Poster Format Guide
(Oct, 2019)

1. General:
Posters should keep text to a minimum and emphasize graphics**.** You do not have to include all of your data. A few key figures are usually sufficient to represent your work. You should tell people what you have done, any new discovery? Is it to convince people that one technique is better than another?

2. Required Elements:

Title – Your poster should include a banner title. Below the title, list the authors and institutions in a slightly smaller font. You should have your institute or company logs on the side.

Introduction – Introduce the research question, give a small amount of background, and identify your hypothesis and the purpose of your study. Consider using bullet points.

Methods – Describe the experiments and protocols employed in your study.

Results – The results of your study appear here, illustrated by the majority of your figures. Present only the most pertinent results. Check that the figures are large and easily read.

Conclusion – Interpret your results. Compare or contrast your findings to those from the scientific literature. Suggest further experiments or research that would build upon your study.

3. Format and Design:
The size of your poster should be A0. Fonts – Your poster should be easily read from a distance of 2 ft. Use contrasting fonts for the title, text and figure legends. (e.g. – Times for the text, and Arial for the title and figure legends)

Layout – Make a scale model of your poster on graph paper using colored paper or post-it notes to design the most effective layout. Design the poster in three or four columns. Related text and graphics should be adjacent. Related text and graphics can be enclosed in a box.

Background color should be white or a neutral color that is easy on the eyes.

Print a miniature version of your poster on A0 paper. Choose 'Fit to size' under the print command, and choose letter-sized paper. If your text is too small to read on the miniature version, it will be too small to read on the final poster. Same is true to pictures and figures – the graphical elements of your poster should be sharp and clear on the miniature printout. Your poster can be either portrait or landscape.

4. Two templates of poster:

Shallow Shear Velocity and Seismic Microzonation of the Urban Las Vegas Basin

www.seismo.unr.edu/hazsurv

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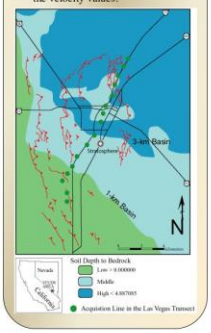
With: *Matt Clark, Chris Lopez, Chris Loughner, Hyunmee Park, Jim B. Scott, Weston Thelen, Aasha Pancha* (all from UNR), *and Bob Greschke* (IRIS-PASSCAL Instrument Center, New Mexico Tech, 100 East Road, Socorro, NM 87801)

Summary

- **Purpose:** to characterize the possible effects of ground shaking from potential seismic sources in the region.
- **Results:** The lowest velocities in the transect (at the NEHRP C/D boundary, 350 m/s) were found near the intersection of Interstate 15 and Lake Mead Blvd.
- The velocities rise smoothly as the transect moves to the south to the highest NEHRP C values (500-650 m/s) near Sahara Blvd.
- From Sahara Blvd. to Tropicana Blvd. there is a slight decline in the velocity values.

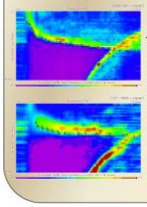


Methods

- 15 km transect beginning at Cheyenne Ave. to the north and ending at Tropicana Blvd. to the south.
- 20 m spacing in 800 m sections, of Texan recorders from the IRIS/PASSCAL Instrument Center at New Mexico Tech.
- Microtremor seismic sources such as trains and car traffic.
- Also included some refraction lines, with a sledge hammer source, to augment the microtremor dispersion data with P velocities.

4.5 Hz geophone attached to Reftek RT-125 Texan spiked into a crack in the sidewalk.

View of transect looking to the south parallel to Interstate 15. The train made an excellent seismic source for microtremor dispersion, down to 1.5 Hz frequency.



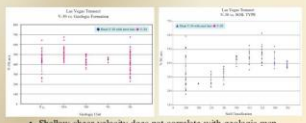
Analysis

Slowness-frequency analyses from two sub-arrays- Flamingo (upper), and Charleston (lower). Red squares are Rayleigh phase-velocity dispersion picks. Velocity-depth profiles are modeled to fit the picks.

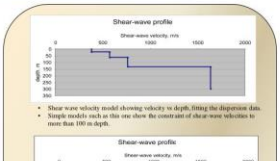
SASW and X-Hole results from B. Luke, UNLV

Discussion

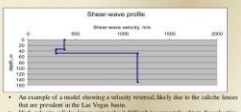
- ReMi transect velocities agree well with nearby SASW and crosshole measurements.
- Only 3 km out of the 15-km-long transect have velocities near or below the NEHRP-C/D boundary (350 m/s).
- The transect shows significant lateral variations, but velocities do not correlate with surface mapping.



- Shallow shear velocity does not correlate with geologic map units. Some USDA soil units do correlate.
- The range of velocities within most map units is greater than the differences between units.



