogenicity on *Actinidia* spp., and several molecular approaches, including repetitive sequence PCR fingerprinting, with BOX and ERIC primers and multi-locus Sequence Analysis (MLSA) of housekeeping genes (McCann et al., 2013; Ferrante and Scortichini, 2015). Rep-PCR has been the most commonly used molecular method to analyse the diversity of bacteria at subspecific level (Louws et al. 1994; Versalovic et al. 1994). On *P. s. pv. actinidiae* MLSA of housekeeping genes revealed more variability than rep-PCR (Vanneste, 2013). Rep-PCR and MLSA analyses are considered a good tool for biovar differentiation, but they are not able to show the variability among strains of the same biovar (Scortichini et al., 2012). Random amplified polymorphic DNA (RAPD) was more resolute in discriminating intraspecific variability in bacterial pathogens (Hartung et al., 1993), also for *P. s. pv. actinidiae*, as reported by Mazzaglia et al. (2011).

Further information about genetic variability could be acquired through the analysis of the sequences of effector genes involved in the Type III Secretion System (T3SS). The pathogenicity of
many Gram-negative bacteria, including *P.s pv. actinidiae*, is linked to this system, that plays a crucial role in the host-pathogen interaction. Genes encoding for this secretion system are called *hrp/hrc* (hypersensitive response and pathogenicity, *hrp* conserved). T3SS is responsible to translocate Avr and Hop (Hrp-dependent outer protein) effector proteins into host cells (Buttner *et al.*, 2009).

The study of intra-pathovar diversity could help to understand the evolutionary process, at subspecies level, that controls plant pathogen population, and to make inferences about adaptation to the host and the environment (Burdon, 1993). After the first occurrence in 2010, few isolates of the pathogen from Northern Italy have been investigated for their intra-pathovar variability (Marcelletti and Scortichini, 2011).

The aim of this research was to investigate the genetic diversity and virulence variations of the isolates of *P.s pv. actinidiae* in the same geographical area at the time of the first epidemic outbreak and four years afterwards, when the pathogen became endemic and established. The identification was verified through a multidisciplinary approach, including molecular and host range test. The intra-pathovar variability of *P.s pv. actinidiae* was investigated in Northern Italy in 2010 and in 2014, with molecular typing using rep-PCR and RAPD-PCR. The pathogenicity and the degree of virulence of the isolates were also evaluated. A MLSA of three effector genes *hopA1*, *avrD1* and *hrpK1*, encoding three different T3SS secreted proteins, were chosen to investigate the possible presence of polymorphic sites related to various functions of the T3SS.

**Materials and methods**

**Microorganisms**

Forty strains of *P.s pv. actinidiae* were used throughout this study. Thirty-three strains were obtained from *Actinidia chinensis* var. *deliciosa* ‘Hayward’ Liang and Ferguson cultivated in four areas of Northern Italy (Piedmont region: provinces of Vercelli (VC), Cuneo (CN), Torino (TO) and Asti (AT)), during two years: twelve were isolated in 2010 and twenty-one in 2014. Five strains from other Italian regions were also included: one isolated from *A. chinensis* var. *deliciosa* ‘Hayward’ and one from *A. chinensis* ‘Hort16A’ (the reference strain of biovar 3 CFBP7286) in Latina province (2008), one from *A. chinensis* ‘Hort16A’ in Rome province (2008), and two from *A. chinensis* ‘Jin Tao’ and *A. chinensis* var. *deliciosa* ‘Hayward’ in Viterbo province (2010). Two reference strains belonging to biovars 1 and 2 were also included: one isolated from Japan in 1984, and one from Korea (Table 1).
**Isolation and pathovar identification**

*Isolation and identification.* Kiwifruit leaves with symptoms of bacterial canker, i.e. necrotic spots, were washed in sterile water and macerated in Luria Bertani (LB) broth (Merck). The resulting medium was spread on Pseudomonas Selective Agar plates with CFC supplement (Merck). After 48 hours incubation at 27°C, single Psa-like colonies were transferred to LB broth and grown on a rotary shaker (120 rpm) at 27°C for 24 hours. DNA was extracted from 100 µl liquid medium using Instagene Matrix (Biorad), according to manufacturer’s instructions. PCR was carried out in a total volume of 25 µl containing: 2.5 µl Buffer 10X, 0.5 µl MgCl₂, 0.75 µl dNTPs (10 mM), 1 µl each primer (10 mM), 0.2 µl Taq DNA polymerase (Qiagen), and 40 ng template DNA.

*P. s. pv. actinidiae* strains were previously identified, through PCR technique described by Rees-George *et al.* (2010) with primers PsaF1, PsaR2 and PsaF3 and PsaR4 and a further amplification of the 16S rRNA region using primers 16F27 (5′-AGAGTTTGATCMTGGCTCAG-3′) and 16R1525 (5′-AAGGAGGTGATCCAGCGCA-3′). The obtained amplicons were run on a 1% agarose gel and compared with positive controls. The sequences obtained were compared with those deposited in GenBank using BLAST programme. To validate the pathovar assignation, the analysis of rep-PCR fingerprinting using BOX and REP primer set following Versalovic *et al.* (1994) and Louws *et al.* (1994) and the duplex-PCR technique following Gallelli *et al.* (2011), were applied.

*Host range test.* A pathogenicity test was performed on lemon (*Citrus lemon*) to distinguish between the pathovars *syringae* and *actinidiae* of *P. syringae* (Andolfi *et al.*, 2014). Fruits were disinfected with sodium hypochlorite (1%) and rinsed with sterile distilled water. Ten µL of the bacterial suspension was inoculated through sterile needle onto the wound. Inoculations with sterile distilled water was used as negative controls. Fruits were kept at room temperature (20-23°C) and pathogenicity was assessed 7 days after inoculation, according to Scortichini *et al.* (2003). The test was carried out on two fruit per isolates and the result has occurred from ten sites each.

**Genetic diversity**

All the strains were studied by Random amplified polymorphic DNA PCR (RAPD-PCR) and repetitive intergenic DNA sequence PCR (rep-PCR), in order to analyse the genetic diversity. Furthermore, we investigated six genes through Multilocus Sequence Analysis (MLSA).

*Molecular fingerprinting using RAPD and rep-PCR.* Fingerprinting analysis on the isolates of *P.s. pv. actinidiae* was performed by RAPD and rep-PCR using the primers listed in Table S1. RAPD-PCR was carried out in a total volume of 25 µl containing: 2.5 µl Buffer 10 X, 0.5 µl MgCl₂, 0.75 µl dNTPs (10 mM), 1 µl each primer (10 mM), 0.2 µl of Taq DNA polymerase (Qiagen) and 20 ng
template DNA. PCR was performed with initial denaturation at 94°C for 1 min, followed by 40 cycles of 1 min at 94°C, 1 min at 36°C for annealing, and 2 min at 72°C for 1 min, with 7 min final extension at 72°C. Rep-PCR with primer GTG₅ was performed following protocols by Versalovic et al. (1994).

Fifteen µl of amplification products were separated by gel electrophoresis using TBE buffer with 2% agarose and 10 µl SYBRSafe® (Invitrogen) at 100 V/cm for 3 hours. Get Pilot 1 kb Plus Ladder (100-10000 bp, Qiagen) was used as molecular marker. Gel profiles were visualized under UV transilluminator using Quantity One program (BioRad Labs). Gel profiles were analysed to build up a concatenated matrix. Cluster analysis was performed on the combined matrix of the fingerprinting obtained from all the molecular markers. A dendrogram of similarity was obtained using an unweight pair group method with arithmetic average (UPGMA) algorithm and Dice similarity index (DC) with Past version 6.5. Branch robustness was evaluated using 1000 bootstrap replicates. Nei’s genetic diversity, effective number of alleles, percentage of polymorphic loci, and Shannon information index were also calculated using GenAlex version 6.5 and PopGene version 1.32. The genetic variation among the population was also evaluated by the analysis of molecular variance (AMOVA) using GenAlex version 6.5. To analyse the relationships between results obtained from fingerprinting analysis, a principal coordinates analysis (PCoA) was also performed using Past version 6.5.

Multilocus sequence analysis (MLSA) On the same collection of strains, a MLSA was performed using the primers listed in Table S2. Effector genes, avrD1, hopA1 and hrpK1 were chosen to allow comparison of data obtained in previous studies about the population of Psa (Ferrante and Scortichini, 2010; Vanneste et al., 2011; Chapman et al., 2012) and to evaluate the presence of additional polymorphic sites. The housekeeping gene cts was sequenced to confirm the haplotype of biovar 3. Furthermore, two housekeeping genes pgi and gapA genes were sequenced, following Sarkar and Guttman (2004).

For the effector genes, the PCR programs were according to Ferrante et al. (2009) and Ferrante and Scortichini (2010), but for hrpK1 gene, the annealing temperature was modified to 67°C. For housekeeping genes, PCR protocols were retrieved from Sarkar and Guttman (2004). PCR products were separated by gel electrophoresis using TAE buffer with 1% agarose and 1.5 µl SYBRSafe® (Invitrogen) at 85 V/cm for 40 minutes. Get Pilot Wide Range Ladder (200-4500 bp, Qiagen) and 100 bp Ladder (100-600 bp, Qiagen) were used to compare the expected size of bands. Bands were visualized under UV transilluminator using Quantity One program (BioRad Labs). The PCR products were purified using QIAquick® PCR purification Kit (Qiagen) and sequenced in both directions by Macrogen Inc. (The Netherlands).
Forward and reverse sequences for each gene were used to create a consensus sequence, using DNA Baser programme (Heracle Biosoft S.R.L., Romania), for multi-alignment using CLUSTALW through MEGA version 6. After cutting the trimmed regions and manual correction, dataset of 380, 887, 550, 518, 681 and 571 bp were obtained, respectively, for the genes hopA1, hrpK1 avrD1, cts, gapA and pgi.

Single nucleotide polymorphisms (SNPs) were assessed on the aligned sequences, and one strain for each haplotype and gene was deposited in GenBank.

Phylogenetic and molecular evolutionary analysis were generated by Neighbor-Joining algorithm using MEGA version 6, branch robustness was evaluated using 1000 bootstrap replicates. GenBank sequences from the National Center for Biotechnology Information (NCBI) were used as references.

