

# Chapter 5

## Establishment of Actinorhizal Symbioses

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### 5.1 Introduction

To cope with nitrogen limitations, some plants have developed the ability to fix atmospheric nitrogen through symbiotic interaction with soil bacteria. The most efficient and intimate of such associations lead to the formation of new root organs called nodules where bacteria are hosted intracellularly and fix atmospheric nitrogen in optimal conditions. Two types of nitrogen-fixing root nodule symbioses (RNS) have been described: the well-studied legume–rhizobial symbiosis (see Part I) and actinorhizal symbioses (Perrine-Walker et al. 2011). The latter involves filamentous bacteria of the genus *Frankia* that interact with more than 200 plant species from eight different families, collectively called actinorhizal plants (Baker and Mullin 1992). Besides *Datisca* these plants are woody shrubs or trees and are present on every continent except Antarctica (Baker and Schwintzer 1990). The efficiency of nitrogen fixation in actinorhizal symbioses is comparable to the one in

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legumes with an estimated rate of 240–350 kg ha<sup>-1</sup> year<sup>-1</sup> (Wall 2000). Because of this, actinorhizal plants play very important roles in various ecosystems, as pioneer species able to colonise poor or degraded soils and to improve their fertility. These plants are used in soil fixation, agroforestry, reforestation, to build windbreaks or as source of timber or firewood (Diem and Dommergues 1990; Zhong et al. 2011).

Interestingly, phylogenetic analyses have demonstrated that all plant-forming RNS belong to the same clade (Rosid I). It was suggested that this common ancestor possessed some kind of predisposition towards RNS formation (Soltis et al. 1995; Doyle 2011). Studies suggest that actinorhizal symbioses appeared 3–4 times independently during evolution (Swensen 1996).

Despite their ecological importance, the establishment and functioning of actinorhizal symbioses are still poorly understood. Progresses have been hindered by the lack of genetic transformation system in *Frankia* and the fact that actinorhizal plants are mostly trees and shrubs thus making genetic approaches difficult. Moreover, no model system to study actinorhizal symbioses as emerged so far and different groups work with different experimental systems. Nevertheless, technical breakthroughs in the last decade have opened new avenues to the study of actinorhizal symbioses. First of all, the genomes of several *Frankia* strains have been sequenced (Normand et al. 2007; Persson et al. 2011) opening the way for comparative genomic studies (e.g. Bickhart et al. 2009; Udwary et al. 2011) and the analysis of global gene expression during symbiosis (Alloisio et al. 2010). Similarly, genomic resources are now available for some actinorhizal plants including ESTs database and microarrays (Hocher et al. 2006, 2011a). Finally, stable and hairy root transformation has now been achieved for actinorhizal plants of the *Casuarinaceae* (Diouf et al. 1995; Franche et al. 1997), *Datisceae* (Markmann et al. 2008) and *Rhamnaceae* (Imanishi et al. 2011) family paving the way for functional plant gene studies through RNAi (Gherbi et al. 2008a, b; Markmann et al. 2008). These new tools have led to advances in our understanding of the molecular mechanisms controlling actinorhizal symbioses formation. In this chapter, we give an overview of the current knowledge on the events leading to actinorhizal symbioses establishment. Multiple reviews addressing specific aspects of actinorhizal symbioses are available for further reading (Péret et al. 2009; Perrine-Walker et al. 2011; Hocher et al. 2011b; Abdel-Lateif et al. 2012; Pawlowski and Demchenko 2012).

## 5.2 Pre-infection, a Molecular Dialogue Between Symbiotic Partners

The first step towards symbiosis is the recognition of compatible symbionts. Host specificity in actinorhizal symbiosis is not as stringent as in legume–rhizobial symbiosis (Pawlowski and Sprent 2008; Pawlowski and Demchenko 2012). Host specificity originates from both partners. Some *Frankia* subgroups like the

“Casuarina” strains evolved high levels of specificity and are able to nodulate only two *Casuarinaceae* genera, *Casuarina* and *Allocasuarina*. On the plant side, some genera like *Gymnostoma* (*Casuarinaceae*) accept a wide range of *Frankia* strains. In legumes, host specificity derives from co-evolution of the bacterial signal molecule and the plant receptor. For the bacterial signal, specificity would result from chemical substitutions on the same chemical backbone (Wall 2000). We can hypothesise that actinorhizal plants with a broad range of bacterial host would recognise a common feature of the signal molecule whereas actinorhizal plants with restricted bacterial hosts would recognise a specific decoration of the signal molecule. On the *Frankia* side, strains able to nodulate divergent plant species would be able to synthesise multiple molecules corresponding to receptors of various plant species (Pueppke and Broughton 1999).

