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BARD

FINAL REPORT

PROJECT NO. IS-2775-96

**Morphogenesis and Light Signal Transduction
in Plants: The p27 Subunit of the COP9-complex**

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BARD Final Scientific Report

Date of Submission of the report: 21.8.2000

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Evaluating Panel: Molecular Biology

Project Title: Morphogenesis and light signal transduction in plants: The p27 subunit of the COP9-complex

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Continuation of (Related to) Previous BARD Project:

☐ Yes

☒ No

Number:

Keywords *not* appearing in the title and in order of importance. Avoid abbreviations.

Arabidopsis, photomorphogenesis, signalosome, light signal transduction

Abbreviations used in the report, in alphabetical order:

Budget: IS: \$ 203,000

US: \$ 93,000

Total: \$ 296,000

Signature

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Publication Summary (numbers)

	Joint authorship	US only	Israeli only	Total
Refereed (published, in press, accepted)	1	1	1	3
Submitted, in review, in preparation	0	0	0	0
Invited review papers	0	1	0	0
Book chapters	0	0	0	0
Books	0	0	0	0
Master theses	0	0	0	0
Ph.D. theses	0	1	1	2
Abstracts	3	2	2	7
Not refereed (proceedings, reports, etc.)				

Patent Summary (numbers)

	Israeli only	US only	Joint	Total
Submitted				
Issued (allowed)				
Licensed				

Cooperation Summary (numbers)

	From US to Israel	From Israel to US	Together, elsewhere	Total
Visits/Meetings	2	2	1	5
Sabbaticals	0	0	0	0
Postdoctorates				

- **Cooperation**, briefly explain whether synergistic, complementary or supportive.

The collaboration was at times synergistic, complementary and supportive. There was free exchange of materials and information between the two laboratories. This resulted in one joint publication (Karniol et al., 1998), and two additional publications. However, by most standards, these other two publications should be considered joint publications. For example, Figure 5 in Karniol et al., (1999) employed materials provided by the Deng lab, while Figure 7 in Serino et al., (1999), used materials provided by the Chamovitz lab.

Dr. Chamovitz visited the Deng lab twice during the funding period, giving two seminars. Prof. Deng visited the Chamovitz lab once, giving a seminar, and his student, G. Serino also spent a week learning a new biochemical technique in the Chamovitz lab, while teaching a new molecular technique to students in the Chamovitz lab.

Introduction

Plants monitor environmental signals and modulate their growth and development in a manner optimal for the prevailing light conditions. The mechanisms by which plants transduce light signals and integrate them with other environmental and developmental signals to regulate plant pattern development are beginning to be unraveled. A large body of knowledge has accumulated regarding the roles of specific photoreceptors in perceiving light signals, and about the downstream developmental responses responding to light (Batschauer, 1999; Chamovitz and Deng, 1996; Deng and Quail, 1999). Still, little is known about the molecular mechanisms connecting the photoreceptors to development, and how these developmental pathways are integrated with additional developmental regulatory pathways to modulate growth.

The multi-subunit protein complex COP9 signalosome (previously referred to as the "COP9 complex") has a central role in mediating the light control of plant development, and in general developmental regulation. Arabidopsis mutants that lack this complex develop photomorphogenically even in the absence of light signals (reviewed in Chamovitz and Deng, 1996, 1997). Various genetic studies have indicated that the COP9 signalosome acts at the nexus of upstream signals transduced from the individual photoreceptors, and specific downstream signaling pathways. Thus the COP9 signalosome was hypothesized to be a master repressor of photomorphogenesis, and that light acts to abrogate this repression. However, the COP9 signalosome has roles beyond the regulation of photomorphogenesis as all mutants lacking this complex die following early seedling development, and an essentially identical complex has also been detected in animal systems (Chamovitz and Deng, 1995; Seeger et al., 1998; Wei et al., 1998).

Our long term objective is to determine the role of the COP9 signalosome in controlling plant development. In this research project we showed that this complex contains at least eight subunits (Karniol et al., 1998; Serino et al., 1999) and that the 27 kD subunit is encoded by the *FUS5* locus (Karniol et al., 1999). The *FUS5* subunit also has a role extraneous to the COP9 signalosome, and differential kinase activity has been implicated in regulating *FUS5* and the COP9 signalosome (Karniol et al., 1999). We have also shown that the COP9 signalosome may work together with the translational-regulator eIF3. Our study of the COP9 signalosome is one of the exciting examples of plant science leading the way to discoveries in basic animal science (Chamovitz and Deng, 1995; Karniol and Chamovitz, 2000; Wei and Deng, 1999).

Outline of Original Objectives and Subsequent Modifications

The general goal of the proposed research was to elucidate the mechanisms by which the COP9-complex suppresses photomorphogenesis in the dark, and promotes photomorphogenetic growth in the light. We saw the first step to elucidating the biochemical function of the COP9-complex as the identification and characterization of its components. To this end we specifically intended to:

1. Clone and sequence the cDNA encoding the p71 subunit of the COP9-complex.

This objective was modified to include the p27 subunit.

2. Develop specific antibodies against p71 in order to further confirm that the gene isolated indeed encodes a subunit of the complex.

This objective was modified to include antibodies against p27.

3. Determine the precise subcellular localization of p71 by confocal analysis of immunostained cells.

Results in the project made this objective irrelevant

4. Use the specific antibodies to examine the possible protein-protein interactions among the different subunits of the complex, and between other available photomorphogenic gene products and the COP9-complex subunits.

5. Map the genomic location of the cloned gene to determine if it corresponds to any of the previously defined photomorphogenic loci.

6. Assay the function of p71 in yeast to determine if p71 is functionally equivalent to yeast NIP1.

Results in the project made this objective irrelevant

7. Employ the yeast two-hybrid interaction trap to isolate proteins which interact with p71.

This objective was modified to isolate p27 interacting proteins.

Results

Cloning and analysis of the gene encoding p71

The p71 protein was identified as it copurifies with the COP9 signalosome. The analysis of this protein indicated that it likely interacts with the COP9 signalosome, but not as a core subunit. This analysis was published in Kamiol et al., 1998: