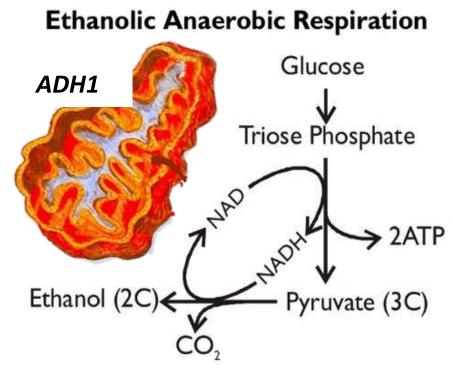
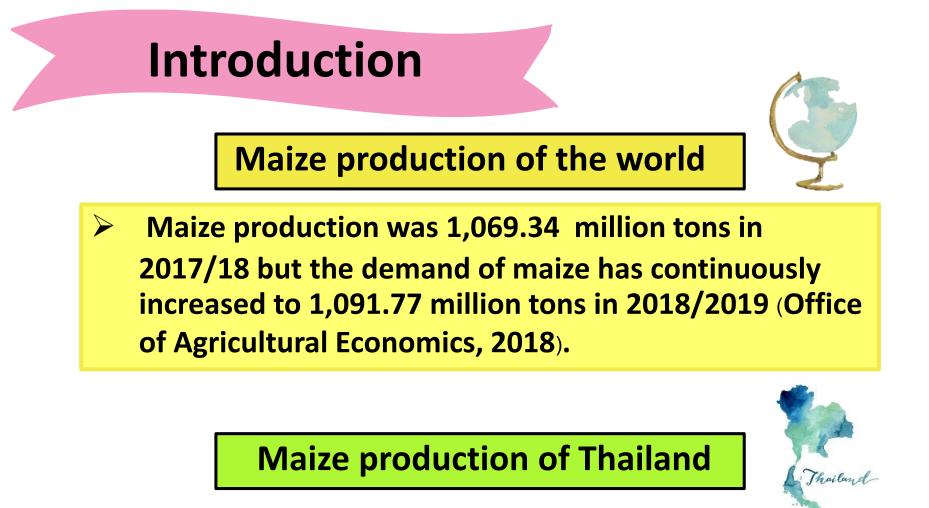
Ethanol Production and Mitochondria-Related Gene Expression of Maize Seed after Artificial Aging