Nevertheless, little is known about the molecular interactions between *Frankia* and host plants in the rhizosphere prior to infection. It was shown recently that aqueous root exudates from the actinorhizal trees *Casuarina glauca* and *C. cunninghamiana* changed *Frankia* physiology and symbiotic properties (Beauchemin et al. 2012). Root exudates increased the growth of *Frankia* and caused hyphal curling, suggesting a chemotrophic response and/or surface property changes. Interestingly, Beauchemin et al. (2012) showed that root exudates altered the bacterial surface properties at the fatty acid and carbohydrate level. More importantly, *Frankia* cells treated with root exudates formed nodules significantly earlier than controls (Beauchemin et al. 2012). These data support the hypothesis of early chemical signalling between actinorhizal host plants and *Frankia* in the rhizosphere. However, the signals involved have not been identified yet. In legumes, flavonoids have been demonstrated to be the symbiotic plant signal attracting rhizobia and initiating the production of bacterial Nod factors (Ferguson et al. 2010). Flavonoids are secondary metabolites derived from the phenylpropanoid pathway. They are widely distributed in plants and fulfil many functions from pigmentation to cell cycle regulation (Abdel-Lateif et al. 2012; Hassan and Mathesius 2012). The impact of root exudates from *C. cunninghamiana* on *Frankia* could not be mimicked by some flavonoids that were shown to be active in the legume–rhizobia symbiosis (Beauchemin et al. 2012). In *Myrica gale*, flavonoids extracted from fruits changed *Frankia* growth and nitrogen fixation according to the symbiotic specificity of strains, inducing compatible and inhibiting incompatible strains (Popovici et al. 2010). This suggests that flavonoids might be plant signals involved in defining symbiotic specificity. In order to analyse the role of flavonoids in actinorhizal nodule formation, *C. glauca* plants with reduced flavonoids biosynthesis were produced by downregulation of *CgCHS1* (Laplaze et al. 1999) using RNA interference. *CgCHS1* encodes a chalcone synthase, the first enzyme of the flavonoid biosynthetic pathway. In these plants, the level of flavonoids in the roots was drastically reduced (Abdel Lateif and Hocher, in preparation). This led to a delay in nodulation and a reduction of the percentage of nodulation (Abdel Lateif and Hocher, in preparation). These results suggest that flavonoids are important for actinorhizal symbiosis formation and might represent symbiotic signals emitted by the root.

Flavonoids might also be involved in actinorhizal prenodule or nodule development by inhibiting auxin transport as demonstrated in legumes (Hassan and Mathesius 2012).

In the legume–rhizobial symbiosis, flavonoids trigger the expression of the bacterial *nod* genes (Chap. 1). These genes encode proteins involved in the biosynthesis of lipo-chitooligosaccharides molecules named Nod factors that act as bacterial symbiotic signals (Chap. 1). Many aspects of the molecular dialogue between rhizobia and legumes have been elucidated from synthesis to perception and transduction of the symbiotic signals (Chap. 1, Jones et al. 2007). In actinorhizal symbioses, the bacterial signal is not yet identified. The recent sequencing of *Frankia* genomes revealed a lack of canonical *nod* genes essential for Nod factors biosynthesis and that symbiotic genes (such as *nif* genes, *hup1*, *hup2* and *shc*) are not organised in symbiotic island and are not induced under symbiotic conditions in *Frankia* (Alloisio et al. 2010; Normand et al. 2007). Altogether, this suggests that *Frankia* might synthesise chemically distinct signalling molecules. Previous attempts to identify symbiotic signals secreted by *Frankia* led to the isolation of an unknown compound found to be heat stable, hydrophobic, resistant to chitinase and smaller than lipo-chitooligosaccharides (C  r  monie et al. 1999). Besides, *Frankia* is known to produce some auxins such as phenylacetic acid (PAA; Wheeler et al. 1984). Treatment of *Alnus glutinosa* plants with PAA was reported to induce nodule-like structure thus suggesting that these molecules might also be involved in pre-infection signalling (Hammad et al. 2003).

