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Data Article

Data set for the proteomic inventory and quantitative analysis of chicken eggshell matrix proteins during the primary events of eggshell mineralization and the active growth phase of calcification

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ABSTRACT

Chicken eggshell is a biomineral composed of 95% calcite calcium carbonate mineral and of 3.5% organic matrix proteins. The assembly of mineral and its structural organization is controlled by its organic matrix. In a recent study [1], we have used quantitative proteomic, bioinformatic and functional analyses to explore the distribution of 216 eggshell matrix proteins at four key stages of shell mineralization defined as: (1) widespread deposition of amorphous calcium carbonate (ACC), (2) ACC transformation into crystalline calcite aggregates, (3) formation of larger calcite crystal units and (4) rapid growth of calcite as columnar structure with preferential crystal orientation. The current article detailed the quantitative analysis performed at the four stages of

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shell mineralization to determine the proteins which are the most abundant. Additionally, we reported the enriched GO terms and described the presence of 35 antimicrobial proteins equally distributed at all stages to keep the egg free of bacteria and of 81 proteins, the function of which could not be ascribed.

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Specifications table

Subject area	*Biology*
More specific subject area	List and putative functions of eggshell matrix proteins present at initial and mid phases of eggshell formation.
Type of data	Raw and processed/analyzed mass spectrometry data obtained by nanoliquid chromatography combined to high resolution tandem mass spectrometry,.xls tables with identified/validated and quantified proteins tables with integrative and functional analysis of protein sequences.
How data was acquired	LC–MS/MS using a LTQ Orbitrap Velos mass spectrometer.
Data format	Raw data: raw.mzml and Processed and analyzed data using Mascot Search engine:.dat. Analyzed: Further assembled sequences using Clustal Omega multi-alignment algorithm and BLAST+suite. GO terms extracted from sequences and enrichment determination.
Experimental factors	Stage of eggshell formation.
Experimental features	Eggshell matrix samples were collected at four stages of eggshell mineralization and digested in gel using trypsin. Resulting peptides were analyzed by LC–MS/MS and further treated using data mining and bioinformatic analysis.
Data source location	Nouzilly, France, INRA Centre Val de Loire.
Data accessibility	Data have been deposited into the ProteomeXchange Consortium [2] via the PRIDE partner repository with the dataset identifier PXD001450.

Value of the data [describe in 3–5 bulleted points why this data is of value to the scientific community]

- Proteomic analysis of 216 chicken eggshell matrix proteins.
- Gene Ontology terms enrichments investigating potential functions of eggshell matrix proteins.
- Quantitative data on protein abundances according to stages of eggshell formation.
- Annotation on quantified eggshell matrix proteins.

1. Collection of eggshell matrix samples and preparation for MS analyses

Eggs were collected on brown-laying hens at 5, 6, 7 and 16 h after previous oviposition as described in [1]. These time intervals correspond respectively to the primary events of mineralization with widespread deposition of amorphous calcium carbonate (ACC), ACC transformation into crystalline calcite aggregates, formation of larger calcite crystal units and rapid growth of calcite and development of a columnar structure with preferential crystal orientation [3]. Eggs were broken and forming eggshells were washed with water, air dried and stored at −20 °C until protein extraction. Eggshell matrix proteins were extracted as described in [1].

A total of 24 individual eggshell protein extracts were used. Six samples collected at the same time point were pooled in equal amounts for each time (5 h p.o., 6 h p.o., 7 h p.o. and 16 h p.o.). The four pooled samples (51 µg of proteins/sample) were fractionated on a 4–20% SDS-PAGE gel (8.3 cm × 7.3 cm × 1.5 mm). Proteins were stained with Coomassie blue and the entire SDS-PAGE lanes were sectioned into 15 bands for each individual pooled sample. Excised proteins were in-gel

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