**Tables:**

Table 1: Baseline characteristics of the 120 patients with SCA

(2 out of the 122 patients had no clinical data available)

|  |  |  |
| --- | --- | --- |
| **Patients with ACS** | **Carrier (8)** | **Non-carrier (112)** |
| **Age (yo)**MeanMedian | 44.7+/-742 | 43.5+/-744 |
| **Gender ratio** (men/women) | 7/ 1  | 91 /21  |
| **Risk factor**TobaccoDiabetesInsulin-resistanceHyperglycemiaGlycaemia (mmol.L)Hb glycated HypertriglyceridemiaTriglyceridemiaCholesterol (mmol.L)LDL (mmol.L)HDL (mmol.L)DyslipidemiaHypertensionObesity/overweightBMICRI | 100% (8/8)13% (1/8)0%63% (5/8)7.86.78%14% (1/7)1.27g/L (7/8)4.25 (7/8)2.86 (6/8)0.81 (6/8)38% (3/8)25% (2/8)75% (6/8)27.7 0% | 80% (89/112)21% (23/109)4% (5/112)49% (55/112)7.646.23% (92/112)36% (41/112)1.79g/L (104/112)3.78 (104/112)2.23 (98/112)0.82 (98/112)34% (38/112)26% (29/112)67% (74/110)27.74% (4/98) |
| **Acute complication post ACS** | 0% | 12% (13/110) |
| **Recurrence** | 25% (2/8) | 31% (35/112) |
| **Familial history** | 50% (4/8) | 37% (41/112) |

Table 2: Bioinformatics software prediction and allelic frequencies in GnomAD: <http://gnomad.broadinstitute.org/> for the 4 mutations identified in *PLIN1*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Nucleotide change in the *PLIN1* gene (rs) | Amino acid change | UMD predictor (score) | Polyphen 2.0 (score) | Sift (score) | Mutation taster (score) | Allelic frequencies in GnomAD |
| c.245C>Trs150004289 | p.Thr82Ile | Probable Polymorphism (59) | Probably Damaging (0.999) | Damaging (0.008) | Disease causing (0.632) | 266/200168 |
| c.269T>Crs139271800 | p.Leu90Pro | Pathogenic (93) | Probably Damaging (1) | Damaging (0.003) | Disease causing (1) | 62/203464 |
| c.820C>Trs8179070 | p.Arg274Trp | Probable Pathogenic (69) | Probably Damaging (1) | Damaging (0.013) | Polymorphism | 84/195866 |
| c.839G>Ars146721183 | p.Arg280Gln | Probably Pathogenic (72) | Probably Damaging (0.988) | Tolerated (0.302) | Polymorphism | 11/205046 |

Table 3: Risks associated with the presence of the mutations (control: GnomAD and cohort: 122 patients with Precocious ACS)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  **Allele’s frequencies (%)** |  |  |  |  |
| **Mutation** |           Control |      Cohort |                OR |      95%CI |   |  p |
| **c.245C>T** | 0.001 | 0.020 | 15.722 | 6.432 | 38.430 | 10-4 |
| **c.269T>C** | 0.0003 | 0.004 | 13.501 | 1.865 | 97.754 | 0.073 |
| **c.820C>T** | 0.0004 | 0.004 | 9.592 | 1.330 | 69.164 | 0.100 |
| **c.839G>A** |           0.00006 | 0.004 | 76.706  | 9.865 | 596.427 | 0.014 |