The mechanisms of perception and transduction of the bacterial symbiotic signal in actinorhizal plants are poorly known. Genetic studies in model legumes have revealed that legume-rhizobial and the more ancient arbuscular mycorrhizal (AM) symbioses (Part III) share part of their genetic programme leading to endosymbiosis including part of the symbiotic signal transduction pathway. This is in accordance with studies that suggest that the legume–rhizobial symbiosis would be derived from the more ancient AM symbiosis (Parniske 2008). Homologues of the genes involved in the common symbiotic transduction pathway have been identified in EST databases from the actinorhizal plants *C. glauca* and *A. glutinosa* (Hocher et al. 2011a, b). Transcriptome analyses showed that some of these genes are more expressed in actinorhizal nodules compared to non-inoculated roots (Hocher et al. 2011a). The receptor kinase SYMRK is part of the common Nod and Myc signalling pathway. A homologue was recently isolated from two actinorhizal species *C. glauca* and *Datisca glomerata* (Gherbi et al. 2008a; Markmann et al. 2008). Knockdown of SYMRK by RNA interference led to inhibition of nodulation and mycorrhisation in these plants when inoculated with compatible *Frankia* bacteria and AM fungi, respectively. Moreover, *C. glauca* SYMRK complemented the *Lotus japonicus* *ljsymrk* mutant for both nodulation and mycorrhisation (Gherbi et al. 2008a; Markmann et al. 2008). This demonstrated that SYMRK is a common signalling element shared between AM, legume–rhizobia and actinorhizal symbioses, supporting the hypothesis that the capacity to accommodate N<sub>2</sub>-fixing bacteria evolved at least partly from the more ancient AM genetic programme. Interestingly, complementation of *ljsymrk* using SYMRK genes

isolated from nodulating and non-nodulating species showed that all the genes tested were able to complement the lack of mycorrhisation but only genes with three LRRs (found in *Tropaeolum majus* and all nodulating plants) were able to complement the nodulation defect (Markmann et al. 2008). The appearance of an additional LRR motif in SYMRK might therefore be one of the evolutionary events that led to nitrogen-fixing RNS apparition in the Fabid clade.

In conclusion, while chemical signalling between *Frankia* and its host plants seems to involve molecules different from Nod factors, the same common symbiotic transduction pathway was recycled from the more ancient AM symbiosis to perceive symbiotic signals in legume–rhizobial and actinorhizal symbioses.

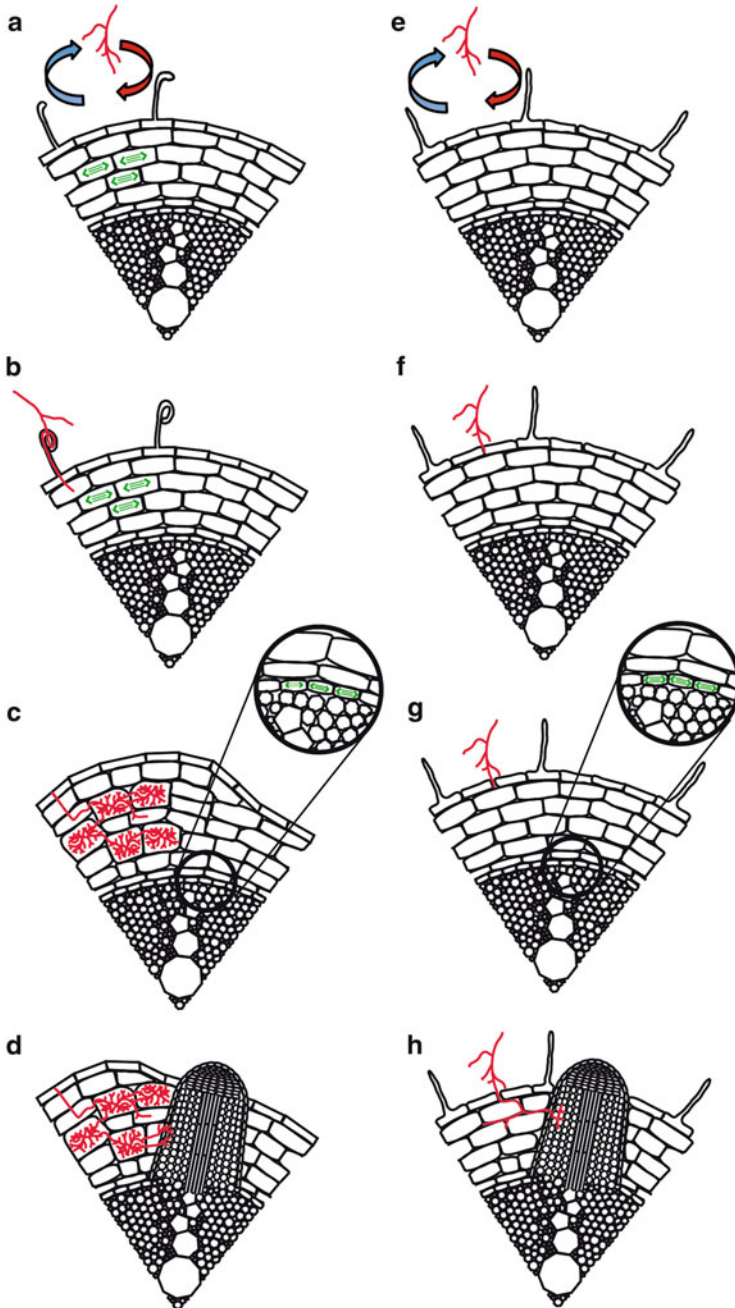
## 5.3 Infection

After pre-infection events, *Frankia* can enter the plant root either intracellularly via root hairs or intercellularly via the middle lamellas of cell epidermal (Obertello et al. 2003; Wall and Berry 2008). The same *Frankia* strains can induce both types of infection in different host plants indicating that the type of infection is controlled by the host plant (Racette and Torrey 1989; Pawlowski and Demchenko 2012).

### 5.3.1 Intracellular Infection

Intracellular infection is found in the *Myrica*, *Comptonia*, *Alnus* and *Casuarina* genera (Berry and Sunnel 1990). *Frankia* bacteria secrete factors that induce root hair deformation (Fig. 5.1a; Callaham and Torrey 1977). Studies carried out by Torrey (1976) demonstrate that all root hairs are deformed during *Casuarina* infection while just some root hairs are deformed in *Comptonia* (Callaham et al. 1979). Sugar-binding lectins produced by *Frankia* might help the bacteria to bind the root hairs in some actinorhizal plants such as *A. glutinosa* (Pujic et al. 2012). *Frankia* hyphae become entrapped by plant cell polysaccharides at the tip of some deformed root hairs and a local hydrolysis of primary cell occurs at the site of *Frankia* penetration (Berry et al. 1986). Surprisingly, recent analyses of *Frankia* genomes did not find any conserved secreted polysaccharide-degrading enzymes that might be responsible for this degradation (Mastronunzio et al. 2008). This might suggest that *Frankia* secretes effector-like molecules to communicate with its host and trigger the local loosening to the cell wall necessary for infection to occur (Mastronunzio et al. 2008). In some deformed root hair, the plasma membrane invaginates and forms an infection thread structure (Fig. 5.1b). Within this structure, growing *Frankia* hyphae are encapsulated by a cell wall-like matrix made of xylan, hemicellulose, cellulose and pectin (Berg 1990).

Root hair deformation occurs 24–28 h after inoculation. However, only growing root hairs are infected by *Frankia* (Callaham et al. 1979). In these infected root



**Fig. 5.1** Establishment of actinorhizal symbiosis through intracellular (a–d) and intercellular infection (e–h). *Frankia* hyphae are shown in red and dividing cells in green. (a, e). Exchange of symbiotic signals between the two partners with, only in (a), deformation of root hairs and metabolic modifications in cortical cells close to the site of perception of the bacterial signal. (b) Penetration of *Frankia* within a curled root hair and initiation of division in cortical cells.

hairs, a high metabolic activity is observed (Berry et al. 1986; Berry and Sunnel 1990). Simultaneously with infection, cell divisions occur in cortical cells adjacent to the infected root hair inducing the formation of a protuberance called the prenodule (Fig. 5.1b). Infected threads grow towards the prenodule and invade some of its cells that become hypertrophied and both the plant cell and bacteria differentiate to fix nitrogen (Fig. 5.1c; Laplaze et al. 2000a). While the prenodule is an obligatory step of the infection process, it is not the precursor of a nodule lobe. As the prenodule develops, cell divisions occur in the pericycle opposite to a protoxylem pole giving rise to a nodule primordium (Fig. 5.1c). The nodule primordium develops into a nodule lobe that is infected by *Frankia* hyphae coming from the prenodule (Fig. 5.1d).