Pathogenicity tests

The isolates from Northern Italy were tested for their pathogenicity through in vitro and in vivo assays and compared to those obtained for reference strains of biovars 1, 2 and 3. Before the tests, the strains were inoculated in healthy plants and reisolated from necrotic spots to avoid the virulence loss. Statistical analyses on the pathogenicity trials were realized by using IBM SPSS statistics version 21 for variance analysis (one-way analysis of variance) using Duncan test $P \leq 0.05$. To assess the reliability of the in vitro pathogenicity assay, the data were compared with the results of the in vivo trials and analysed with Student’s t-test at 95% confidence level and correlation coefficient ($R^2$). A disease index scale for the in vitro and in vivo tests is reported in Figure 1. The symptoms observed (leaf spotting, necrotic area and water-soaked area) for the isolates from Northern Italy were those typical of biovar 3.

In vitro pathogenicity assay

Bacterial suspension was prepared after 24 hours growth in LB broth at 27°C on a rotary shaker (120 rpm). For in vitro assay, leaf discs (2 cm diameter) were prepared from fourteen days-old leaves of A. chinensis var. deliciosa ‘Hayward’ (1-year old plant) and were placed on 10 ml sterile water in not sealed three sector Petri dishes. The leaf disks were inoculated with bacterial suspension ($10^8$ CFU/ml) at three equidistant points (three drops of 30 µl each per leaf disc). Control leaves were prepared similarly with sterile deionized water.

Disease index (0-5) was assigned to the symptoms observed on the disks kept at 20°C in the dark for 12 days, corresponding to: 0=healthy leaves; 1= small necrotic spots or streaks (1-4% infected area); 2= necrotic spots or larger veins (5-10%); 3= spots or converging necrotic areas (11-30%); 4= converging necrotic areas (≥50%); 5= completely necrotic leaves. The experiment was carried out
in three replicates for each strain (9 leaf discs per strain were scored). The pathogenicity assay was performed twice.

**In vivo pathogenicity assay** The assay was performed in greenhouse on 1 year-old plants of *A. chinensis* var. *deliciosa* ‘Hayward’ inoculated by directly spraying a bacterial suspension (10^8 CFU/ml) of each strain of *P.s. pv. actinidiae* onto kiwifruit leaves. Potted plants (30–40 cm high) were inoculated on 25 March, 2014 and 24 September 2014 and kept in the greenhouse at approximately 20 °C, RH 70-80% with natural daylight. After pathogen inoculation in the evening, plants were covered with plastic film for 72 hours. Control plants were prepared similarly but inoculated with sterile deionized water.

A disease index (D.I.), ranging from 0 to 5, was assigned, by observing 6 leaves per plant,12 days after inoculation: 0= no symptoms; 1= 1-4% infected area; 2= 5-10% infected; 3= 11-30% infected area; 4= ≥50% infected area; 5= completely necrotic. The classes of infection, used to describe the severity of symptoms, were four: not pathogenic strain (NP; D.I. 0.0- 0.4), low virulent strain (LV; D.I. 0.5-1.9); moderate virulent strain (MV; D.I. 2.0-2.9); virulent strain (V; D.I. 3.0-3.9); highly virulent strain (HV; D.I. 4.0-5.0). The experiment was performed with three replicates for each strain (18 leaves per strain). The pathogenicity assay was carried out twice.

**Results**

**Pathogen identification**

Thirty-three bacterial isolates from symptomatic leaves of kiwifruit cultivated in Northern Italy confirmed to belong to *P.s. pv. actinidiae* by amplification of two expected bands of 280 and175 bp, after PCR reaction with two primer pairs of Rees-George *et al.* (2010) and sequencing of 16S region (two sequences were deposited in GenBank with accession numbers KP794939 and KP794940). The pathovar assignation was validated through duplex PCR with the amplification of two PCR product for all strains and, typical fingerprinting profile using rep-PCR with ERIC primer (Fig. 2). By considering the host range test, the populations did not induce any disease symptom on the inoculated lemon fruits tested. Control fruits did not show any disease symptoms.

**Molecular characterization**

The molecular fingerprinting of strains of *P.s. pv. actinidiae* generated a band profile reproducible in replicated experiment. Rep-PCR through ERIC primer produced a profile showing an identical molecular pattern for all the Italian strains analysed (Psa 3) and allowed the differentiation of the
Korean strain –K2 (Psa 2) and the Japanese KW11 (Psa 1). UPGMA dendrogram divided the two
biovars from biovar 3 (Fig. 2). Rep-PCR through GTG\textsubscript{5} primer revealed also variability within
biovar 3, as shown in supplementary Figure S1.

One example of RAPD-PCR using OPB13 primer is reported in Fig. 3. The concatenated matrix of
the fingerprinting of the strains of \textit{P.s. pv. actinidiae} was used to generate a dataset, and a
dendrogram of similarity (Fig. 4) was obtained by using Dice coefficient and UPGMA clustering
algorithm. The co-phenetic correlation coefficient obtained was 0.9474, well supporting the
dendrogram resulting from matrix used. The dendrogram showed a cluster of the strains of \textit{P.s. pv.
actinidiae} belonging to biovar 3, which was significantly separated from the two reference strains
of biovar 1 and biovar 2 (Fig. 4). The Japanese strain (biovar 1) and the Korean one (biovar 2) were
separated at a similarity level of 0.70 supported by a high bootstrap value (99) and separated from
Italian strains at similarity level 0.54 (bootstrap value 83). Among the Italian strains, all belonging
to the biovar 3, two main clusters, with a Dice coefficient (DC) of 0.46, supported by a high
bootstrap value (100), were generated: Cluster I included all the strains from Northern Italy, and
Cluster II included all the strains from Central Italy. Furthermore, the strains from Northern Italy
could be divided in two sub-clusters well supported by bootstrap values, according to the year of
isolation: sub-cluster Ia (bootstrap: 89), with all the strains isolated in 2014, and sub-cluster Ib
(bootstrap: 98), with all the strains isolated in 2010.

The high bootstrap value and the length of the branches, measured with the Dice coefficient (DC),
showed a great variability of the strains isolated in 2014. Sub-cluster Ia showed a DC ranging from
0.68 (between strains RC1 and RC2/RC4) to 0.90 (between strains RL1 and RL2), with a mean DC
in the sub-cluster of 0.79.

Within sub-cluster Ib, the strains of 2010 showed on average a higher similarity compared with the
strains of 2014. The DC ranged from 0.75 (between 38/10 and 36/10c1) to 0.92 (between 41/11 and
39/10), with a mean DC in the sub-cluster of 0.89.

**Genetic diversity and principal coordinates analysis**

Genetic diversity parameters of the three populations of \textit{P.s. pv. actinidiae} are shown in Table 2.
The highest diversity was observed for the population of \textit{P.s. pv. actinidiae} isolated from Northern
Italy in 2014, with the highest number of alleles (Ne=1.38), gene diversity (H=0.23), and Shannon
index (I=0.35), and 71.79% of polymorphic loci.

The genetic distance (Table S3) was 0.207 between the populations of Northern Italy of 2014 and
2010, 0.278 between the population of Northern Italy of 2014 and the Central Italy population, and
0.317 between the population of Northern Italy of 2010 and the Central Italy population. A high
variability of the three populations of \textit{P.s. pv. actinidiae} was shown by the value of the total genetic
diversity (\(H_T = 0.321\)), while \(H_S\) within the population was 0.199. The \(G_{ST}\) value (35%) showed the proportion of genetic diversity linked to the number of individuals of the population. The AMOVA was used to analyse the population structure (Table S4), showing that 58% of the variation was within the population, while 42% was among the populations.

The scatter diagram of the principal coordinate analysis (Fig. 5) showed three distinct groups, two for the populations of \(P. s. pv. actinidiae\) from Northern Italy and one heterogeneous group including the strains from Central Italy and the strains of biovar 1 and 2. The Japanese and the Korean strain showed to be more clearly separated in the dendrogram (Fig. 4). These strains were grouped with strains of Central Italy because the PCoA analysis visualization reduces the dimension of complex data matrix into a bidimensional space. The first coordinate explained 25.67% of the total variability (eigenvalue 1.07), while the second one explained 24.83% (eigenvalue 0.87), therefore the two coordinates could explain over half of the variance.

**Multilocus sequence analysis (MLSA)**

A DNA sequence dataset, with partial sequences of \(cts\), \(avrD1\), \(hopA1\) and \(hrpK1\) was built. Phylogenetic analysis was performed for each gene sequence dataset. The partial gene sequences of \(pgi\) and \(gapA\) were 100% identical for all the isolates considered (data not shown).

Figures S2a and S2b show two major clades for \(cts\) and \(avrD1\) genes. For \(cts\) gene, two clades are shown (Figure S2a; bootstrap value: 88%): clade I, including all Italian isolates, with two cytosines in position 251 and 431, and a clade II, including the Japanese and Korean isolates, with a thymine in position 251 and an adenine in position 431. The same clustering, supported by 64% bootstrap value, is shown for \(avrD1\) gene (Figure S2b), with all Italian isolates with two adenines in position 43 and 528, and the Japanese and Korean isolates, with a cytosine in position 43 and a guanine in position 528.

Figures S3a and S3b show the Neighbour-Joining analysis of \(hrpK1\) and \(hopA1\) genes. Sequences alignment showed very low sequence diversity, but six single nucleotide polymorphisms (SNPs) occurred in four strains isolated in Northern Italy in 2014: two in \(hopA1\) and four in \(hrpK1\). Among the SNPs in \(hopA1\) and \(hrpK1\), two resulted in amino acid variation, while four were silent (Table 3). Amino acid variation occurred from isoleucine (ATC) to phenylalanine (TTC) in strain PSA1 at position 107 and from serine (AGC) to threonine (ACC) at position 82 for RL5 strain. For the Japanese and Korean strains, \(hopA1\) gene was not amplified.
Pathogenicity tests

In both pathogenicity tests, one *in vitro* and another *in vivo*, the first symptoms, necrotic spots, were observed six days after inoculation of *P. s. pv. actinidia* on the leaves. Uninoculated control remained healthy.

By considering the results of the two Northern Italy populations *in vivo*, the strains of 2014 showed a higher variability in the virulence (D.I. ranging from 0.59 to 3.93), compared to the strains of 2010 (D.I. ranging from 0.71 to 3.21). The strains with the highest virulence were five isolated in 2014 (QV2; D.I.: 3.93; QV3: 3.57; QV4: 3.09; RL4: 3.93; and PSA1: 3.21), and one isolate of 2010 (41/11: 3.21). The isolates were divided in three categories according to their virulence *in vivo* (Figure S4) and the strains of 2014 confirmed on average a higher virulence: 24% were virulent (V), 48% moderately virulent (MV), and 29% low virulent (LV). The strains of 2010, divided in the same three categories, showed a different sharing: 9% virulent, 17% moderately virulent, and 75% low virulent.

