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Crystal structure optimization and micro-structural properties of 3-cyano-4-methylquinoline-2(1H)selenone ($C_{11}H_8N_2Se$)

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ABSTRACT

Crystal structure optimization studies were performed on one of of selenium containing heterocycles namely 3-cyano-4-methyl-quinoline-2(1H)selenone ($C_{11}H_8N_2Se$) which consider good model to investigate role of selenium-ion and its effects on the structural and micro-structural features of selected selenone. Visualization of molecular structure of selenium containing moiety was accurately investigated. The theoretical investigations were concerned by bond distances, torsions on angles of investigated compound to clarify role of H-bonding on the structure formed. Beside comparison with other crystal data to optimize crystal structures of substituted selenones which found monoclinic crystal form with *P* 21/*c* space group.

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KEYWORDS

Synthesis;
Selenium;
H-bond;
XRD;
SEM;
Visualization;
Crystal structure.

INTRODUCTION

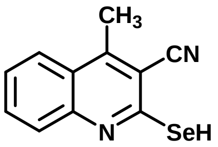
It is well known that the quinoline ring system is an important structural unit widely existing in alkaloids, therapeutics and synthetic analogues with interesting biological activities[1-3]. A large variety of quinoline derivatives have been used as antimalarial, anti-inflammatory, antiasthmatic, antibacterial, antihypertensive and platelet derived growth factor receptor tyrosine kinase (PDGF-RTK) inhibiting agents[4,5].

Recent studies reveal that the intra-molecularly stabilized organo-selenium and sulfur compounds play an important role in the catalytic antioxidant activity[6,7]. Since, Se resembles sulfur (S) in many of its properties, it is isosteric[8,9]. The biological and pharmaceutical activities of different selenium compounds are of special interest because they are active sites of a large number of ◄selenium►dependent enzymes, such as glutathione peroxidase (GSHPx)[10,11] and help in prevention of cancer[12]. In the same field of research, results of many studies[13,14] have related Se deficient bioavailability and intake to human cancer mortality. New synthetic ◄selenium►compounds may provide a way to minimize toxicity associated with higher ◄selenium►intake. Recently, several forms of organoselenium have been studied for their cancer preventive activities. The dietary p-methoxybenzeneselenol, a synthetic organoselenium compound, was found to inhibit azoxymethane-induced hepatocarcinogenesis in rats without clinical signs of toxicity[15].

Recently Jasinskia et al.[16] were investigated synthesis, crystal structures and theoretical studies of four Schiff bases derived from 4-hydrazinyl-8-(trifluoromethyl) quinoline trying to optimize the structure of these compounds. Many research were devoted to understand crystal structure, effect of substituent's on the different crystallographic data obtained from single crystal data and their biological and catalytic activity of substituted pyridine[17-24].

The major goal of the present investigation is to optimize crystal structure of substituted quinoline and comparing the theoretical crystallographic data of selected selenium containing simplest hetero-cycle such as 3-Cyano-4-Methyl-quinoline-2(1H) selenone ($C_{11}H_8N_2Se$) with experimental data. Beside confirming the validity of using XRD- powder diffraction as quantitative tool for estimating different phases for small nucleus of organic compound. Furthermore accurate investigations of micro-structural parameters that responsible for their biological activity.

EXPERIMENTAL



3-cyano-4-methylquinoline-2(1H)selenone ($C_{11}H_8N_2Se$)

The compound of selenium containing hetero-cycles namely, 3-cyano-4-methylquinoline-2(1H) selenone ($C_{11}H_8N_2Se$) was carefully synthesized and structurally established by one of the authors themselves see ref.[25] according to the following briefs.

A mixture of the corresponding chloro-quinoline derivative 1 (2.02 g, 10 mmol), selenium metal (1.0 g, 12 mmol) and sodium borohydride (1.2 g, 32 mmol) was refluxed in ethanol (50 mL) for 5 h. The mixture was cooled and poured in cold HCl. The solid precipitate was filtered, dried, and recrystallized from ethanol.