A gene encoding a protease of the subtilase family called *Cg12* or *Ag12* in *C. glauca* and *A. glutinosa*, respectively, is specifically expressed in plant cells infected by *Frankia* (Laplaze et al. 2000b; Ribeiro et al. 1995; Svistoonoff et al. 2003). No expression was found during intracellular symbiosis with the AM fungus *Glomus intraradices* (Svistoonoff et al. 2003). It has been proposed that these proteases might be involved in cell wall remodelling or the processing of peptidic signals during symbiotic infection. A recent comparative transcriptome analysis of genes induced during actinorhizal, rhizobial and AM symbioses indicates that protease-encoding genes are among the core genes that are induced in all three endosymbioses (Tromas et al. 2012). This suggests that proteases are important component for setting endosymbioses and that some of the genes encoding proteases involved in the ancient AM symbiosis have been recycled to form RNS. Interestingly, the infection-specific induction of a *ProCG12::GUS* construct was retained in the model legume *M. truncatula* (Svistoonoff et al. 2004) indicating that gene regulation during infection in legume–rhizobial and actinorhizal symbioses might use conserved regulators.

Several studies suggest a role of the phytohormone auxin during infection by *Frankia*. A gene named *CgAUX1* encoding a functional auxin influx carrier is expressed in plant cells infected by *Frankia* but not by the AM fungi *G. intraradices* in *C. glauca* (Péret et al. 2007, 2008). Inhibition of auxin influx using 1-naphthoxy acetic acid (1-NOA) delays actinorhizal nodule formation and leads to the formation of small nodules in *C. glauca* (Péret et al. 2007). *Frankia* produces auxins, indole-3-acetic acid (IAA) and phenylacetic acid (PAA), in vitro (Wheeler and Henson 1979; Hammad et al. 2003; Perrine-Walker et al. 2010). Recent immunolocalisation experiments showed specific accumulation of both IAA and PAA in plant cells infected by *Frankia* in *C. glauca* (Perrine-Walker et al. 2010). Gene expression, immunolocalisation and modelling experiments suggest that this specific accumulation is due to auxin production by *Frankia in planta*



**Fig. 5.1** (continued) (f) Penetration of *Frankia* in between epidermal cells. (c) Branching of *Frankia* hyphae within the prenodule and divisions of pericycle cells at the site of initiation of the nodule, in front of a xylem pole. (g) Initiation of the nodule without formation of a prenodule. (d, h) emergence of the nodule colonised by *Frankia*

and the specific localisation of auxin influx and efflux carriers in *C. glauca* nodules (Perrine-Walker et al. 2010). Altogether, these studies link symbiotic infection to auxin accumulation in *C. glauca*. However, we do not know if this is a common feature of actinorhizal symbioses. Moreover, the role, if any, of auxin in those cells infected by *Frankia* is still unknown. We are currently addressing this question by inhibiting auxin signalling specifically during *Frankia* infection in *C. glauca* (Laplaze, unpublished data).

### 5.3.2 Intercellular Infection

Intercellular infection occurs in some actinorhizal plant genera such as *Elaeagnus*, *Ceanothus*, *Cercocarpus*, *Hippophae*, *Shepherdia* and *Discaria* (Miller and Baker 1985; Berry and Sunnel 1990; Valverde and Wall 1999; Imanishi et al. 2011). During intercellular infection, some signal exchange must occur between the two partners but no root hair deformation is observed (Fig. 5.1e). Instead, *Frankia* enters through the middle lamella between adjacent epidermal cells (Fig. 5.1f) and then progresses intercellularly in the root cortex (Fig. 5.1g). As in intracellular infection, this is associated with pectolytic activity that might be of plant rather than bacterial origin (Mastrorunzio et al. 2008). During intercellular infection, prenodule formation has not been reported. However, some cortical cell divisions occur in *Ceanothus* but these new cells are not infected by *Frankia* (Berry and Sunnel 1990). Nodule primordium formation occurs through cell divisions in the pericycle in front of a xylem pole. The nodule lobe primordium is then colonised by intercellular hyphae (Fig. 5.1g). *Frankia* hyphae become intracellular when they invade cortical cells of the young nodule primordium.

