

Dear Luis, Alex, Scott, and Kevin,

June 17, 2009

Please find enclosed 11 strains that have been tested in my lab and can be used for sequencing.

Strains of *Phycomyces blakesleeanus*

	Strain <sup>1</sup>	Genotype <sup>2</sup>	Origin <sup>3</sup>
10433	C47	<i>madA35</i> (-)	NRRL1555, NTG
10430	B2	<i>madC452</i> (-)	NRRL1555, ICR170
10435	A905	<i>madC406</i> (-)	NRRL1555, ICR170
10447	C68	<i>madD59</i> (-)	NRRL1555, NTG
10448	C149	<i>madD120</i> (-)	NRRL1555, NTG
10449	C110	<i>madE102</i> (-)	NRRL1555, NTG
10450	C6	<i>madF48 carRA12</i> (-)	NRRL1555, NTG
10451	<b>C307</b>	<b><i>madG131</i></b> (-)	<b>C288 X NRRL1555</b>
10452	<b>A284</b>	<b><i>madG131</i></b> (-)	<b>A56 X C307</b>
10453	L151	<i>madI714</i> (-)	NRRL1555, NTG
10454	L153	<i>madI716</i> (-)	NRRL1555, NTG
10458	NRRL1555		
10459	URC21		
10460	A56		

<sup>1</sup>Strains with prefix A come from Prof. Arturo P. Eslava (Universidad de Salamanca, Spain); C, from the late Prof. M. Delbrück (California Institute of Technology, Pasadena, CA, U.S.A.); L, from Prof. E. D. Lipson (Department of Physics, Syracuse University, Syracuse, NY, U.S.A.); S, from Prof. Cerdá-Olmedo (Universidad de Sevilla, Spain); B, from Max Planck Institute für Molekulare Genetik (Berlin, Germany)

<sup>2</sup>Mutations labelled *mad* affect the phototropism of the sporangiophore; *pde*, cAMP phosphodiesterase; *car*, beta-carotene biosynthesis; *nic*, biosynthesis of nicotinic acid; *ura*, biosynthesis of uracil; *fur*, resistance to 5-fluorouracil; *lys*, biosynthesis of lysine. The mating type is indicated by the symbol (-) or (+).

<sup>3</sup>The standard wild type NRRL1555 was obtained originally from the Northern Regional Research Laboratory, USDA, Peoria, IL, USA. A56 is the (+) isogenic strain of NRRL1555. Mutants were obtained previously by N-methyl-N'-nitro-N-nitrosoguanidine mutagenesis (NTG) or by 2-methoxy-6-chloro-9-[3-(ethyl-2-chloroethyl) aminopropylamino] acridine-2HCl mutagenesis (ICR170).

**NOTE:** The mutations in *madA* and *madB* strains (C21, C47, A893, and C109) have been identified in the corresponding genes. These strains could be used as controls.

Strains in bold may have some genetic background from a + strain that is not fully isogenic with NRRL1555. They may be compared with C107 that has the same *madG* allele.

Regards  
Arturo