MS m/z (% ref. int.): 248 (18) [M^+], other important fragments 207; (5), 167 (25), 140 (100), 113 (20). M.P. 298-300^{0}C, Mwt (247.15); IR: 2200 (CN). 1HNMR: DMSO-d_6 : 14.95 (s, 1H SeH, exchangeable); 7.40 - 8.10; (m, 4H Ar-H); 2.70 (s, 3H, CH_3)

The details of spectroscopic and structural data was reported in refe.[25].

X-ray diffraction (XRD)

The X-ray diffraction measurements (XRD) were carried out at room temperature on the fine ground 3-Cyano-4-methylquinoline-2(1H)selenone ($C_{11}H_8N_2Se$) in the range (2θ =10-70^o) using Cu-Kα radiation source and a computerized [Steo-Germany] X-ray diffractometer with two theta scan technique. A visualized studies of crystal structure were made by using Diamond Molecular Structure version 3.2 package, Germany and Mercury 2.3-BUILD RC4-UK. A visualization study made is concerned by matching and comparison of experimental and theoretical data of atomic positions, bond distances, oxidation states and bond torsion on the crystal structure formed. Some of these data can be obtained free of charge from The Cambridge Crystallographic Data Centre via www.ccdc.cam.ac.uk/data_request/cif, or by emailing data_request @ccdc.cam.ac.uk, or by contacting ICSD-Fiz-Karlsruhe-Germany.

Scanning electron-microscope (SEM)

Scanning electron microscope (SEM) measurements were carried out using small pieces of prepared samples on different sectors to estimate the actual molar ratios by using "TXA-840, JEOL-Japan" attached to XL30 apparatus with EDX unit, accelerant voltage 30kv, magnification 10x up to 500.000x and resolution 3 nm. The samples were coated with gold.

RESULTS AND DISCUSSIONS

Structural measurements

Structural identification

The X-ray diffraction of pure 3-cyano-4-methylquinoline-2(1H)selenone ($C_{11}H_8N_2Se$) Which recrystallized from ethanol was performed and supported by single crystal data supplied from ICSD-data bank Karlsruhe Germany see TABLE 1.

Analysis of the corresponding 2θ values and the interplanar spacing d (A^o) by using computerized program proved that the compound is mainly belongs to monoclinic crystal structure with *P21/c* space group as confirmed in crystallographic data in TABLE 1.

Figure 1_a Shows the experimental XRD-profile recorded for highly pure solid product of 3-cyano-4-methylquinoline-2(1H) selenone ($C_{11}H_8N_2Se$) the most intense reflection peaks of monoclinic phase was marked with red squares as clear in Figure 1_a. The indexed peaks are representing the major monoclinic phase in case of powder diffraction while the non-indexed reflections refer to impurity phases. To confirm the validity of using XRD- powder diffraction as quantitative tool for estimating different phases for small nucleus of organic compound (Quinoline nucleus) a visualized XRD- for single crystal of 3-cyano-4-methylquinoline-2(1H)selenone ($C_{11}H_8N_2Se$) was constructed depending up on lattice coordinates of pure single crystal as clear in Figure 1_b.

TABLE 1 : R.T. crystal data of 3-cyano-4-methyl-quinoline-2(1H)selenone ($C_{11}H_8N_2Se$).

Formula	($C_{11}H_8N_2Se$)
Formula weight	408.22
ICSD-Code-767,163	
Crystal size (mm)	0.51 × 0.35 × 0.31
Crystal system	Monoclinic
Space group	*P 21/c*
Formula weight	(247.15)
a (Å)	8.4995(3)
b (Å)	14.0844(5)
c (Å)	14.1922(6)
α (°)	90
β (°)	98.076(4)
γ (°)	90
Volume (Å3)	1662.51(11)
Z	4
Dcalc (Mg m?3)	1.731
F (0 0 0)	816
Reflections, total	10,971
Reflections, Ind [R(int)]	4909(0.0287)
θmax (°) with Cu Kα	32.33
R, Rw [I > 2σ(I)]	0.0441, 0.0819
Goodness of fit on F2	0.890
(Δρ)max/min (e Å?3)	0.347/?0.387
Measurement	GEMINI (Oxford Diffraction, 2007)
Refinement	Full-matrix least-squares on F2 (SHELXL97)

The comparison between the fundamental fingerprints of experimental lines (those with red squares) for 3-cyano-4-methylquinoline-2(1H) selenone in Figure 1_a with those in Figure 1_b one can observe that the most intense reflection peaks (lines with [002], [011], [102], [014], [113] and [025]) are located nearly in the same position at two theta ~ 4.2, 12.4, 15, 18, 21, 24 and 32 respectively. The differences between the two positions less than half theta due to different kinds of hydrogen bonding environment inside the unit cell of packing 3-cyano-4-methylquinoline-2(1H)selenone ($C_{11}H_8N_2Se$). These results are in full agreement with those reported by[26,27] who were confirming that there are strong correlation between the intermolecular H-bonding and solid crystal structure of the investigated compound.

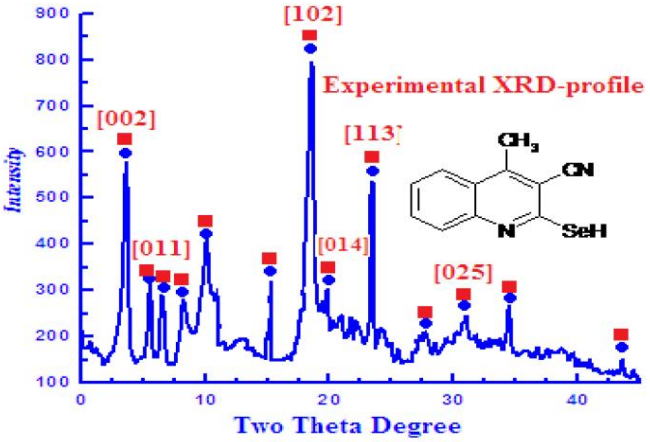
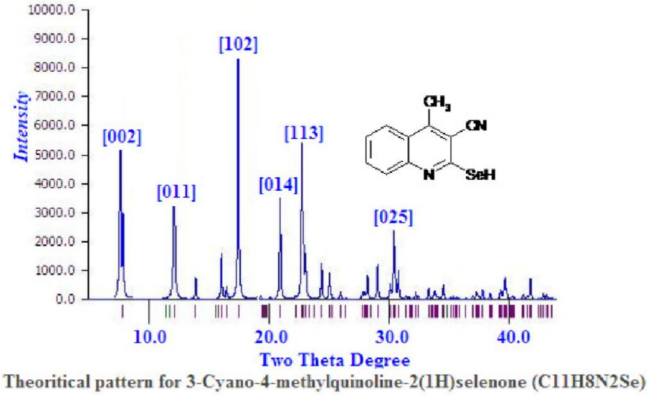


Figure 1_a : R.T. experimental XRD-profile recorded for 3-cyano-4-methylquinoline-2(1H) selenone, where red squares = monoclinic pure phase with P21/c space group.



Theoritical pattern for 3-Cyano-4-methylquinoline-2(1H)selenone (C11H8N2Se)

Figure 1_b : Theoretical pattern XRD-profile recorded for 3-cyano-4-methylquinoline-2(1H) selenone.

For accurate identification of peak position in the case of experimental XRD-profiles Figures 1c was constructed as high resolution zoom in diffractogram in the range of two theta =1-6 Θ.

It was concluded that characteristic experimental line with reflection peak (lines with [002]) was lying accurately at two theta degree (2theta = 4.7) which is identical to the same line in the visualized XRD-profile see Figure 1_b. Furthermore the most intense reflection line I_o indexed by [102] in experimental XRD lies at two theta = 17.7 which is identical value to that recorded in visualized XRD as clear in Figure 1_b.

Figure 1_d displays the different types of intermolecular hydrogen bonding that could be found together in the 3D-unitcell of 3-cyano-4-methylquinoline-2(1H) selenone causing the formation of H-bonded monoclinic crystal structure.

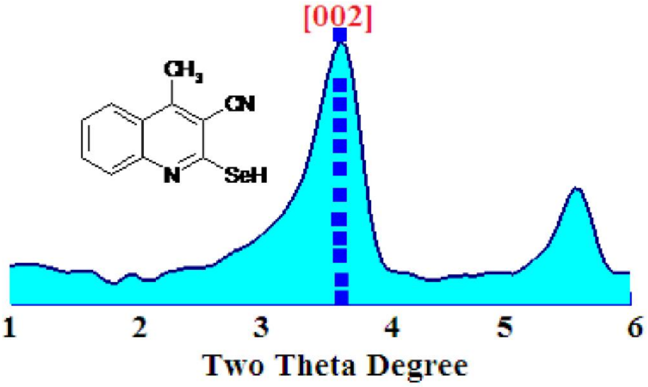


Figure 1_c : High-resolution XRD-profile recorded for 3-cyano-4-methylquinoline-2(1H) selenone.

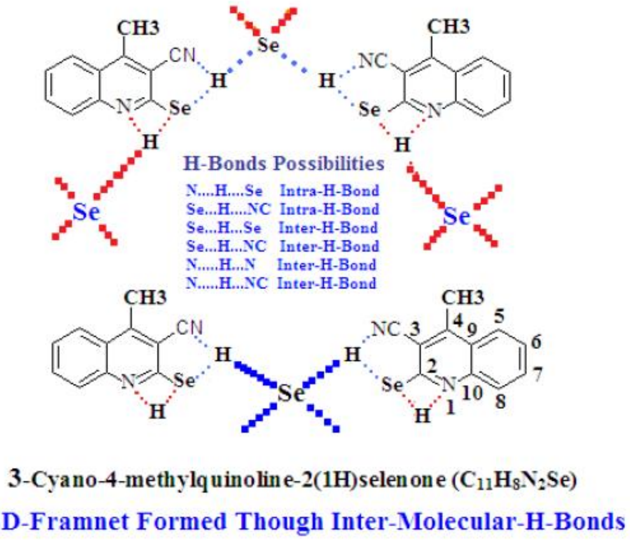


Figure 1_d : Possibilities of H-bond inside crystal lattice of 3-cyano-4-methylquinoline-2(1H) selenone.

From Figure 1_d one can indicate that there are five types of H-bonding two are intra-H-bond in the same molecule of 3-cyano-4-methylquinoline-2(1H) selenone which are Se…H….CN and Se….H….N while the others three inter-H-bond are Se…H…..N and Se….H….Se and Se….H…NC. These five types of hydrogen bonding are responsible for forming 3D-framnet of 3-Cyano-4-methylquinoline-2(1H) selenone as solid crystal.

Venkatachalam et al.[28] repoted that the are strong correlation between structural variation imparts molecular anisotropy (H-bonding) in solid state by preferentially forming intermolecular and intramolecular hydrogen bonds. In particular examination of crystal structure of a group of structurally similar compounds revealed the importance of the individual groups in their structure and how they influence the molecular lattice framework.

Structural visualization of 3-cyano-4-methylquinoline-2(1H) selenone

To confirm the crystallographic data obtainable from experimental XRD and single crystal data reported in TABLE 1 a visualized unit cell with minimum 90 atoms was constructed by using both of DIAMOND -IMPACT CRYSTAL-Germany /and MERCURY 2.3Build RC4-UK visualizer - see Figure 2_a,2_b, TABLES 2, 3, 4, 5 and 6.

The study concerned by matching and comparison of lattice constants, torsion of bonding, bond lengths, lattice volume, atomic coordinates and symmetry operation.

Figure 2a,b show the geometry of four molecules of 3-cyano-4-methylquinoline-2(1H) selenone and display-

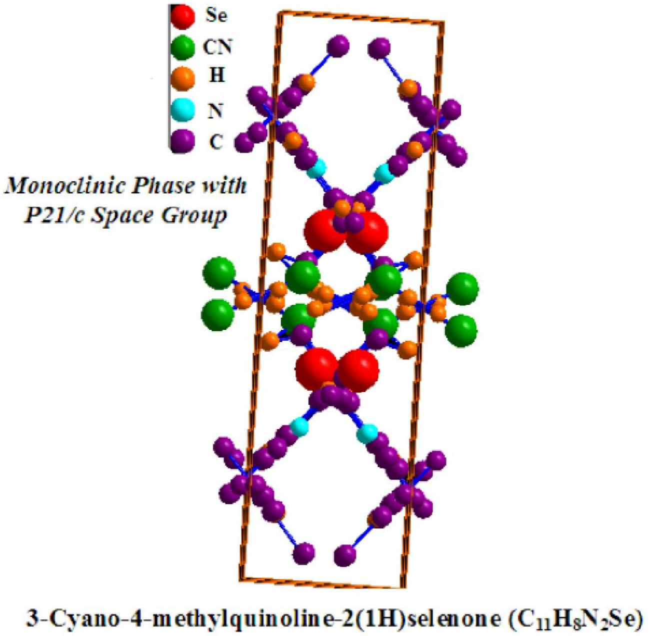
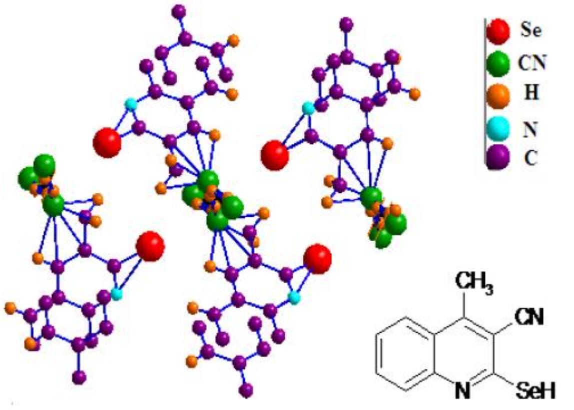


Figure 2_b : Unit cell of 3-cyano-4-methylquinoline-2(1H) selenone with *P21/c* space group.



3-Cyano-4-methylquinoline-2(1H)selenone ($C_{11}H_8N_2Se$)

Figure 2_a : Geometry of four molecules of 3-cyano-4-methylquinoline-2(1H) selenone showing different environment surrounded selenium ion.

ing different environment surrounding selenium atom and unit cell of 3-cyano-4-methylquinoline-2(1H) selenone respectively. Quinoline nucleus has three substituent R_1= Se…H, R_2= CN^-, R_3 = CH_3. The molecules are strongly hydrogen-bonded two/three-dimensional sheets. The mean separation between the sheets of molecules is ~ 3.521 (7) A °, corresponding to~ quarter of the c axis. There are no stacking interactions in this structure. The molecules form a mesh and the symmetry-related molecules in the adjacent planes lie above or below the gaps in the mesh. There are no strong interactions visible between the molecular layers inside unit cell.

It was observed that selenium has important role as nucleation center such that selenium can form five types of H-bonding as clear in Figure 1_d two are intra-H-bonds in the same molecule of 3-cyano-4-methylquinoline-2(1H) selenone which are Se…H….CN and Se….H….N while the other three inter-H-bond are Se…H…..N1, Se….H….Se and Se…..H….NC.

The observed changes in the Se….H distances in the fully protonated structures are small and may be due to some uncorrected experimental error. The shape of the hydrogen-bond potential-energy well must change due to slight changes in the local environment as suggested by Wilson[29].

From TABLE 2 it was observed that there are more than one type of hydrogen bonding as clear in TABLE 2 namely N_2…H_1 =0.864(3) Å, Se_1….H_{2D} =0.819(4) Å, Se_1….H_1 =0.822(1)Å, N_{1D}…H_2 = 0. 818(3) Å and Se….H_1 = 0.825(4) Å.

TABLE 2 : Some selected bond distances and angles inside unit cell of 3-cyano-4-methylquinoline-2(1H) selenone.

$Atom_1$	$Atom_2$	Symm. Op2	d_{1-2}Å	atom3	Symm. Op3	d_{1-3} Å	Angle ^213
Se1	C2	x, y, z	1.7564	H6	1-x, y, 0.5-z	2.2717	125.123
N1|C1	H2	x, y, z	0.8198	H1	x, y, z	0.8202	109.494
	H2	x, y, z	0.8198	H2	1-x, 1-y, 1-z	1.9132	12.165
	H1	x, y, z	0.8202	H1	1-x, 2-y, 1-z	1.9109	13.418
	C11	x, y, z	1.4185	H1	1-x, 2-y, 1-z	1.9109	119.384
	H1	1-x, 2-y, 1-z	1.9109	H2	1-x, 1-y, 1-z	1.9132	118.785
	H6	x, y, z	1.9666	H7	x, y, z	1.9668	47.016
	H7	x, y, z	1.9668	C3	x, y, z	2.4083	54.437
	C3	x, y, z	2.4083	H3	x, y, z	2.4352	48.549

For non-hydrogen bonding as Se_1-C_2, Se_1-C_{11} and Se_1-C_3 bond distances were found to be d_{1-2} 1.754(5), 1.413(5) and 2.408(6) Å respectively while some of hydrogen-bonded distances are found to be 0.823(4), 0.814, 1.966(6) and 1. 966(6) Å respectively correspond to Se_1-H_1, Se_1-H_2, Se_1-H_7 and Se_1-H_7 bond distances.

These observations confirm that selenium anion make as nucleation center through different possibilities of H-bond formation that enhance 3D-nucleation process of 3-cyano-4-methylquinoline-2(1H) selenone.

The five possibilities of H-bonding as clear in Figure 1_d two are intra-H-bond in the same molecule of 3-cyano-4-methylquinoline-2(1H) selenone which are Se…H….CN and Se….H….N while the others three inter-H-bond are Se…H…..N, Se….H….Se and N1….H…N2C.

These types are slightly short in contrast with normal H-bond compared with similar hydrogen bonds reported in[29] since O—H and H….O distances show no abnormalities compared with O—H….O hydrogen bonds of similar length Steiner and Saenger[30] reported that there is no evidence of disorder in the anisotropic displacement parameters of the protons. These distances reported in TABLE 2, 3, 4, 5, 6 lie in the region where the proton position has been found to be near the centre of the hydrogen bond.

The analysis of structural properties of monoclinic phase shows the values of selected bonds torsion in the packing unit cell of 3-cyano-4-methylquinoline-2(1H) selenone Figure 2_b the torsion on the most cases are equilibrated that reflect the high stability inside unit cell. These equilibrated bonds such as C_1-N_1-Se_1-H_1 with positive 48.56(3) and C_1..N_1..Se_1..H_{1B} with negatively value -45.56(3) consider good model that reflects stability of lattice.

TABLE 3

Atom$_1$	Atom$_2$	Symm. Op2	d_{1-2}Å	atom3	Symm .Op3	d_{1-3}Å	Angle ^213
H2	N1|C1	x, y, z	0.8198	H2	1-x, 1-y, 1-z	1.1252	159.004
	N1|C1	x, y, z	0.8198	H1	x, y, z	1.3392	35.263
	N1|C1	x, y, z	0.8198	C11	x, y, z	1.8599	45.976
	N1|C1	x, y, z	0.8198	N1|C1	1-x, 1-y, 1-z	1.9132	167.835
	N1|C1	x, y, z	0.8198	H1	1-x, 2-y, 1-z	2.3374	49.596
	H2	1-x, 1-y, 1-z	1.125	H1	x, y, z	1.3392	158.402
	H2	1-x, 1-y, 1-z	1.1252	C11	x, y, z	1.8599	132.494

TABLE 4

Atom$_1$	Atom$_2$	Symm. Op2	d_{1-2} Å	atom3	Symm. Op3	d_{1-3} Å	Angle ^213
C5	C4	x, y, z	1.4053	C6	x, y, z	1.4122	123.442
	C4	x, y, z	1.4053	C10	x, y, z	1.4177	118.071
	C4	x, y, z	1.4053	C7	x, y, z	2.3946	152.777
	C6	x, y, z	1.4122	C10	x, y, z	1.4177	118.486
	C6	x, y, z	1.4122	H3	x, y, z	2.0295	99.901
	C10	x, y, z	1.4177	H3	x, y, z	2.0295	141.611
	C10	x, y, z	1.4177	C3	x, y, z	2.4159	89.263