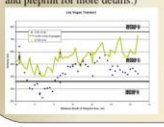
- Shear wave velocity model showing velocity vs depth, fitting the dispersion data.
- Simple models such as this one show the constraint of shear-wave velocities to more than 100 m depth.



- An example of a model showing a velocity reversal, likely due to the caliche lenses that are prevalent in the Las Vegas basin.
- High-velocity caliche lenses can make it difficult to accurately obtain the velocities below, limiting depth penetration.

Conclusions

- This survey suggests a medium-scale transect with a limited budget can be completed in a short time.
- The transect adds crucial new data to the characterization of ground shaking effects.
- Creating shaking amplification maps for urban basins in Nevada cannot rely on surface mapping; additional direct measurements are needed.
- We have completed similar studies in the Los Angeles and the Reno basins. (See the website and preprint for more details.)



Shear velocity averaged to 100 meters depth (V_{s30}) compared to V_{s30} across the transect.

IDENTIFICATION OF GENES INVOLVED IN RICE (*Oryza sativa*, indica) GRAIN FILLING

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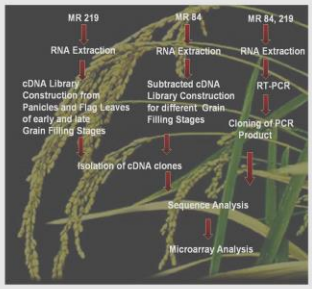
ABSTRACT

For decades, rice has been the staple crop for more than half the world's population. The challenge to produce sufficient rice for the future is overwhelming, as the current rate of population growth outpaces that of rice production. Grain filling is a vital factor that directly affects the yield of rice. A functional genomic study has been undertaken to comprehend rice grain filling at the molecular level. High and poor yielding Malaysian varieties of rice, MR 219 and MR 84 respectively, were chosen for this study. To achieve the objectives, several approaches have been attempted. Firstly, cDNA libraries were constructed from the panicles of early, and late grain filling stages and the flag leaf of the high yielding variety, to represent the genes that are involved in grain filling. Secondly, subtraction cDNA libraries were constructed to identify the genes involved during different stages of grain filling in the MR 84 variety. The clones isolated from all the cDNA libraries will be used for cDNA microarray analysis in the future. Lastly, genes encoding large and small subunits of ADP-glucose pyrophosphorylase, the key enzyme in the starch biosynthesis; and the gene for rice endosperm B-zip (REB), a transcriptional factor associated with protein storage in rice endosperm; were obtained by RT-PCR.

Comparisons of MR 84 and MR 219

	MR84	MR219
Maturity days	115	105
No. of panicles/plant	13-17	14-18
No. of spikelets/plant	130	150
Weight of 1000 grains (g)	26	27.1
Production (tons/h.a.)	4.0 - 6.2	6.0 - 10.7

METHODOLOGY



RESULT & DISCUSSION

cDNA Library Analysis

	Early grain filling stage	Late grain filling stage	Flag leaf library
Primary library	$5.6*10^5$pfu/ml	$4*10^6$pfu/ml	$8*10^5$pfu/ml
Amplified library	$6.9*10^7$pfu/ml	$1.5*10^8$pfu/ml	$6.5*10^8$pfu/ml

A total of 1152 clones from flag leaf library and 3098 clones from panicle library were obtained. Some of them are:

Clone number	Putative Function	Score (bits)
OP46	Ribosomal L-9 like protein	307
OFL6F6	Transcription factor	256
OP123	Glutelin	416
OP101	26S Proteosome reg. subunit	405

A total of 2366 subtracted cDNA clones were isolated from 4 subtraction cDNA libraries. A few examples are:

Clone number	Putative Function	Score (bits)
Sub1 68	Wheat adenosylhomocysteinase-like protein	447
Sub1 101	Mechanosensitive ion channel protein	169
Sub1 162	Putative CDPK-related protein kinase	510

RT-PCR

ADP-glucose pyrophosphorylase

Small subunit

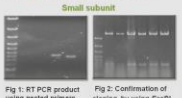


Fig 1: RT PCR product using nested primers.

Fig 2: Confirmation of cloning by using *EcoR*I.

Large subunit

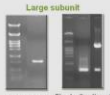


Fig 3: RT PCR product.

Fig 4: Confirmation of clone by (1) PCR; (2) *EcoR*I digestion.

Rice Endosperm bZIP

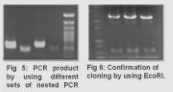


Fig 5: PCR product by using different sets of nested PCR primers.

Fig 6: Confirmation of cloning by using EcoRI.

CONCLUSION

- cDNA library and subtraction libraries have been successfully constructed.
- A total of 6616 clones were obtained from all libraries.
- Partial sequence encoding small and large subunit of ADP-glucose pyrophosphorylase and rice endosperm Bzip were obtained by using RT-PCR.

ACKNOWLEDGEMENTS

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