The correlation coefficient ($R^2$) between the two disease indexes was 0.87, showing a high reliability of the *in vitro* test compared to the *in vivo* test. In addition, the Student’s t-test applied to both assays showed no significant differences ($P \geq 0.05$). In the *in vitro* test, the strains of *P. s. pv. actinidia* isolated in 2014 were significantly more virulent ($P \leq 0.05$), with a higher disease index (average D.I.: 1.80; Table 1), than the strains isolated in 2010 (average D.I.: 1.18). The same tendency was observed in the *in vivo* test (Table 1), where the strains of 2014 showed an average D.I. of 2.27, higher compared to the average D.I. (1.57) of the strains of 2010 ($P \leq 0.05$).

Discussion

In a collection of *P. s. pv. actinidia* strains isolated in two Italian regions, Piedmont (Northern Italy) and Latium (Central Italy), during the first severe outbreak in 2010 and after four years (2014), species, pathovar and biovar were assigned through different methods including rep-PCR using BOX and ERIC primers and duplex PCR. The molecular fingerprinting, in accordance with Ferrante and Scortichini (2010) and Mazzaglia *et al.* 2011, permitted to generate unique and repeatable genetic patterns for the strains of *P. s. pv. actinidia*, discriminating the Italian strains (biovar 3) from the Asian strains (biovars 1 and 2). The analysis on Northern Italy strains showed that the use of rep-PCR through ERIC produced the same pattern profile for all the strains of *P. s. pv. actinidia*, as already reported in the analysis of isolates from Latium and from other Italian regions (Marcelletti and Scortichini, 2011).

The molecular fingerprinting, obtained by the concatenated matrix of rep-PCR through GTG5 primer and RAPD PCR analysis, revealed a high level of variability in the population of strains of *P. s. pv. actinidia* from Northern Italy, according to Mazzaglia *et al.* (2011) for the analysis of Psa
Italian strains. These techniques enabled also to differentiate the population of Italian *P.s. pv. actinidiae* both depending on geographical origin and year of isolation. In particular, strains from Northern Italy clustered together (Cluster I), while the strains from Central Italy formed another group (Cluster II). The effect of the geographical origin on the genetic diversity of the isolates was already reported by several authors. Genetic diversity was also associated to the year of isolation and the strains were divided in two major clades. This diversity could be related to the pressure of different weather conditions at the collection site, which could influence the structure of bacterial population (Scortichini, 2005; Kolliker *et al.*, 2006).

Furthermore, compared to the initial clonal population of 2008-2010 present in Italy, *P.s. pv. actinidiae* isolated in 2014 showed a higher variability, also supported by a lower similarity index. These results were also confirmed by the results from *Na, Ne, H, I* and polymorphic loci, that attributed the highest diversity within population to the strains isolated in Northern Italy in 2014. The AMOVA also showed the highest percentage of genetic variance within the population of Northern Italy isolated in 2014. An intra-pathovar diversity was also demonstrated for other bacterial pathogens, as reported by Picard *et al.* (2008) for *Xantomonas axonopodis pv. allii* and Giovanardi *et al.* (2016) for *X. arboricala pv. pruni*.

The highest genetic identity was shown between the two populations of Northern Italy (0.813). This identity could be attributed to the limited geographic area of isolation, as reported for other *Pseudomonas* species (Sisto *et al.*, 2007).

Intra-pathovar variability was also shown for the virulence. Few papers considered the *in vivo* virulence of the strains, mostly focusing on the different biovars of *P. syringae pv. actinidiae* (Koh *et al.*, 2014). We demonstrated, through *in vivo* pathogenicity test, the occurrence of different levels of virulence in both Northern Italy populations. A higher disease index was shown for strains isolated in 2014, compared with strains of 2010. There was no correlation between the fingerprinting clusters and the virulence groups (Figure S5), as already reported for other bacterial pathovars (Picard *et al.*, 2008; Giovanardi *et al.*, 2015).

Moreover, a new *in vitro* test was developed. The time after inoculation was optimized and the highest correlation with *in vivo* test was found at 12 days after inoculation. The *in vitro* test could be used for virulence evaluation to speed up the *in vivo* virulence assessment, showing a good correlation coefficient.

A MLSA of some effector genes belonging to the T3SS, a conserved secretion system involved in pathogenicity (Lindeberg *et al.*, 2012), was performed to evaluate if the variability in virulence observed could be associated with mutations in these genes. The analysis revealed only four SNPs for the strains of Psa isolated in 2014, while for the strains of 2010 no mutations were observed.
Among the SNPs, only two resulted in different amino acidic sequence. Thus, no positive correlation was found between SNPs and virulence levels. The mutations found in the genes of virulence could be related to the process of genetic differentiation, by considering that these classes of genes are evolving at a faster rate than the genome as a whole (Remenant et al., 2010). The few SNPs found in the effector genes are not sufficient to justify the different levels of virulence, as the pathogenicity in P. s. pv. actinidiae is controlled by several effector genes (Marcelletti et al., 2011). By comparing the whole genome of two strains of P. aeruginosa with different virulence, Lee et al. (2006) found that the pathogenicity is the result of a large pool of pathogenicity-related genes.