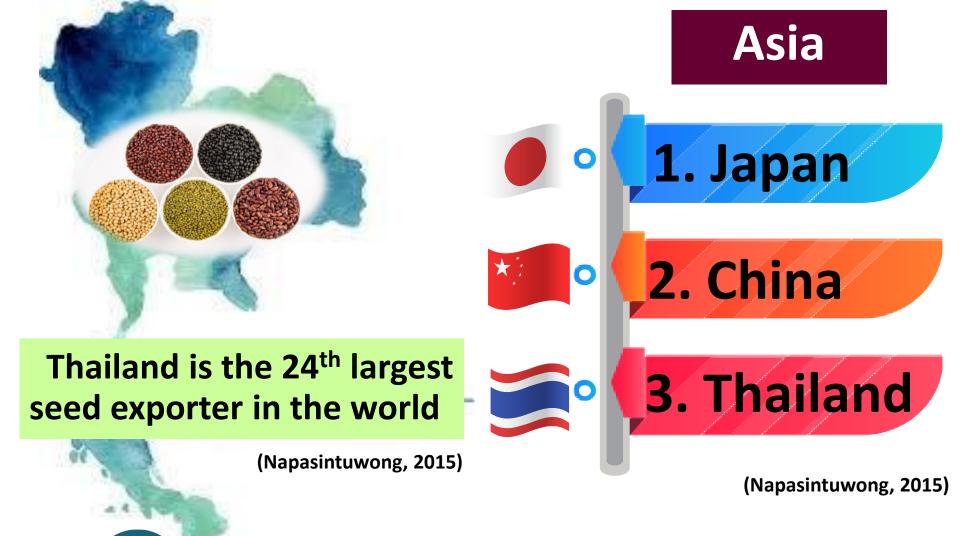




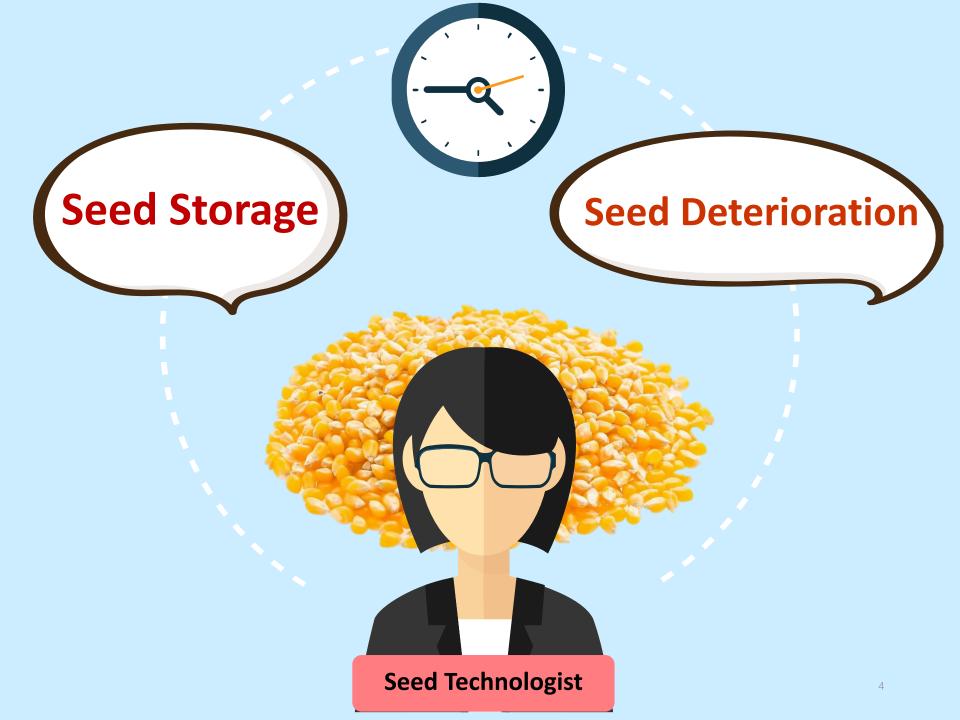
Chalisa Chaengsakul Thesis committee : Damrongvudhi Onwimol, Ph.D. Asst. Prof. Pasajee Kongsil, Ph.D. Department of Agronomy Kasetsart University



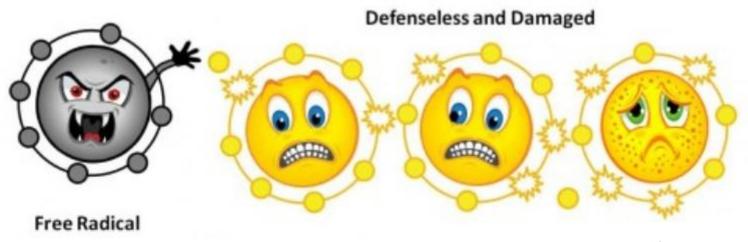
Maize production was 4.93 million tons in 2017/18 tons but the demand of maize has continuously increased to 6.6 million tons in 2019 (Office of Agricultural Economics, 2018; Thai Feed Mill Association, 2018).



The export of value of maize seed form Thailand was estimated at about 1.72 billion bath in 2016 and 2.12 billion bath in 2017 (Thai Seed Trade Association, 2018).



A model of seed deterioration is forwarded arguing that free radical assault on mitochondrial membranes may be a primary cause of seed deterioration (McDonald, 2006).



Damage of inner mitochondrial membrane results in impairment of aerobic energy metabolism and reduced oxidative phosphorylation (Benamar *et al.*, 2003).

Seed produces metabolic energy by anaerobic fermentation, of which the end products are ethanol and lactic acid (Kennedy *et al.*, 1992).





One alternative towards assessing the quality of seed is to monitor the concentration of certain volatiles (acting as biological markers) evolved from the seeds; examples are ethanol (EtOH), acetaldehyde (Bicanic *et al.*, 2003.)

Kodde *et al.* (2012) succeeded in test with cabbage seed (*Brassica oleracea* L.) by modified breath analyser in "Agri" version and called "fast ethanol assay".



Pathogens borne in maize seed



Aflatoxin *Aspergillus flavus* Aflatoxins are primarily a problem associated with maize, as it is infested with Aspergillus flavus and Aspergillus parasiticus in the field as well as storage (Nasir & Jolley, 2002).

Fungi separate from maize can produced aflatoxin such as *Aspergillus flavus, Aspergillus parasiticus and Aspergillus nomius* (Saito and Tsuruta, 1993).

