Despite the fungus colonizes the bark and the wood of the plane trees, Cfp-susceptible or resistant clones leaves from *P. acerifolia* and *P. occidentalis* were demonstrated to maintain the own susceptibility and resistance level when leaves are inoculated with Cfp conidia (El Modafar *et al.*, 1995; Clérivet and Alami, 1999). Nevertheless, susceptible *Platanus acerifolia* leaves respond actively to CP treatments producing extracellular and intracellular phenolic compounds and undergoing to a cell structural disorganization (Bennici *et al.* 2004, Scala *et al.* 2004). In the previous works it has been showed that in the standard experimental conditions (ten µl droplets of CP 1.5 x 10^-4 M applied to the lower leaf surface) the concentration of CP protein diminished into the droplets completely 48 hours after treatment. Contemporaneously, CP caused a rapid accumulation of phytoalexins together with a fungal restriction after Cfp conidia addition. CP was active at the minimum concentration of about 10^-5 M, and the Cfp growth was inhibited until to 72 hours after treatment. The main hypothesis emerged from the whole frame of results, that CP adhered to leaf surface and/or more probably was absorbed into the leaf tissues where it elicited effective defence responses against the pathogen. In the present work we have showed that CP acted at low concentrations like some very active substances able to elicit defence responses in plants, such as, for example, the α-elicitins and the oligogalacturonides (Huet *et al.*, 1995; Le Berre *et al.*, 1994). From the relative PCR results emerge that CP succeeds to mime the *Ceratocystis* action but stimulating different answers probably because it must not be the only active fungus protein. Furthermore, in situ hybridization results seem to confirm the capacity of CP to stimulate an answer in the plant like the fungus, but seem also to confirm that differences in expression are due to the fact that the fungus has other proteins which can be able to set off an answer in the plant and then also several under the point of time and space view. SSH is an effective method which has been developed to isolate expressed sequences that are specifically and differentially transcribed under various conditions or in response to various biotic and abiotic stresses. There are no
many works about plant interactions with pathogen or elicitors, one of the first of which was from Dellagi et al (2000) which described the characterization of the gene \textit{St-WRKY1} that was up-regulated in potato leaves after inoculation with \textit{Erwinia carotovora} subsp. \textit{atroseptica}. WRKYs are elicitor-induced proteins that bind to the sequence TGAC, or W box, in the promoters of \textit{PR} genes and appear to be responsible for upregulation of these genes. In general, new and interesting imputs on the genes involved in defence reaction have been shown in the last years. Kong \textit{et al.}, 2003, inoculated \textit{Triticum aestivum} “Ning7840”, one of few wheat cultivars with resistance to \textit{Fusarium graminearum}, and demonstrated that some defence related genes, like as the chitinase, were certainly involved in resistance. Degenhardt \textit{et al.}, 2005, showed that many genes were differentially transcribed in apple leaves resistant and susceptible to \textit{Venturia inaequalis}. They found that typical defence genes, like as β-1,3 glucanase, cysteine protease inhibitor, superoxide dismutase, were over-transcribed only in the resistant cultivar. Recently, Lotan-Pompan et al (2007), combining the SSH and cDNA-amplified fragment-length polymorphism (cDNA-AFLP) techniques, isolated a significant number of clones which were similar to genes that have been formerly described as stress- or defence related.

In the our work CP was shown to alter the expression pathways for many individual genes at various regulation steps involved the gene accessibility, the initiation of transcription and the synthesis of RNA. Important transcriptional variations were observed at level of protein synthesis/turnover and primary metabolism. The turnover is very important in stress responses. The proteome can change over time not only by protein synthesis but also through the removal of proteins whose functions are not longer required. In cells subjected to stresses an increased rate of proteolysis and major modifications in primary metabolism were reported (Gottesman 1999, Mladenova, 1990). Modifications in primary metabolism could be important not only to provide building blocks and energy for the biosynthesis of defence compounds but also for a cross talk between defence responses and other signalling pathways (Schenk \textit{et al.}, 2000).

A total of 78 new \textit{P. acerifolia} gene sequences were identified, the majority of which were long more than 600bp. A high percentage of these sequences
belonged to genes known to be involved in defence reaction, three of which have been presented with the complete CDS (clones L8A, C5H and A12D). The clone L3A corresponded to the *Rar1* gene that codifies a protein that regulates R-gene mediated resistance in various plant species, indicating conservation of its defence function (Freialdenhoven *et al*., 1994; Liu *et al*., 2002). Recent evidence suggests that *Nicotiana benthamiana* *Rar1* (*NbRar1*) also is an essential component of the *N* gene–mediated resistance response to *Tobacco mosaic virus* (TMV) (Liu *et al*., 2002). This is interesting because the *N* gene belongs to the TIR-NBS-LRR class of *R* genes (Whitham *et al*., 1994), thus, *Rar1* may represent an example of a signalling component involved in defence pathways. *Rar1* encodes a cytosolic protein of unknown function containing two (CHORD) Zn2+ binding domains (Shirasu *et al*., 1999).