In conclusion, our study confirms that the biovar can be differentiated generating unique fingerprinting patterns by rep-PCR. RAPD technique showed an increased level of resolution in evaluating the genetic diversity within the biovar, at least with the set of primers used in this study. Through this multidisciplinary approach, we can state that a significant diversity occurs within the strains of P. s. pv. actinidiae from Northern Italy, both in genetics and in virulence. The study of the genetic diversity and virulence of the isolates of P. s. pv. actinidiae in the same geographical area at the first epidemic outbreak and four years afterwards, when the pathogen became endemic and established, highlighted an increase of average virulence of the strains and a higher level of genetic diversity. All the parameters considered – Na, Ne, H, I, polymorphic loci, and AMOVA – showed a higher genetic diversity within the population of Northern Italy isolated in 2014, compared to the older population. This constitutes a proof to the hypothesis that the initial epidemics started from a uniform population (Shapiro, 2016).

As previously demonstrated, P. s. pv. actinidiae has an overall clonal population structure, but the genomes carry a marked signature of recombination within the pathovar (McCann et al., 2013). P. s. pv. actinidiae has a high multiplication rate (Choi et al., 2014), that permits to rapidly introduce polymorphisms, confirmed also by the SNPs found in the effector genes, and to modify the genetic structure of the population in a relatively short time span (Schuenzel et al., 2005).

The fast and dramatic epidemics caused by P. s. pv. actinidiae could become an interesting model to study the changes of pathogen genetic diversity, but further investigation through genome sequencing and comparative genome analysis could clarify the higher intraspecific variability within the same biovar.

Acknowledgments
The Authors wish to thank the financial support of Piedmont Region in the framework of the project “PRO.ACT.IN.” (PSR FEASR 2007/2013, European Fund for Rural Development, Measure 124, Action 1). The Authors gratefully acknowledge Dr. Luca Nari and Dr. Graziano Vittone from
Agrion, and the growers for their support in sampling, Dr. Giorgio Balestra (Università della Tuscia) for providing the Central Italy and Asian strains, and Dr. Fabiano Sillo (University of Turin) for the support in molecular data analysis.

Compliance with Ethical Standards

- There are no potential conflicts of interest.
- The research does not involve human participants nor animals.
- The research does not involve informed consent.
References


