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CERTIFICATE OF ANALYSIS

SAMPLE INFORMATION

Customer:	Nature4science.com, Nature4science.com	**Report #:**	01-893-2
Customer Address:	5753-G573 E. Santa Ana Cyn Rd Anaheim, ORANGE 92807	**Received Date:**	01/05/2017
Sample #:	Garlic/crop 2017-2018	**Testing Date:**	01/06/2017
Description:	dry flakes	**Report Date:**	01/12/2017
Species:	*Allium sativum*		

TEST INFORMATION See attached Appendix for more detailed information.

Method: DNA Species Identification SOP AT-SP-278-X
Instrument: Ion torrent Personal Genome Machine Next Generation DNA Sequencer
References: Proprietary HERB™ reference DNA sequence database
Analysts: ANB, TKH, SNC, NWH, DLC
Tests: FP-1

RESULTS

The sample was analyzed using a universal plant DNA test, which identified it as a hybrid or mixture of Allium species, including Allium sativum, Allium ampeloprasum and another Allium species. The exact identity of this last Allium species cannot be confirmed because it is divergent from all reference DNA sequences. No other plant species were identified in the sample. This report is an update to the previous version 01-893-1 to identify the lot number of the sample. This report supersedes all previous versions.

Fig 1. Species Identification Test Results. The Y-axis is the total number of sequences identified for each species; ***this value is not representative of weight or volume*** of the species. "Other" category (if applicable) represents sequences not specifically identified.

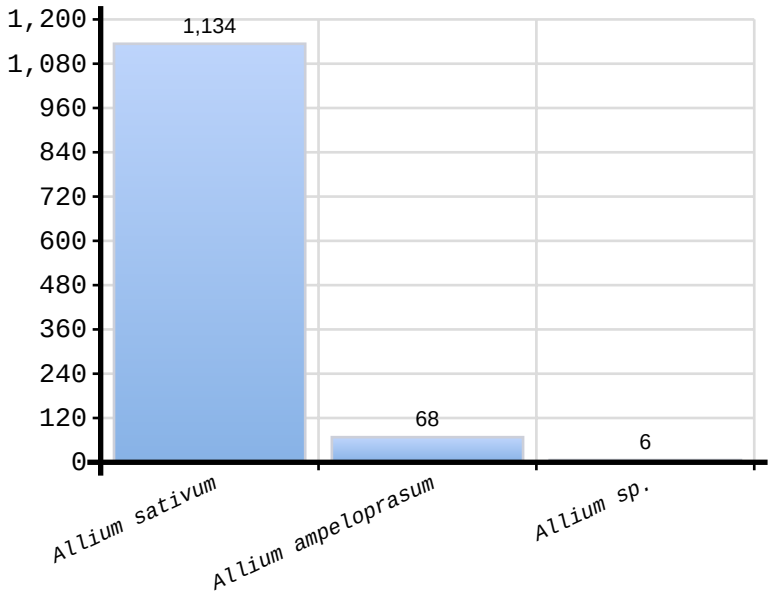

Fig 2. Clean Screen Test Results. The Y-axis is the total number of sequences detected for each species. *LOD = 50 pg DNA.

No Clean Screen Test was performed.

Verified by:
Darragh Clancy

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CERTIFICATE OF ANALYSIS APPENDIX

Method
All test samples are analyzed using NSF AuthenTechnologies' proprietary procedure for DNA species identification (SOP AT-SP-278-X). A single sample is randomly selected and the DNA is extracted. Then, carefully selected primers are used to amplify specific gene regions using Polymerase Chain Reaction (PCR). The DNA is sequenced using a Next Generation Sequencer where up to thousands of sequences are obtained for the sample. Sequences are compared to our proprietary HERB™ reference DNA sequence database for identification of the species. To ensure the validity of the results, all test samples are run alongside positive and negative controls throughout the process.

References
AuthenTechnologies' proprietary reference database contains thousands of verified, validated DNA sequences from authenticated voucher specimens and publications. Specimens are obtained from numerous major academic and research institutions around the country, primarily the University of California, Berkeley and Harvard University. The database contains sequences from most commercially used species and adulterants.

Tests
All samples are analyzed using the same general procedure (SOP AT-SP-278-X), but specific primers, or tests, are used based on the species and the nature of the material. For most raw materials universal primers are used, which will detect any species of plant, animal, or fungi. For some raw materials, complex blends, and all processed plants, fungi, and animals specific primers that only detect the target species and closely related nontarget species are used. These primers are designed to detect shorter, more fragmentary DNA as would be expected in processed or degraded materials. The universal or specific tests used are indicated on the report.

Results
For each sample, a brief synopsis of the test results is provided, which typically includes information on whether or not the target species was identified, and if any other species were detected in the sample. No test results are categorized as "pass" or "fail" as these decisions must be made by the customer. More specific information about the results is illustrated in the figures, as described below. For universal Plant, Animal, or Fungi tests, the presence of most species of Plants, Animals, or Fungi will be determined; for group-specific tests, only the presence of closely related species (i.e. in the same genus) will be determined.

Fig 1. Species Identification Test Results
All of the results from the species identification tests are summarized in a bar graph. On the X-axis is a list of each of the species identified in the sample. On the Y-axis is the total number of sequences identified for each species, including a zero (0) for test results where no DNA was identified. A negative result may be due to either (a) the species is not present in the material or (b) the DNA is undetectable due to degradation or processing. It is important to understand that this value is not representative of the weight or volume of the species in the starting material. The total number of sequences obtained and the relative abundance of species identified may vary from sample-to-sample, or run-to-run. Therefore, the numbers of sequences and/or relative ratios of species in a mixed sample should be interpreted as qualitative assessments of the presence or absence of a species in the sample. Depending on the complexity and nature of sample data, some non-target species sequences may not be specifically identified and will be categorized in the figure as "Other". These sequences may represent species with trace abundance, or otherwise not reported and may be further characterized if requested for a fee.

Fig 2. Clean Screen Test Results
All of the results for the Clean Screen tests are summarized in a bar graph. On the X-axis is a list of all the plant species being screened for. On the Y-axis is the number of sequences detected for each species in the sample, including a zero (0) for negative test results. A negative result may be due to either (a) the species is not present in the material or (b) the DNA is undetectable due to degradation or processing. For species with an asterisk (*), the Limit of Detection (LOD) has been validated to 50 picograms (pg) of DNA; for those species not marked with an asterisk, the LOD is higher than 50 pg but has not been specifically determined. It is important to note that the number of sequences detected for each species is not a quantitative assessment of the volume or weight of the species in the starting material. Therefore, the numbers of sequences for species in the sample should be interpreted as qualitative assessments of the presence or absence of a species in the sample.