TABLE 5

Atom$_1$	Atom$_2$	Symm. Op2	d_{1-2}Å	Atom3	Sym. Op3	d_{1-3} Å	Angle ^213
C6	H4	x, y, z	0.9302	C7	x, y, z	1.3537	119.987
	C7	x, y, z	1.3537	C5	x, y, z	1.4122	119.923
	C5	x, y, z	1.4122	C8	x, y, z	2.4259	90.480
	H5	x, y, z	1.9778	C10	x, y, z	2.4319	113.433
	C8	x, y, z	2.4259	C4	x, y, z	2.4813	118.681
	C10	x, y, z	2.4319	C4	x, y, z	2.4813	59.026

TABLE 4-6 explain some selected bonds angles in the packing unit cell of 3-cyano-4-methylquinoline-2(1H) selenone. One can indicate that no violation in most of bond distances such as H_2….N_1…H_2 d_{1-2} = 0.8198 Å and d_{1-3}=1.125(2) Å or angles as clear in TABLE 4, 5, 6. The angles with selenium center as ($H_1Se_1N_1$^) = 89.5(1)° are good example for representing stability of this 3-cyano-4-methylquinoline-2(1H) selenone that enhanced by H-bonds as proved in structure analysis in the present investigations.

TABLE 6

Atom$_1$	Atom$_2$	Symm. Op2	d_{1-2}Å	atom3	Symm. Op3	d_{1-3} Å	Angle ^213
C10	N2	x, y, z	1.3752	C5	x, y, z	1.4177	120.802
	C5	x, y, z	1.4177	C9	x, y, z	1.4231	120.762
	C9	x, y, z	1.4231	C2	x, y, z	2.2789	148.570
	C2	x, y, z	2.2789	C6	x, y, z	2.4319	121.354
	C8	x, y, z	2.4163	C4	x, y, z	2.4207	121.548
	C4	x, y, z	2.4207	C6	x, y, z	2.4319	61.505
C11	H6	x, y, z	0.9696	H7	x, y, z	0.9701	107.961
	H7	x, y, z	0.9701	N1|C1	x, y, z	1.4185	109.418
	C3	x, y, z	1.5001	H2	x, y, z	1.8599	105.514
	H2	x, y, z	1.8599	H1	x, y, z	1.8600	42.201
H6	C11	x, y, z	0.9696	H7	x, y, z	1.5689	36.030
	H7	x, y, z	1.5689	N1|C1	x, y, z	1.9666	66.501
	N1|C1	x, y, z	1.9666	C3	x, y, z	2.0386	73.902
	H2	x, y, z	2.0996	H1	x, y, z	2.2903	35.185
	Se1	1-x, y, 0.5-z	2.2717	H1	x, y, z	2.2903	97.341
H7	C11	x, y, z	0.9701	H6	x, y, z	1.5689	36.009

SE-microscopy measurements

Figure (3a-c) show the SEM-micrographs for pure 3-cyano-4-methylquinoline-2(1H) selenone applied on the ground powders that prepared in ethanolic solution.

The average grain size was calculated and found in between 0.91 and 3.71μm.

The EDX examinations was performed on random spots in the same sample confirmed and are consistent with our XRD analysis for monoclinic phase with $P2_1/c$ space group, such that the differences in the molar ratios EDX are fitted with molecular formula of 3-cyano-4-methylquinoline-2(1H) selenone. From Figure (3a-c) it is so difficult to observe inhomogeneitiy within the micrograph due to that the powders used are very fine and the particle size estimated is too small.