Table 1 – Strain name, cultivar, geographical location, year of isolation and results of the pathogenicity assay in vitro and in vivo for the P. s. pv. actinidiae strains used in this study.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Cultivar</th>
<th>Geographical location*</th>
<th>Year</th>
<th>Mean ±SD in vitro</th>
<th>Mean ±SD in vivo</th>
<th>Class infection</th>
</tr>
</thead>
<tbody>
<tr>
<td>RC1</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>1.50 ± 0.55</td>
<td>2.14 ± 1.11</td>
<td>MV***</td>
</tr>
<tr>
<td>RC2</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>1.67 ± 0.52</td>
<td>2.02 ± 1.14</td>
<td>MV</td>
</tr>
<tr>
<td>RC4</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>1.33 ± 1.37</td>
<td>1.79 ± 0.99</td>
<td>LV</td>
</tr>
<tr>
<td>RC6</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>1.83 ± 0.98</td>
<td>2.02 ± 0.84</td>
<td>MV</td>
</tr>
<tr>
<td>RL1</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>1.17 ± 0.98</td>
<td>1.19 ± 0.98</td>
<td>a</td>
</tr>
<tr>
<td>RL2</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>0.33 ± 0.52</td>
<td>0.59 ± 0.70</td>
<td>ac</td>
</tr>
<tr>
<td>RL4</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>3.50 ± 0.55</td>
<td>3.93 ± 0.39</td>
<td>V</td>
</tr>
<tr>
<td>RL5</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>2.00 ± 2.10</td>
<td>2.62 ± 1.08</td>
<td>MV</td>
</tr>
<tr>
<td>CC1</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>1.67 ± 0.52</td>
<td>2.26 ± 1.05</td>
<td>MV</td>
</tr>
<tr>
<td>CC2</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>1.67 ± 1.86</td>
<td>2.29 ± 1.16</td>
<td>MV</td>
</tr>
<tr>
<td>CC5</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>1.17 ± 0.75</td>
<td>2.14 ± 1.28</td>
<td>MV</td>
</tr>
<tr>
<td>CC6</td>
<td>Hayward</td>
<td>Italy - Piedmont (TO)</td>
<td>2014</td>
<td>0.83 ± 0.41</td>
<td>0.71 ± 0.90</td>
<td>ab</td>
</tr>
<tr>
<td>PSA1</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>3.17 ± 1.03</td>
<td>3.21 ± 0.99</td>
<td>eg</td>
</tr>
<tr>
<td>PSA3</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>0.83 ± 0.41</td>
<td>0.84 ± 0.84</td>
<td>ab</td>
</tr>
<tr>
<td>PSA8</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>1.00 ± 1.55</td>
<td>1.66 ± 1.08</td>
<td>ad</td>
</tr>
<tr>
<td>PSA2</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>2.00 ± 1.10</td>
<td>2.62 ± 0.98</td>
<td>MV</td>
</tr>
<tr>
<td>QV2</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>2.83 ± 2.04</td>
<td>3.93 ± 0.60</td>
<td>g</td>
</tr>
<tr>
<td>QV3</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>2.50 ± 0.55</td>
<td>3.57 ± 0.90</td>
<td>fg</td>
</tr>
<tr>
<td>QV4</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>2.17 ± 0.75</td>
<td>3.09 ± 1.67</td>
<td>dg</td>
</tr>
<tr>
<td>QV5</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2014</td>
<td>1.50 ± 0.84</td>
<td>2.14 ± 1.43</td>
<td>be</td>
</tr>
<tr>
<td>BA3</td>
<td>Hayward</td>
<td>Italy - Piedmont (VC)</td>
<td>2014</td>
<td>3.00 ± 0.63</td>
<td>2.86 ± 1.36</td>
<td>ab</td>
</tr>
<tr>
<td>38/10</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>0.83 ± 0.41</td>
<td>0.84 ± 0.54</td>
<td>ab</td>
</tr>
<tr>
<td>310</td>
<td>Hayward</td>
<td>Italy - Piedmont (VC)</td>
<td>2010</td>
<td>1.00 ± 0.89</td>
<td>0.95 ± 1.08</td>
<td>ab</td>
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<td>74/10</td>
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<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>1.17 ± 0.75</td>
<td>1.31 ± 0.84</td>
<td>ac</td>
</tr>
<tr>
<td>41/11</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>2.33 ± 0.52</td>
<td>3.21 ± 1.17</td>
<td>eg</td>
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<tr>
<td>229</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>1.33 ± 2.07</td>
<td>2.26 ± 0.54</td>
<td>bf</td>
</tr>
<tr>
<td>309</td>
<td>Hayward</td>
<td>Italy - Piedmont (VC)</td>
<td>2010</td>
<td>0.83 ± 1.17</td>
<td>1.19 ± 0.59</td>
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</tr>
<tr>
<td>39/10</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>1.17 ± 1.17</td>
<td>1.79 ± 2.01</td>
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<tr>
<td>36/10 c1</td>
<td>Hayward</td>
<td>Italy - Piedmont (AT)</td>
<td>2010</td>
<td>1.67 ± 0.52</td>
<td>1.91 ± 1.61</td>
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<td>34/10</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>1.33 ± 0.52</td>
<td>2.26 ± 1.23</td>
<td>bf</td>
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<tr>
<td>314</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>1.00 ± 0.89</td>
<td>1.19 ± 1.16</td>
<td>ac</td>
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<tr>
<td>313</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>0.67 ± 1.03</td>
<td>0.71 ± 0.90</td>
<td>ab</td>
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<tr>
<td>36/10 c2</td>
<td>Hayward</td>
<td>Italy - Piedmont (CN)</td>
<td>2010</td>
<td>0.83 ± 0.98</td>
<td>1.19 ± 1.16</td>
<td>ac</td>
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<tr>
<td>CFBP7286</td>
<td>Hort16A</td>
<td>Italy - Latium (LT)</td>
<td>2008</td>
<td>3.00 ± 0.00</td>
<td>3.83 ± 0.63</td>
<td>V</td>
</tr>
<tr>
<td>K2</td>
<td>-</td>
<td>Korea - Jeonnam</td>
<td>unknown</td>
<td>1.17 ± 0.75</td>
<td>2.68 ± 0.40</td>
<td>MV</td>
</tr>
<tr>
<td>KW11</td>
<td>-</td>
<td>Japan - Shizuoka</td>
<td>1984</td>
<td>3.33 ± 0.52</td>
<td>3.67 ± 0.94</td>
<td>V</td>
</tr>
<tr>
<td>VT439</td>
<td>Jin Tao</td>
<td>Italy - Latium (VT)</td>
<td>2010</td>
<td>1.67 ± 0.82</td>
<td>-</td>
<td>-</td>
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<tr>
<td>VT511</td>
<td>Hayward</td>
<td>Italy - Latium (VT)</td>
<td>2010</td>
<td>1.00 ± 0.89</td>
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<td>-</td>
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<tr>
<td>LT23</td>
<td>Hayward</td>
<td>Italy - Latium (LT)</td>
<td>2008</td>
<td>2.00 ± 0.63</td>
<td>-</td>
<td>-</td>
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<tr>
<td>RM310</td>
<td>Hort16A</td>
<td>Italy - Latium (RM)</td>
<td>2008</td>
<td>2.83 ± 0.41</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>
* Letters in brackets indicate the Italian province of isolation: AT stands for Asti; CN for Cuneo; LT for Latina; RM for Roma; TO for Torino; VC for Vercelli; VT for Viterbo.

** Values in the same column followed by the same letter are not statistically different by Duncan’s multiple range test ($P \leq 0.05$)

*** Severity of symptoms in vivo: low virulent strain (LV; D.I. 0.5-1.9); moderate virulent strain (MV; D.I. 2.0-2.9); virulent strain (V; D.I. 3.0-3.9)
Table 2- Genetic diversity parameters of the three populations of *P. s. pv. actinidiae* considered in this study.