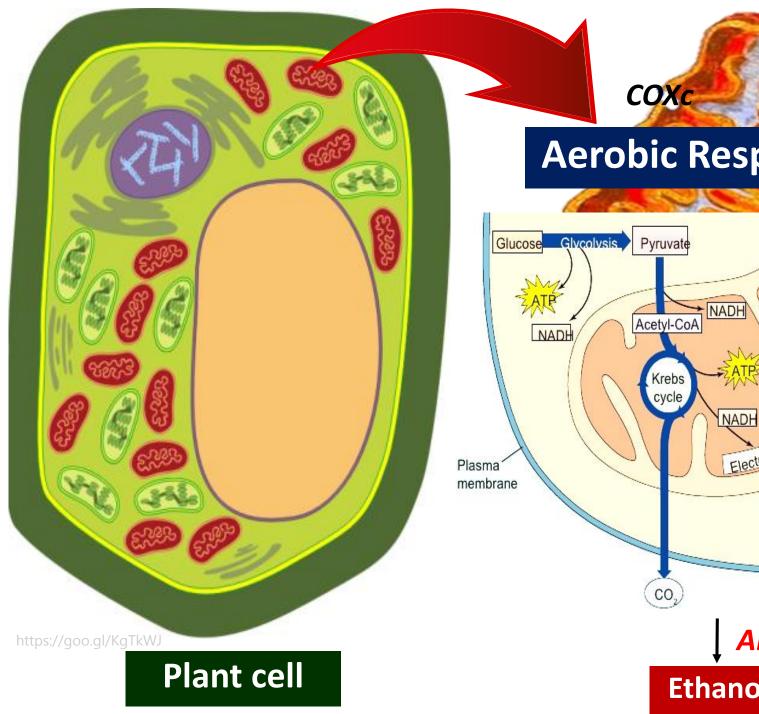
Pathogens borne in maize seed

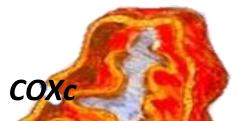
Aflatoxin



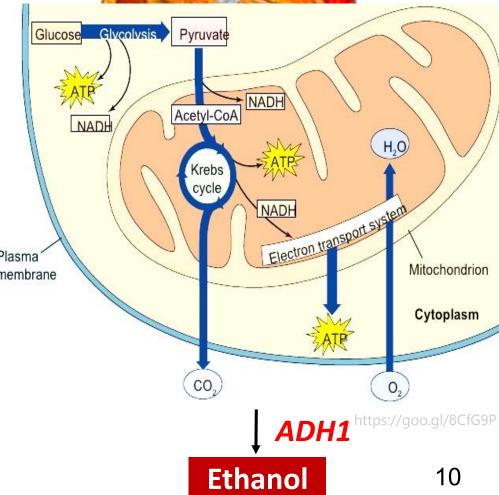
https://goo.gl/KdyPnV

Thailand found *Aspergillus flavus* more than *Aspergillus parasiticus* (Moss,1998)





Aerobic Respiration



AOX1

AOX1 were expression when include abiotic stresses such as low temperature, drought, and nutrient deficiency, as well as biotic stresses such as bacterial infection (Vanlerberghe, 2013).

ATPase

Yin *et al.* (2016) reported the assembly of mitochondrial ATP synthase was inhibited in aged seed, causing ATP production to decrease.



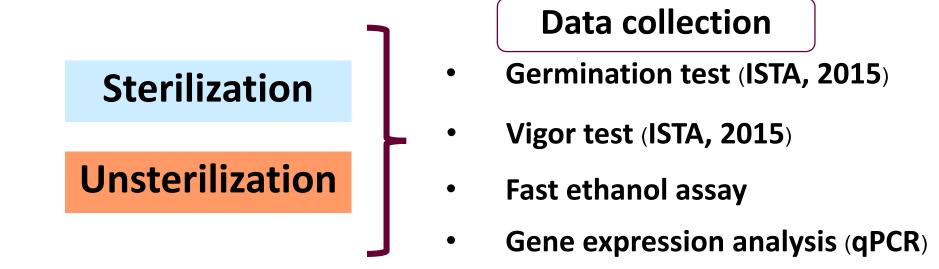
To evaluate mitochondria degradation via gene expression analysis including fast ethanol assay for detecting ethanol production from seed after artificial aging

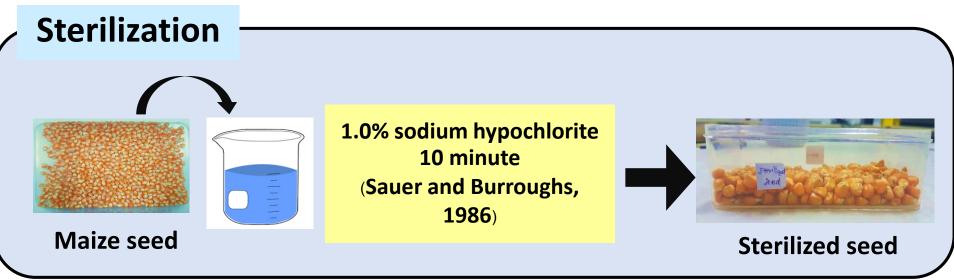
Materials and Method

Maize F1 hybrid seed



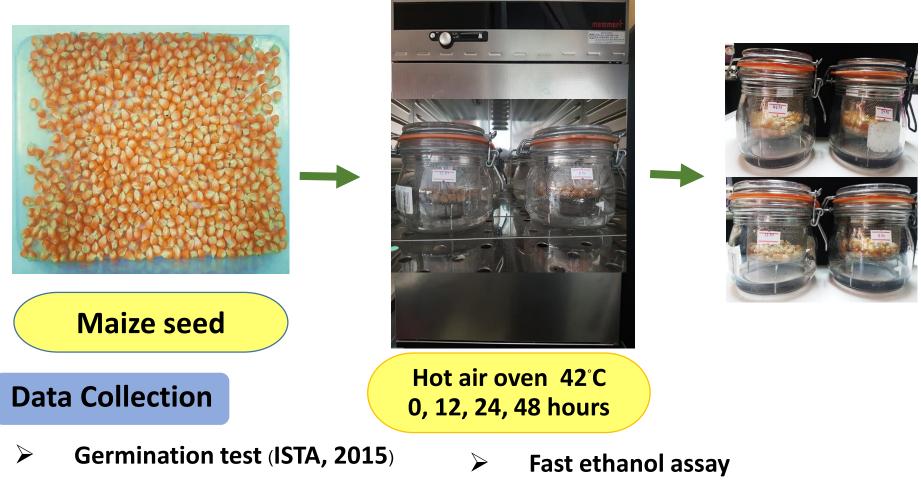
Sterilization





Artificial Aging by Hot Humid Treatment

Experimental design: CRD

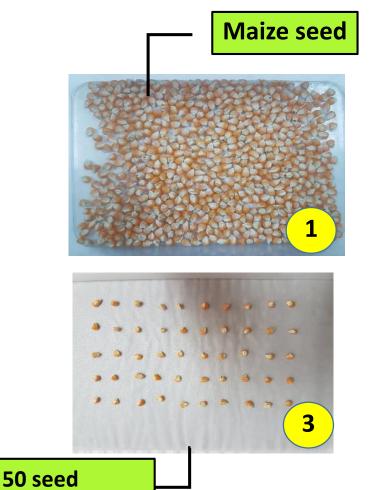


Vigor test (ISTA, 2015)

Gene expression analysis (qPCR)

Germination test (ISTA, 2015)

Between paper-BP- techniques



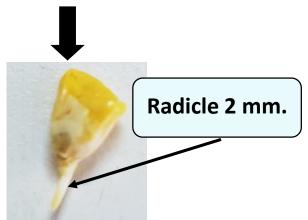


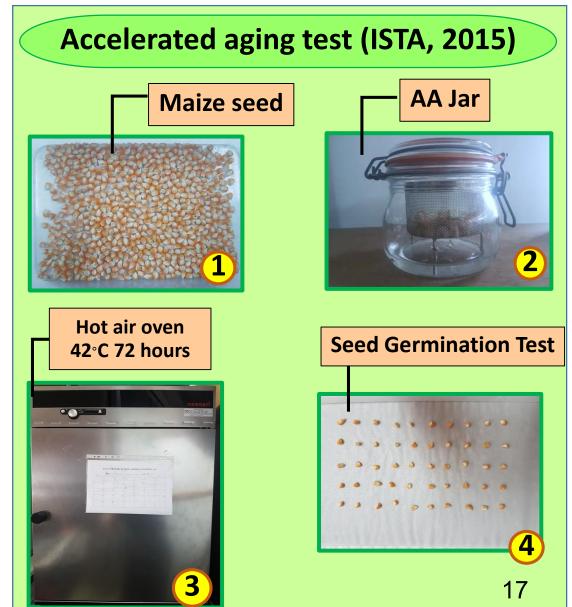
Vigor tests (ISTA, 2015)

Single count of radicle emergence (modified by ISTA, 2015)



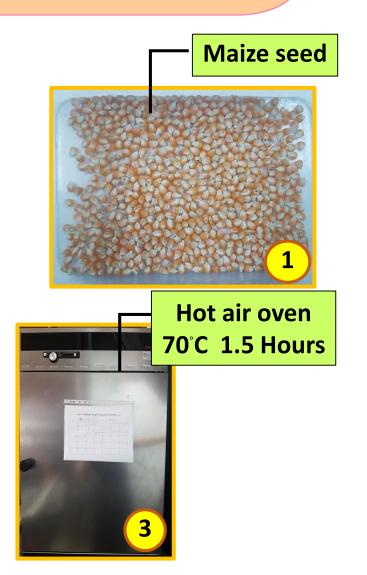
After germination 50 hours 25°C, (modified by ISTA, 2015)







Fast ethanol assay



10 seed and add water for 20% SMC





Modified breath analyser "Agri" version

Gene Expression Analysis (qPCR)





Seed grinder (MICRO HAMMER CUTTER MILLLABORATORY GRINDER 601 MHCM)





https://goo.gl/0R1hCG

Gene Expression Analysis (qPCR)



RNA Extraction

(Modified by Lodhi *et al.,* 1994)



CTAB and PVP Buffer



NanoDrop[®](scientific)

Gene Expression Analysis (qPCR)

4

cDNA

(Thermo Scientific Revert Aid First Strand cDNA Synthesis Kit)





Table. 1 Primer for gene expression analysis (qPCR)

| Gene | Accession | Types | Sequence (5'→3') | Annealing temperature | |
|-----------------------|----------------|----------------|----------------------|--------------------------|--|
| Alcohol dehydrogenase | | Forward primer | GGTTCGACAGTGGCTGTTTT | | |
| (Adh1-S) | L23548.1 | Reverse primer | TGTGGTCTTTTGGGTTCACA | 58 ⁰ C | |
| ATP synthase | NM_001158454.1 | Forward primer | TGAAGATAAGCAGCGTGGTG | 60 ^о С | |
| | | Reverse primer | TAGGAGCAACAGGAGCGACT | | |
| Alternative oxidase | AY059646.1 | Forward primer | AAGAAAATGCCTGGCTGCTA | 58 ⁰ C | |
| | | Reverse primer | CCTTCGTTGCTCCTTTTCAG | | |
| | EU976023.1 | Forward primer | ACCTTGGCACAAGAGACGAT | 59 ⁰ C | |
| Cytochrome c oxidase | | Reverse primer | TGGGCCCATCACTTAAAAAG | | |
| Elongation factor 1- | | Forward primer | AGGTCCACCAACCTTGACTG | - 58 ⁰ C | |
| alpha (EF1-A) | U76259.1 | Reverse primer | ACGTCCAACAGGGACAGTTC | | |

Results and Discussions

Seed qualities after artificial aging

Table. 2 Germination and seed vigour of maize seed cv. A aftersubjected in different periods of time of hot-humid treatment.

| Hours after hot-humid treatment | Germination (%) nent | | Accelerated aging test (%) | | Single count of radicle emergence (%) | |
|------------------------------------|-------------------------|------|-------------------------------|--------|---|---|
| 0 (control) | 74.5 a | | 60 a | | 47.5 a | |
| 12 | 61.5 b | | 59 a | | 40.5 ab | |
| 24 | 61 b | | 56 a | | 35 b |] |
| 48 52.5 | | 44 b | | 29.5 b | | |
| F-test | * | | * | | * | |
| C.V. (%) | 11.91 | | 9.61 | | 20.72 | |

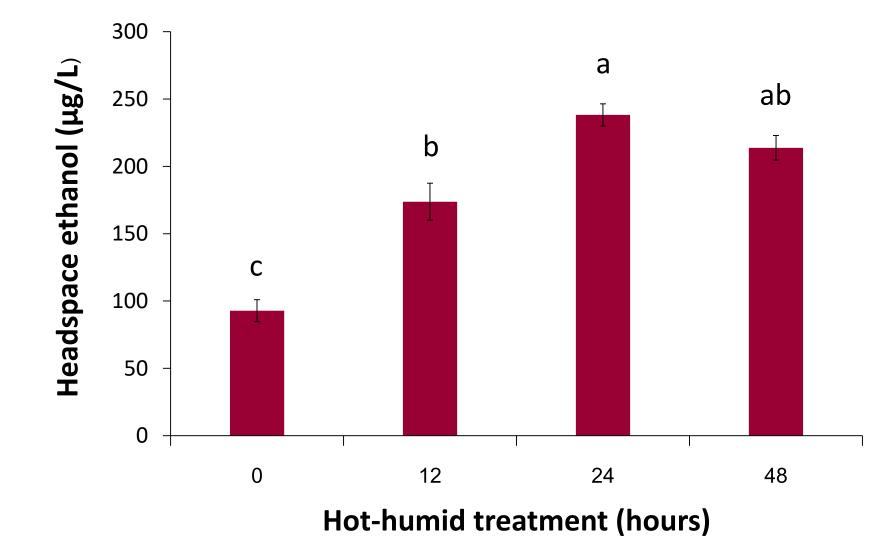
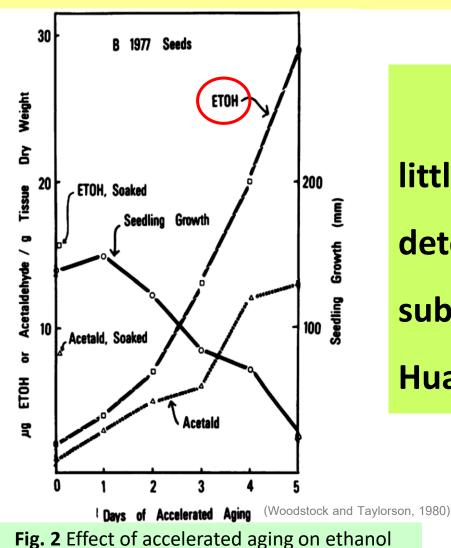


Fig. 1 Effect of time period during hot-humid treatment on ethanol production of maize seeds (cv. A). Headspace ethanol was measured above 1,200 mg seed samples at 20% moisture in 20 mL vials after 1.5h incubation. Error bars denote the S.E. (n = 4).