Mutational analyses of CHORD-encoding genes indicate that *Rar1* represents a *R* gene-dependent signalling component and it can exist a link between *Rar1* and the Skp1-Cullin F-box protein (SCF) complex for the protein degradation pathway (Shirasu, 1999). Different SCF components have been shown to interact with COP9 signalosome (CSN) (Lyapina *et al*., 2001), a multiprotein complex involved in protein degradation through the 26S proteasome (Wei and Deng, 1999). CSN is associated with a large number of proteins, most of which are substrates or regulators of the ubiquitin system (Wei and Deng, 2003). The CSN is thought to cooperate with the Ubiquitin/26 S proteasome system in the regulation of protein stability (Sun *et al*., 2002). The removal must be selective so that only the correct proteins are degraded. Proteins are continuously synthesized and degraded in all living organisms to maintain the level of the structural molecules, enzymes and regulatory proteins like transcription factors (Vierstra, 1996). Ubiquitin/26S proteosome-dependent proteolytic pathway has emerged as a powerful regulatory mechanism in a wide range of cellular processes (Ciechanover, 1998; Zeng *et al*., 2006). Several evidences have recently been suggested that ubiquitin mediated protein degradation may also act as a regulatory mechanism in the plant defence removing negative regulators of the resistance response (Muskett and Parker, 2003). Interestingly, in the present work both 26S proteasome non-ATPase regulatory subunit 1 and ubiquitin have been demonstrated to be involved in the resistance response of plane leaves to CP.
Three other ESTs corresponded to pathogenesis-related (PR) proteins, which are induced and accumulate in host plants as a result of pathogen infection or abiotic stress conditions (Kim and Hwang, 2000). Thaumatin-like proteins (TLPs) belong to group 5 (PR-5), they are proteins commonly found both in monocotyledonous and dicotyledonous species in response to pathogen infection and known like antifungal compound. The precise mechanism by which PR-5 proteins exert their defence activity has not been clearly elucidated (Min Jung et al., 2005). Another PR protein consisted of β-1,3 glucanase (PR-2), which are endoglycohydrolase enzymes widely distributed in higher plants (Meins et al., 1992). There are many reports on the β-1,3 glucanase expression and their action into the cell wall and intercellular spaces where it encounters the invading fungus (Krishnaveni et al., 1999). TLPs belong to PR-14 class which have also been used as one marker of systemic acquired resistance in dicotyledonous (Yamakawa et al., 1998) as well as in monocotyledonous (Morris et al., 1998). Moreover, the genes ribulose-phosphate 3-epimerase and transketolase are two key-genes of the pentose-phosphate pathway, which is the main source of phenolic compounds in plants and is known for a long time to be associated with defence mechanisms (Agrios 1997, Buchanan et al., 2000).

Many other genes, even if were not included in the macro-group “Defence and/or stress related proteins”, can be indirectly involved in pathogen- and abiotic stress-responses. For example, the histone acetylation is involved in plant response to abiotic stresses (Kim et al., 2004; Lee et al., 2005; Song et al., 2005; Sridha and Wu, 2006). From these studies it emerges that the gene expression, during the plant responses to abiotic stresses, may be controlled by an antagonistic mechanism of histone acetylation and deacetylation on the target genes. In addition, about a possible role of the hystone deacetylase in pathogen defence, it has been demonstrated the over expression of the HDA19 gene in Arabidopsis induced ethylene and jasmonate-regulated PR gene expression and resulted in increased resistance to a plant pathogen, suggesting that this gene may play an important function in ethylene and jasmonate signalling and pathogen response (Zhou et al., 2005). The first report of stress induced helicase gene in the plants was in cDNA microarray analysis of 1300 Arabidopsis genes where the authors reported a DEAD-box helicase gene as a
cold stress-inducible gene suggesting a new role of helicases in stress signalling (Seki et al., 2001). It has been suggested a cross talk between defence responses and other signalling pathways, in particular, it has been observed CAB genes induction after salicylic acid (SA) treatments (Schenk et al., 2000). Because the phytochrome signal precedes and controls the activation of genes related to light, it has been suspected that light must have a function in the SA-controlled defence. This may occur at various levels, the most evident being the photosynthetic apparatus. Examining variegated mutants forming chloroplast-deficient leaf zones near to intact green areas it has been observed that signal resulting from both the SA (salicylic acid) and phytochrome pathways control the regulation of the HR induced by an avirulent pathogen, while the expression of PRs is not modified by the reduction of active chloroplasts (Genoud et al., 2002). It has been also observed that photosynthesis-related proteins, such as Rubisco small subunit, several photosystem subunits and chlorophyll a/b binding proteins, were significantly down-regulated during the proteasome-mediated PCD, but up-regulated during HR cell death (Kim et al., 2006).