<table>
<thead>
<tr>
<th>Population</th>
<th>N. strains</th>
<th>Na</th>
<th>Ne</th>
<th>H</th>
<th>I</th>
<th>PL (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Piedmont 2014</td>
<td>21</td>
<td>1.72 ± 0.029</td>
<td>1.38 ± 0.023</td>
<td>0.23 ± 0.012</td>
<td>0.35 ± 0.017</td>
<td>71.79</td>
</tr>
<tr>
<td>Piedmont 2010</td>
<td>12</td>
<td>1.54 ± 0.033</td>
<td>1.23 ± 0.019</td>
<td>0.15 ± 0.011</td>
<td>0.24 ± 0.016</td>
<td>54.70</td>
</tr>
<tr>
<td>Latium</td>
<td>5</td>
<td>1.47 ± 0.033</td>
<td>1.28 ± 0.022</td>
<td>0.17 ± 0.013</td>
<td>0.26 ± 0.019</td>
<td>46.58</td>
</tr>
<tr>
<td>Mean (± SE)</td>
<td>-</td>
<td>1.58 ± 0.031</td>
<td>1.26 ± 0.021</td>
<td>0.18 ± 0.012</td>
<td>0.28 ± 0.017</td>
<td>62.39</td>
</tr>
</tbody>
</table>

Na: observed number of alleles; Ne: effective number of alleles; H: Nei’s genetic diversity; I: Shannon information index; PL: Polymorphic loci (%).
Table 3 - Polymorphic sites on four strains of *P.s. pv. actinidiae* isolated in 2014. Bases and triplet with the corresponding amino acids codification for references are indicated in italics, variant are indicated in regular type, whereas different amino acids are indicated in bold. K stands for lysine, I for isoleucine, F for phenylalanine, P for proline, G for glycine, S for serine, and T for threonine.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Accession Number</th>
<th>HopA1</th>
<th>HrpK1</th>
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<tbody>
<tr>
<td></td>
<td>Reference</td>
<td></td>
<td></td>
</tr>
<tr>
<td>QV3 (2014)</td>
<td>KU984444</td>
<td>G</td>
<td>A</td>
</tr>
<tr>
<td>PSA1 (2014)</td>
<td>KU984445</td>
<td>-</td>
<td>T</td>
</tr>
<tr>
<td>RC6 (2104)</td>
<td>KU984442</td>
<td>-</td>
<td>C</td>
</tr>
<tr>
<td>RL5 (2014)</td>
<td>KU984443</td>
<td>-</td>
<td>C</td>
</tr>
<tr>
<td></td>
<td>Reference</td>
<td></td>
<td></td>
</tr>
<tr>
<td>QV3 (2014)</td>
<td>KU984447</td>
<td>AAG (K)</td>
<td>-</td>
</tr>
<tr>
<td>PSA1 (2014)</td>
<td>KU984448</td>
<td>ATC (I)</td>
<td>TTC (F)</td>
</tr>
<tr>
<td>RC6 (2104)</td>
<td>KU984451</td>
<td>CCC (P)</td>
<td>GGT (G)</td>
</tr>
<tr>
<td>RL5 (2014)</td>
<td>KU984450</td>
<td>ACC (T)</td>
<td>TCC (S)</td>
</tr>
</tbody>
</table>
Figures captions

Fig. 1 – Disease severity indices to evaluate the pathogenicity of the *P. s. pv. actinidiae* strains inoculated on plant and leaf discs of *Actinidia chinensis* var. *deliciosa* ‘Hayward’.

Fig. 2 – ERIC PCR fingerprinting of representative strains of *P.s. pv. actinidiae* from different geographic area (a). Lane M – 1 kp plus ladder (Qiagen). Lanes 1-6: strains isolated in 2014. Lanes 7 and 9: strains K2 and KW11. Lanes 8 and 11: strain VT439 and RM310. Lanes 12-14: strains isolated in 2010. Dendrogram (b) generated after cluster analysis of genetic similarity based on ERIC PCR fingerprinting of all the strains of *P.s. pv. actinidiae*. The dendrogram was constructed using UPGMA method and Dice similarity index.

Fig. 3 – RAPD PCR fingerprinting obtained with OPB-13 primer for genomic DNAs of *P.s. pv. actinidiae* strains. Lanes 1-12: Piedmont strains 2010, L1 - 38/10; L2 - 36/10 c1; L3 - 36/10 c2; L4 - 309; L5 - 314; L6 - 74/10; L7 - 310; L8 - 41/11; L9 - 229; L10 - 313; L11 - 39/10; L12 - 34/10; Lanes 13-19: Japanese, Korean and Latium strains, L13 - K2; L14 - KW11; L15 - vt511; L16 - vt439; L17 - lt23; L18 - CFBP7286; L19 - rm310; Lanes 20-40: Piedmont strains 2014, L20 - rc1; L21 - rc2; L22 - rc4; L23 - rc6; L24 - rl1; L25 - rl2; L26 - rl4; L27 - rl5; L28 - cc1: L29 - cc2; L30 - cc5; L31 - cc6; L32 - psa1; L33 - psa3 ; L34 - psa8; L35 - psa9; L36 - qv2; L37 - qv3; L38 - qv4; L39 - qv5; L40 - ba3; Lane 41 - Positive control ; Lane C: Negative control ; M: 1 kb Plus ladder (Qiagen).

Fig. 4 - Dendrogram of similarity generated by rep and RAPD-PCR fingerprinting of *P. s. pv. actinidiae* strains. Cluster analysis was performed on combined dataset matrix of concatenated fingerprinting markers using Dice similarity index and UPGMA clustering algorithm. The scale indicates the degree of similarities between strains. Number at nodes represent bootstrap percentage estimated from 1000 replications of the dataset.

Fig. 5 - Principal Coordinates analysis (PCoA) obtained from the dataset matrix of fingerprinting generated by rep and RAPD-PCR of *P.s. pv. actinidiae* strains analysed in this study. The figure displays the diagram of Coordinate 1 versus Coordinate 2.