Results and Discussion Maize seed after artificial aging

• Fast ethanol assay of maize seed after artificial aging



High-vigor seed accumulated little or no ethanol while deteriorated seed accumulated substantial ethanol (Buckley and Huang ,2011)

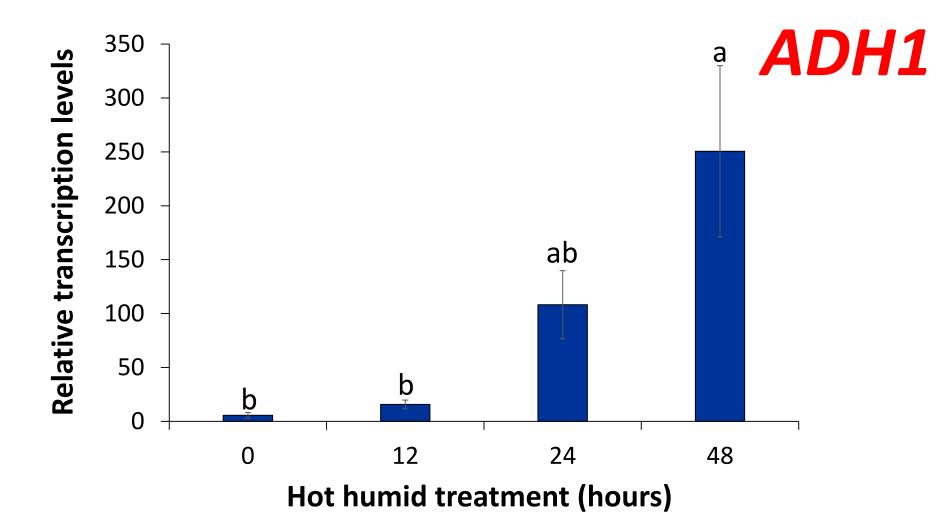
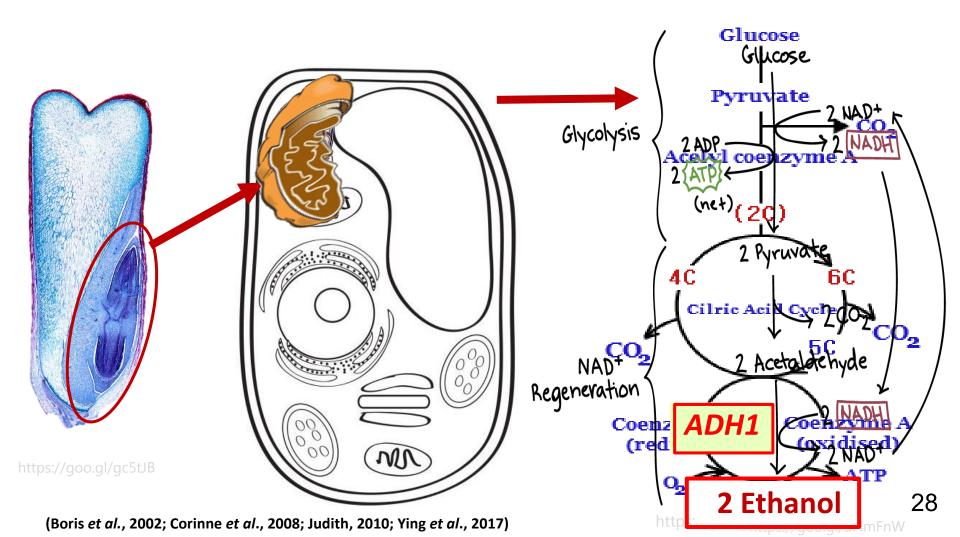


Fig. 3 Effect of time period during hot-humid treatment on energy metabolism gene (ethanol metabolomics gene) expression. Maize seeds (cv. A) were subjected in 100%RH at 42 °C for 0, 12, 24 and 48 hours. The quantitative RT–PCR was measured the change of expression of *Alcohol* dehydrogenase (*ADH1*)-Maize. Error bars denote the S.E. (n = 4).