The grain size for 3-cyano-4-methylquinoline-2(1H) selenone monoclinic -phase was calculated according to:

Scherrer's formula[31],

$B = 0.87\lambda/D\cos\theta$(1)

where D is the crystalline grain size in nm, θ, half of the diffraction angle in degree, λ is the wavelength of X-ray source (Cu-K∝) in nm, and B, degree of widening of diffraction peak which is equal to the difference of full width at half maximum (FWHM) of the peak at the same diffraction angle between the measured sample and standard one. From SEM-maping, the estimated average grain size was found to be (1.13 and 2.91μm) which is relatively large in comparison with that calculated applying Scherrer's formula for pure 3-cyano-4-methylquinoline-2(1H) selenone monoclinic -phase (D ~ 0.73 μm). This indicates that, the actual grain size in the material bulk is smaller than that detected on the surface morphology. Similar behavior was reported by[32-34].

These results estimated from Scherrer's calculations are consistent with those deduced from structure visualization of 3-cyano-4-methylquinoline-2(1H) selenone in the current study in which selenium ion make as nucleation center through different possibilities of H-bond formation that enhance and reinforce 3D-nucleation process of 3-cyano-4-methylquinoline-2(1H) selenone and consequently lead to corresponding decrease in the grain size estimated of 3-cyano-4-methylquinoline-2(1H) selenone

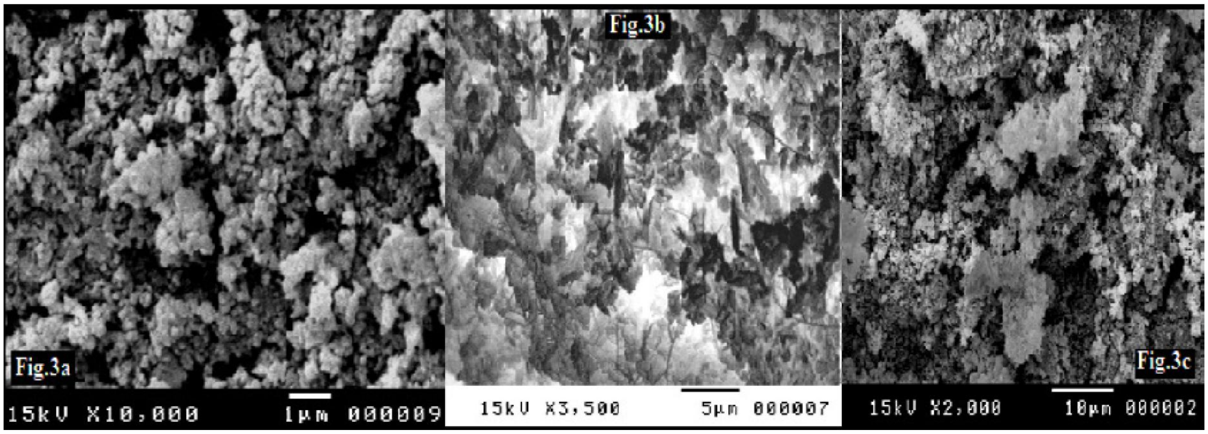


Figure 3$_{a-c}$: Scaning electron micrographs captured for pure 3-cyano-4-methylquinoline-2(1H) selenone with three different magnification factors (a) 1 μm (b) 5 μm and (c) 10 μm.

CONCLUSIONS

The conclusive remarks inside this article can be summarized in the following points;

1- Compound 3-cyano-4-methylquinoline-2(1H) selenone is mainly belongs to monoclinic crystal structure with *P21/c* space group as confirmed in crystallographic data and visualized study.

2- XRD- powder diffraction could used as quantitative tool for estimating different phases for small nucleus of organic compounds as quinoline nucleus.

3- There are five types of H-bonding two are intra-H-bond in the same molecule of 3-cyano-4-methylquinoline-2(1H) selenone which are Se…H….CN and Se….H….N while the others two inter-H-bond are Se…H…..N and Se….H….Se, these five types of hydrogen bonding are responsible for forming 3D-framnet of 3-cyano-4-methylquinoline-2(1H) selenone as solid array material.

4- The visualized investigations exhibited good fitting with experimental data.

5- The average grain size was calculated and found in between 0.91 and 3.71μm which is relatively high in contrast with that calculated throughly applying Scherrer's formula for pure 3-cyano-4-methylquinoline-2(1H) selenone monoclinic -phase (D ~ 0.73 μm).

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