## 5.4 Actinorhizal Nodule Formation

Actinorhizal nodule lobes are formed from cell divisions occurring in the pericycle in front of a xylem pole. New nodule lobes are formed by branching, giving rise to a coralloid actinorhizal nodule formed of multiple lobes. Each lobe contains a meristem at its apex, a central vascular bundle and a periderm. In the nodule, four zones have been defined: (1) the meristematic zone, (2) the infection zone, (3) the fixation zone and (4) the senescence zone. The *meristematic zone* is localised at the apex and produces new cells responsible for the indeterminate growth of actinorhizal nodules. The *infected zone* is adjacent to the apical zone. In this zone, *Frankia* hyphae infect some of the new cells. The *fixation zone* is composed of infected and uninfected cells. Infected cells are filled with *Frankia* hyphae and hypertrophied. Vesicles differentiate and nitrogen fixation occurs. Assimilation of the fixed N probably occurs in uninfected cells (Wall 2000). The *senescence zone* is



localised at the base of old nodules. In this zone, the host cytoplasm and the bacteria degenerate.

Because of its origin, i.e. cells divisions in the pericycle in front of xylem poles and its structure, the actinorhizal nodule lobe has been considered as a modified lateral root (Pawlowski and Bisseling 1996). Moreover, in some actinorhizal plants such as *C. glauca*, a structure called nodular root is formed. The nodular root is a very specialised root showing negative geotropism (growing upward) and cortical aerenchyma and lacks a root cap and root hairs. It has been suggested that it plays an important role under flooding or waterlogged conditions by increasing gas exchange between the nodule and the atmosphere (Silvester et al. 1990). Furthermore, study carried out by Schwintzer et al. (1982) shows a correlation between the external oxygen tension and the length of the modified root. The formation of lenticels is noted at the nodule periderm of certain actinorhizal genera (*Alnus*, *Coriaria* and *Datisca*). This structure is also involved in nodule aeration (Silvester et al. 1990). The presence of both structures, lenticel and root nodule in some *Datisca* species, has been reported by Pawlowski et al. (2007).

## 5.5 Conclusions

Nitrogen availability is one of the major limiting factors of crop production worldwide. The high price of nitrogen fertilisers and their environmental impact has recently renewed the interest of the plant science community and funding charities for research on the transfer of biological nitrogen fixation to crops such as cereals (Den Herder et al. 2010; Beatty and Good 2011). Two groups of plants evolved the ability to form nitrogen-fixing RNS: the rhizobial symbiosis is restricted to the *Fabaceae* with the notable exception of the genus *Parasponia* (*Cannabaceae* family), while actinorhizal symbioses occur in eight angiosperm families. Interestingly, molecular phylogenies studies showed that (1) all these plants belong to a single  $N_2$ -fixing clade (Soltis et al. 1995) and (2) that nodulation appeared several times independently in both groups (Doyle 2011). This led to the suggestion that the common ancestor of the  $N_2$ -fixing clade had a yet unknown genetic predisposition to form RNS. Recent results have shown that actinorhizal and rhizobial symbioses rely on similar molecular components that were recycled from the ancient and widespread AM symbiosis (reviewed in Geurts et al. 2012). More studies on actinorhizal and rhizobial symbioses (including the atypical *Parasponia*–*Rhizobium* symbiosis) are needed to understand how during evolution RNS appeared in the nitrogen-fixing clade. Moreover, because actinorhizal (and *Parasponia*) nodules are simpler structure (modified lateral roots) that appeared independently in different plant families, it might represent a better model for the transfer of nodulation to other plants. New strategies are being developed to characterise the molecular mechanisms of actinorhizal symbioses formation and functioning. This should shed a new light on the evolution of root endosymbioses and hopefully pave the way to the transfer of nitrogen fixation to important crops.

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