Results and Discussion Maize Seed after Artificial Aging

Mitochondria-related gene expression



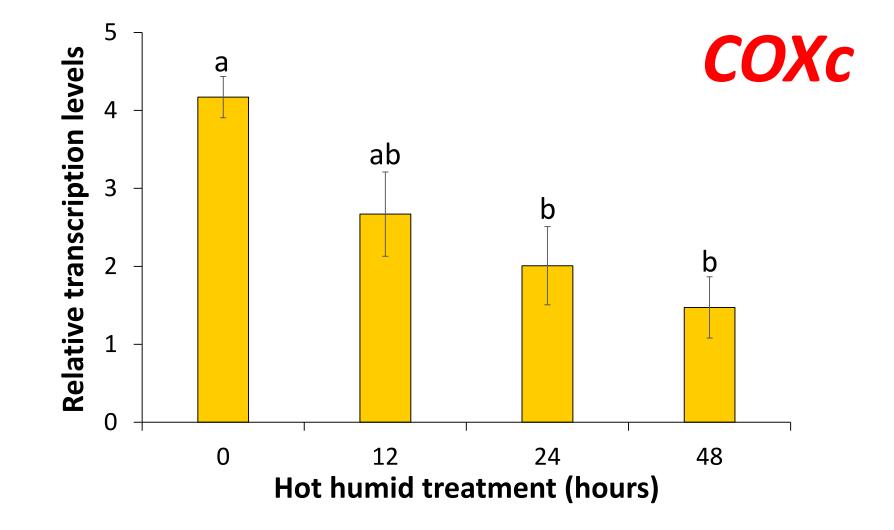
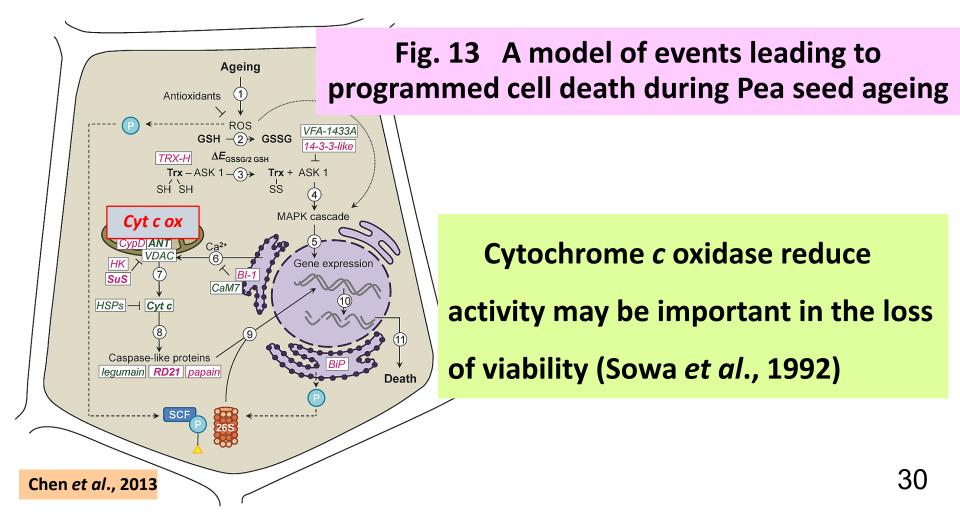


Fig. 4 Effect of time period during hot-humid treatment on energy metabolism gene(ethanol metabolomics gene) expression. Maize seeds (cv. A) were subjected in 100%RH at 42 °C for 0, 12, 24 and 48 hours. The quantitative RT–PCR was measured the change of expression of cytochrome c oxidase (*COXc*)-*Maize*. Error bars denote the S.E. (n = 4).

Results and Discussion Maize Seed after Artificial Aging

Mitochondria-related gene expression



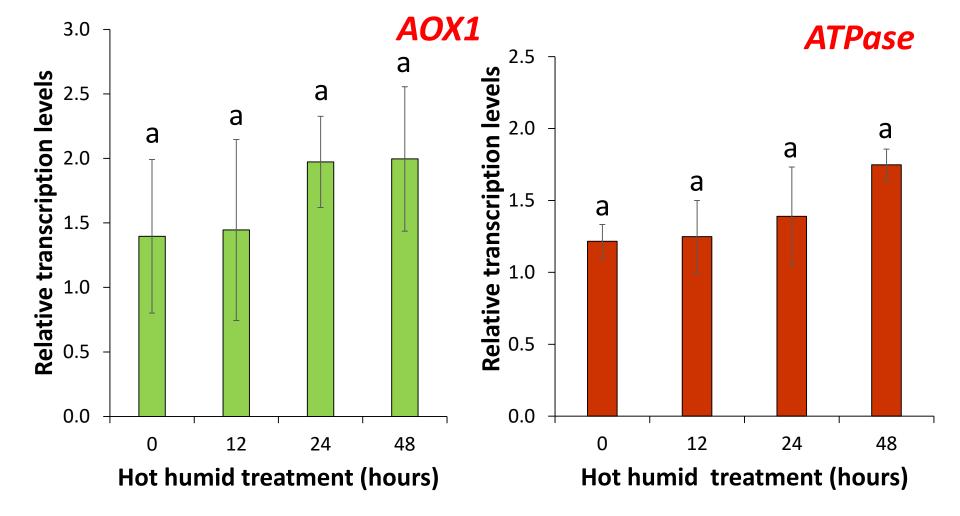


Fig. 7 Effect of time period during hot-humid treatment on energy metabolism gene (ethanol metabolomics gene) expression. Maize seeds (cv. A) were subjected in 100%RH at 42 °C for 0, 12, 24 and 48 hours. The quantitative RT–PCR was measured the change of expression of Alternative oxidase (AOX1) and ATP synthase (*ATPase*)-*Maize*. Error bars denote the S.E. (n = 4).

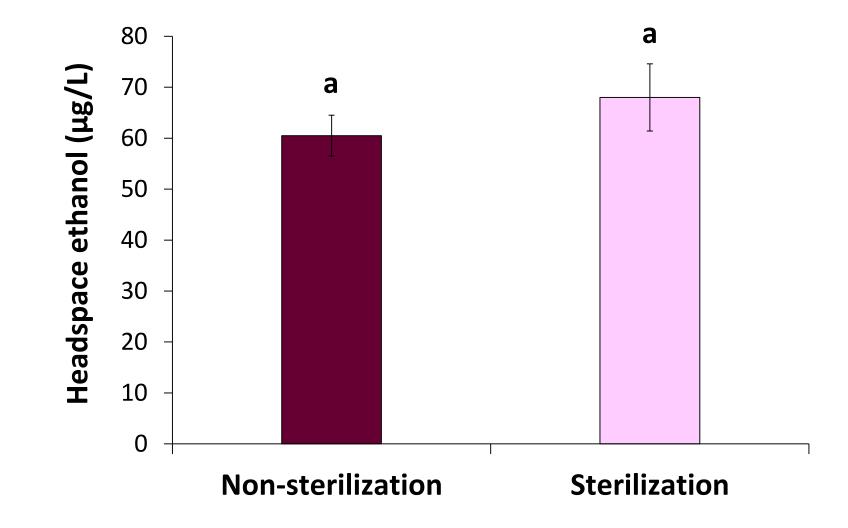


Fig. 8 Effect of seed surface sterilization on ethanol production. Maize seeds cv. B were surface sterilized in 1.0% sodium hypochlorite for 10 minutes, then subsequently washed with sterile water for 10 minutes. Non-sterilized seed and sterilized seed were and , respectively. Headspace ethanol was measured above 1,200mg seed samples at 20% moisture in 100 mL vials after 6h incubation. Error bars denote the S.E. (n = 4).

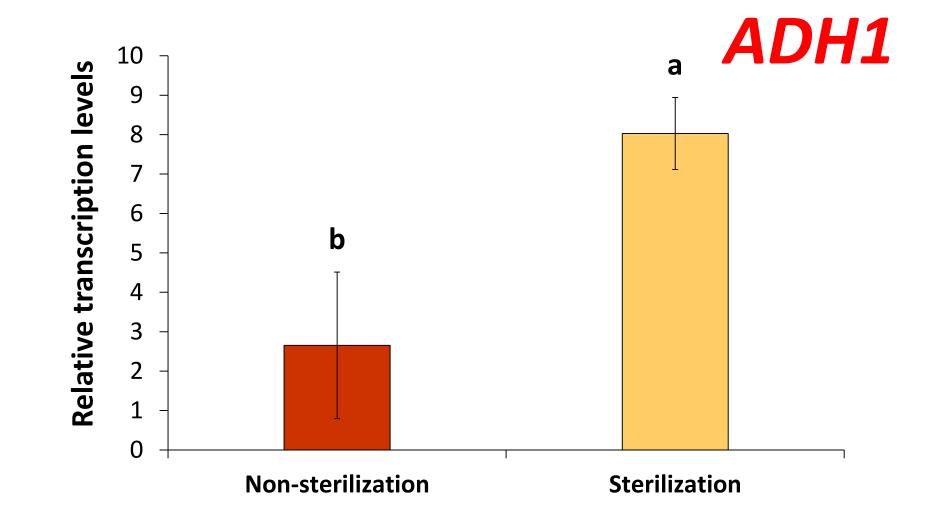
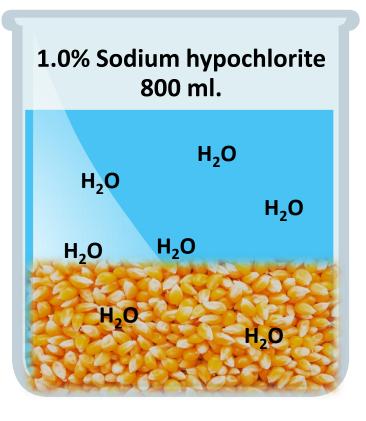


Fig. 9 Effect of seed surface sterilization on relative transcription levels gene expression of *alcohol dehydrogenase* (*ADH1*)-*Maize*. Maize seeds cv. B were surface sterilized in 1.0% sodium hypochlorite for 10 minutes, then subsequently washed with sterile water for 10 minutes. Non-sterilized seed and sterilized seed were and , respectively. Error bars denote the S.E. (n = 4). An independent-samples t-test was conducted to compare ambient condition and control condition.



The relative transcription levels of ADH1 of maize seed sterilized has more than seed non-sterilized. Kibinza (2006) seed moisture content is key factor of aging is discussed with regards to energy metabolism and may be including the transcription of cell.

Conclusion

Artificial aging of maize seed shown low vigor and germination including the transcription level of gene involving in mitochondria degradation especially the increase of transcription of *ADH1* gene according with ethanol that investigated by fast ethanol assay.



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"Thank you for your attention"

